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Please provide a detailed statement of th Include the elected species or structures, utility of the invention. Define any term known. Please attach a copy of the cover	keywords, synonyms, s that may have a spec	acronyms, and registry numial meaning. Give examples	bers, and combine	with the concept	or f
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## Fig. 13.

AlaGlnGluProValLysGlyProValSerThr

ELI1

AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACT

GCTCGAGCCATGGTATGGACGTATACGAGTTCTTGGTCAATTCCAGGACACAGATGA

LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsnArg

63 ELI3

AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT

TTCGGTCCAAGAACAGGATAATAGAACTAAGCAACGCGATACAATTTGGGTGGATTGGCA
ELI2

CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet

ELI5

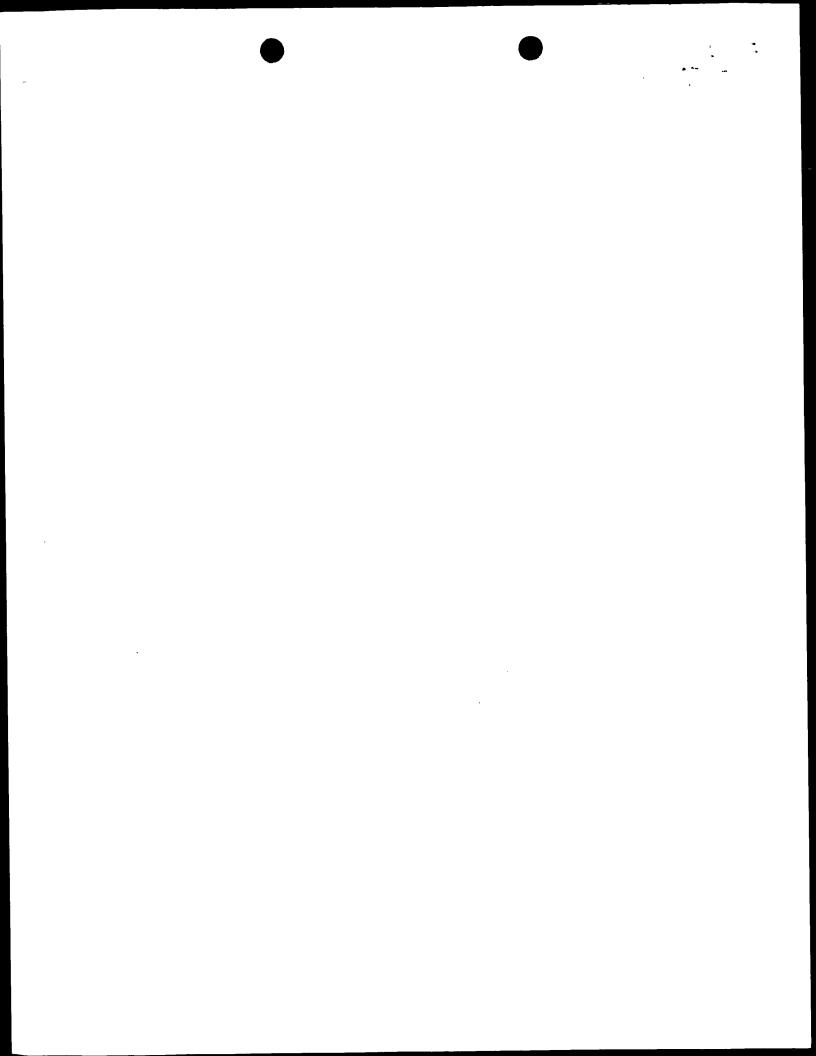
TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG

ACAAACTTCCTGTGACTAACAGGTCCATAGTTTTTCACGACACTTCCAAGGACGCCATAC

ELI4

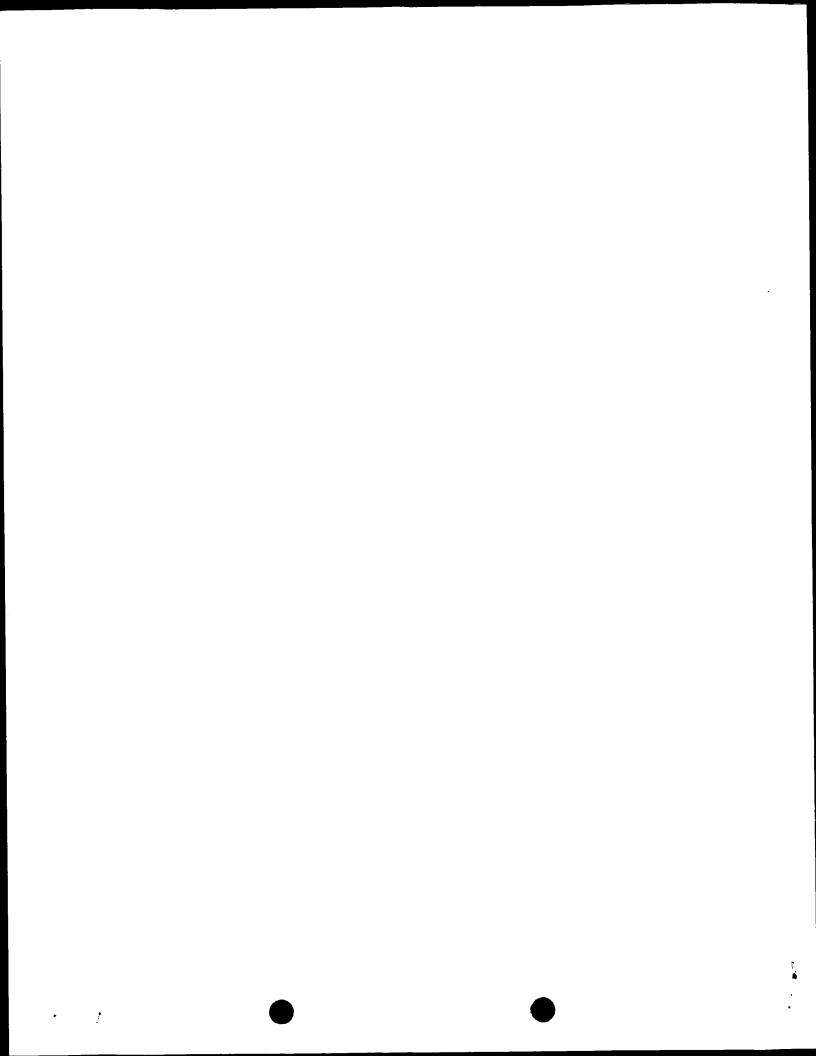
AlaCysPheValProGlnEndEnd
183 GCTTGTTTCGTTCCACAATAATAG

CGAACAAAGCAAGGTGTTATTATCCTAG 210 ELI6 ←



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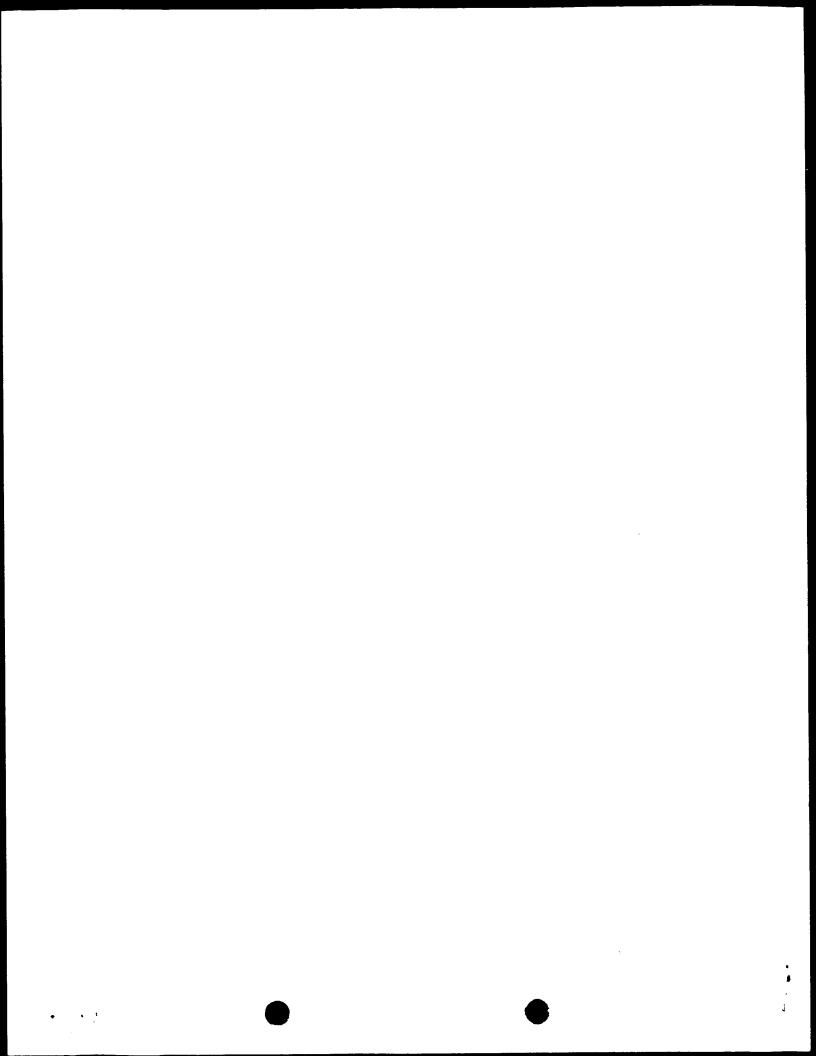


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TTCTTGTCCTATTATCTTGATTCGTTGGGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGAT
TGTCCAGGTATCAAAAAGTGCTGTGAGGTTCCTGCGGTATGTTTCGTTCCACAATAATAG1

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acaggataatagaactaagcaacgcgatacaatttgggtggattggcaacaacttcctgtggctacaag
gtccatagtttttcacgacacttccaaggacgccataccgaacaaagcaaggtgttattatcctag1

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"Primary structure of the human elafin precursor preproelafin deduced from the nucleotide sequence of its gene and the presence of unique repetitive sequences in the prosegment.";
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Characterization and gene sequence of the precursor of elafin, an
elastase-specific inhibitor in bronchial secretions.";
Am. J. Respir. Cell Mol. Biol. 8:439-445(1993).
                                           01-FEB-1991 (Rel. 17, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
11-DUN-2002 (Rel. 41, Last annotation update)
Elafin precursor (Elastase-specific inhibitor) (ESI) (Skin-derived antileukoproteinase) (SKALP).
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Saheki T., Ito F., Hagiwara H., Saito Y., Kuroki J., Tachibana S.,
Hirose S.;
                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93280175; PubMed=7685029; Molhuizen H.O.F., Alkemade H.A.C., Zeeuwen P.L.J.M., de Jongh G.J., Mieringa B., Schalkwijk J.; "SKAF/elafin: an elastese inhibitor from cultured human "SKALF/elafin: an elastese inhibitor from cultured human keratinocytes. Purification, cDNA sequence, and evidence for transglutaminase cross-linking."; J. Biol. Chem. 268:12028-12032(1993).
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Prancart C., Dauchez M., Alix A.J.P., Lippens G.;

Francart C., Dauchez M., Alix A.J.P., Lippens G.;

Francart C., Dauchez M., Alix A.J.P., Lippens G.;

J. Mol. Biol. 268:666-677[937].

-!- FUNCTION: NEUTROPHIL AND PANCREATIC ELASTASE-SPECIFIC INHIBITOR OF SKIN. IT MAY PREVENT ELASTASE-MEDIATED TISSUE PROTEOLYSIS.

-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: CONSISTS OF TWO DOMAINS: THE TRANSCUTAMINASE SUBSTRATE DOMAIN: CONSISTS OF TWO DOMAIN SERVES AS AN ANCHOR TO LOCALIZE ELAFIN COVALENTLY TO SPECIFIC SITES ON EXTRACELLULAR MATRIX
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MEDLINE=9115923; PubMed=2001428;
Schalkwijk J. de Roo C., de Jongh G.J.;
Schalkwijk d. de Roo C. (e Jongh G.J.;
"Skin-derived antileukoproteinase (SKALP), an elastase inhibitor from human keratinocytes. Purification and biochemical properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                    Sallenave J.-M., Marsden M.D., Ryle A.P.;
"Isolation of elafin and elastase-specific inhibitor (ESI) from
bronchial secretions. Evidence of sequence homology and immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsunemi M., Matsuura Y., Sakakibara S., Katsube Y.; "Crystal structure of an elastase-specific inhibitor elafin complexed with porcine pancreatic elastase determined at 1.9-A resolution."; Blochemistry 35:11570-11576 (1996)
            Wiedow O., Schroeder J.-M., Gregory H., Young J.A., Christophers E., "Elatin: an elastase-specific inhibitor of human skin. Purification, characterization, and complete amino acid sequence."; J. Biol. Chem. 265:14791-14795(1990).
                                                                                                                                      Wiedow O., Schroeder J.-M., Gregory H., Young J.A., Christophers E.; J. Biol. Chem. 266:3356-3356(1991).
                                                                                                                                                                                                                                                               Sallenave J.-M., Ryle A.P.;
"Purification and characterization of elastase-specific inhibitor.
Sequence homology with mucus proteinase inhibitor.";
Biol. Chem. Hoppe-Seyler 372:13-21(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1096:148-154(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. Hoppe-Seyler 373:27-33(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96387196; PubMed=8794736;
MEDLINE=90368643; PubMed=2394696;
                                                                                                                                                                                                                                          MEDLINE=91248412; PubMed=2039600;
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92162196; PubMed=1536690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L10343; AAA36483.1; -. AL049767; CAB53524.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z18538; CAA79223.1; -.
EMBL; D13156; BAA02441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D13156; BAA02441.1; -. S58717; AAB26371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR, JH0614, JH0614.
PIR, S13607, S13607.
PIR, A46749, A46749.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 85-100.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 61-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cross-reactivity."
                                                                                                                                                                                                     SEQUENCE OF 70-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR.
                                                                                                                                                                                                                           TISSUE-Sputum;
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Sputum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEINS
                                                                                                                       ERRATUM.
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 271:7012-7018(1996).
-!- FUNCTION: NEUTROPHIL AND PANCREATIC ELASTASE-SPECIFIC INHIBITOR OF
SKIN. IT MAY PREVENT ELASTASE-MEDIATED TISSUE PROTEOLYSIS (BY
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                              ELAFIN.
2 X TANDEM REPEATS OF SVP-1 LIKE MOTIF.
SVP-1 CLOTTING 1.
SVP-1 CLOTTING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                     61 AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 117
                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823,
                                                                                                                                                                                                                                                                                                                                                                      1 AQEPVKGPVSTKPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
                                                                                                                                                                                                                                                                                                                   cn 100.0%; Score 327; DB 1; Length 117; sl Similarity 100.0%; Pred. No. 4.3e-29; 57; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96215132; PubMed=8636131;
Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
Tachibana S., Hirose S.;
                                                                                                   PROSITE; PS00313; SVP_I; 2.
PROSITE; PS00317; 4 DISULFIDE CORE; 1.
Serine procease inhibitor; Signal; Repeat; 3D-structure.
SIGNAL
                                                                                                                                                                                                                                                                     RC -> CP (IN REF. 7).
C -> R (IN REF. 8).
C -> S (IN REF. 8).
; A51D46257E5B03EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARIIII.
TISSUE SPECIFICITY: TRACHEA AND LARGE INTESTINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                          INTERFORM SAP I.
INTERFORM SAP I.
INTERFORM SAP I.
PERMITS, PROGOGOS, WAD I.
PRINTS, PROGOGOS, 4DISULPHCORE.
SMART; SMO0217; WAP; I.
                                                                                                                                                                                                                                                                                                     12270 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D50319; BAA08854.1; -.
HSSP; P19957; 2REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                              1117
72
54
72
1117
1105
1109
                    Genew; HGNC:8947; PI3.
 PDB; 1FLE; 11-JAN-97.
PDB; 2REL; 07-JUL-97.
                                                                                                                                                                                                                                                                91
92
98
117 AA;
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                MIM; 182257;
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ELAF PIG
ID ELAF PIG
AC Q29125;
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DISULFID
DISULFID
DISULFID
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CHAIN
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2 QEPVKGP-----VSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACF 54
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Kuroki J., Hosoya T., Itakura M., Hirose S., Tamechika I.,
Yoshimoto T., Ghoneim M.A., Nara K., Kato A., Suzuki Y., Furukawa M.,
Tachibana S.;
                                                                                                                                                                                                                                                                                                                           TANDEM REPEATS OF SVP-1 LIKE MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, characterization, and tissue distribution of porcine SPAI, a protein with a transglutaminase substrate domain and the WAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sodium/potassium ATPase inhibitor SPAI-2 precursor (WAP-2 protein).
                                                                                                                                        12 X 6 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBL_TaxID=9823,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.7%; Score 221.5; DB 1; Length 167; ilarity 61.9%; Pred. No. 1.7e-17; Conservative 5; Mismatches 12; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=96215132; PubMed=8636131;
Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.,
Tachibana S., Hirose S.;
                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; Z5932EA1A459D9CA CRC64;
                                                                                                                                                                                                                                                                                                                                         SVP-1 CLOTTING 1.
SVP-1 CLOTTING 2.
InterPro; IPR002221; WAD.
Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
SWART; SW00217; WAD; 1.
PROSITE; PR00317; 4 DISULFIDE CORE; 1.
Serine protease inhibitor; Signal; Repeat.
21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 22-58
                                                                                                               POTENTIAL.
                                                                                                                            ELAFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Biol. Chem. 270:22428-22433(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                         17923 MW;
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                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                                                                         167 AA;
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                                                                                                             Sus scrofa (Pig)
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P16225;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SODIUM/POTASSIUM ATPASE INHIBITOR SPAI-2.
                                                                                                                                                                                                                                                                                                                      PTM: THE SHORT FORM (AA 127-187) MAY BE AN ARTIFACT DUE TO THE STRONGLY ACIDIC CONDITIONS OF THE DUODENUM. THE PRO-SPAI FORM MAY BE THE NATIVE FORM.
                                                                                                                                                                                                                                                                AGAINST NA+.
-!- TISSUE SPECIFICITY: SMALL INTESTINE...LARGE INTESTINE. THE PLASMA
                                                                                                                                                                                                                                                                                  CONTAINS THE PRO-SPAI FORM CIRCULATING.
DOMAIN: THE REPETITIVE DOMAIN OF PRO-SPAI SERVES AS A SUBSTRATE
FOR TRANSGLUTAMINASE.
"Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVP-1 CLOTTING 1.
14 X 6 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                          Araki K., Kuwada M., Ito O., Kuroki J., Tachibana S., "Four disulfide bonds' allocation of Na+, K(+)-ArPase inhibitor
                                                                               MEDLINE-90026425; PubMed-2553020;
Araki K., Kuroki J., Ito O., Kuwada M., Tachibana S.;
"Novel peptide inhibitor (SPAI) of Na+, K+-ATPase from porcine
                                                                                                                                                                                                                                 Biochem, Biophys, Res. Commun. 172:42-46(1990).
-!- FUNCTION: INHIBITS NA+, K+ ATPASE BY THE COMPETITIVE MODE
                                                                                                                                     Biochem. Biophys. Res. Commun. 164:496-502(1989).
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00313; SVP_I; 2.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
Signal; Repeat.
                      members.";
J. Biol. Chem. 271:7012-7018(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, D17756; BAA04603.1; --
EMBL, D17754; BAA04603.1; JOINED.
EMBL, D17755; BAA04603.1; JOINED.
EMBL, D83667; BAA12037.1; --
EMBL, D50320; BAA08855.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.
                                                                                                                                                                                WEDLINE=91025070; PubMed=2171523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002098; SVP_I.
InterPro; IPR002221; WAP.
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PIR, B33429, B33429.
PIR, C33429, C33429.
HSSP, P19957; 2REL.
                                                          SEQUENCE OF 127-187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1227
627
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82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                    2 QEPVKGP-----VSTKPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACF 54
                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91155942; PubMed-2293019;
Farmer S. U., Fliss A.E., Simmen R.C.M.;
"Complementary DNA cloning and regulation of expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- INDUCTION: BY ESTROGEN AND PROGESTERONE; IN UTERUS.
-!- PIM: COMPARED TO HUMAN ALP, IT SEEMS TO LACK A CLEAVABLE
                                                                                                                       54.9%; Score 179.5; DB 1; Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DEVELOPMENTAL STAGE: MAXIMAL EXPRESSION AT MID- AND LATE
                                                                                                                                                8; Mismatches 17; Indels
WAP. PYRROLIDONE CARBOXYLIC ACID.
                                                              MISSING (IN SPAI-1).
R -> G (IN SPAI-3).
S -> G (IN SPAI-3).
; 12F5BD0813AF5E27 CRC64;
                                                                                                                                      Pred. No. 6.7e-13;
                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL PEPTIDE.
-!- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0003; 4DISULPHCORE.
ProDom; PD001224; WAP; 1.
                                                                                                      20471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M57446; AAA63446.1; -.
                                                                                                                                      49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A36113; A36113.
HSSP; P19957; ZREL.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 2.
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00217; WAP; 2.
187
122
175
179
174
183
148
                                                                                                                                                                                                                                                                                                                                                               Antileukoproteinase.
                                                                                                                                        Similarity
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GESTATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissue=Uterus;
                                                                                                                                                                                                                                              185 YPK 187
                                                                                                                                                   31;
                                                                                                                                                                                                                        55 VPQ 57
                                                                                                                                                                                                                                                                                  RESULT 4
ALK1_PIG
ID ALK1_PIG
 DOMAIN
MOD RES
DISÜLFID
                                             DISULFID
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MEDLINE=97271386; PubMed=9126337;
Zitnik N.J., Zhang U., Kashem M.A., Kohno T., Lyons D.E., Wright C.D.,
Rosen E., Goldberg I., Hayday A.C.;
"The cloning and characterization of a murine secretory leukocyte
protease inhibitor cDNN.";
                                                                   TRYPSIN INHIBITORY SITE (PROBABLE).
ELASTASE OR CHYMOTRYPSIN INHIBITORY SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jin F.-Y., Nathan C.F., Radzioch D., Ding A.,
"Secretory leukocyte protease inhibitor: a macrophage product induced
by and antagonistic to bacterial lipopolysaccharide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukoprotease inhibitor gene in the mutine lung.",

Am. J. Respir. Crit. Care Med. 156:1235-1240(1997);

-!- PUNCTION: ACID-STABLE PROTEINASE INHIBITOR WITH STRONG AFFINITIES
FOR TRYPSIN, CHYMOTRYPSIN, ELASTASE, AND CATHEPSIN G. MAY PREVENT
ELASTASE-MEDIATED DAMAGE TO ORAL AND POSSIBLY OTHER MUCOSAL
TISSUES (BY SIMILARITY).

-!- TISSUES (BY SIMILARITY)

-!- TISSUE SPECIFICITY: HIGHES EXPRESSION IN LUNG, SPLEEN,
INTESTINE AND EPIDIDYMIS WITH LOWER LEVELS IN LIVER AND SEMINAL
VESICLE. NO EXPRESSION IN BRAIN, HEART, KIDNEY AND MUSCLE.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                          ALK1_MOUSE STANDARD; PRT; 131 AA.
P97430; O09081; O09082;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Antileukoproteinase 1 precursor (ALP) (Secretory leukocyte protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6 X CBA; TISSUE=Lung;
MEDLINE=98011992; PubMed=9351627;
Abe T.; Paminaga Y., Kikuchi T., Watanabe A., Satoh K., Watanabe Y.,
Nukiwa T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacterial pneumonia causes augmented expression of the secretory
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                                                                                                                                                                                                                                                                                               5 VKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                        21; Indels
               TRYPSIN INHIBITORY DOMAIN.
ELASTASE INHIBITORY DOMAIN.
                                                                                                                                                                                                                    C8C937E997815BCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 232:687-697(1997).
                                                                                                                                                                                                                                               Score 165; DB 1;
Pred. No. 1.7e-11;
                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                         SIMILARITY.
SIMILARITY.
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SIMILARITY.
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                                                                                                                                                                                                                    12518 MW;
                                                                                                                                                                                                                                                            48.18;
 inhibitor;
                                                                                                                                                                                                                                                       Local Similarity 48.19 tes 25, Conservative
                                        59
113
28
82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 88:417-426(1997).
                                                                                                                                                                                                                 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
Serine protease
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14
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34
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72
72
88
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                 ELASTASE OR CHYMOTRYPSIN INHIBITORY SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 271:7012-7018(1996).
-!- TISSUE SPECIFICITY: LARGE INTESTINE (RELATIVELY LOW LEVELS).
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                    TRYPSIN INHIBITORY SITE (PROBABLE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96215132; PubMed=8636131;
Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A.
Tachibana S., Hirose S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                               TRYPSIN INHIBITORY DOMAIN.
ELASTASE INHIBITORY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A57C9E30FE711B8F CRC64;
                                                                                                                                                                                                                                                    Serine protease inhibitor; Repeat; Signal.
SIGNAL 1 25 BY SIMILARITY.
CHAIN 26 131 ANTILEUKOPROTEINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.2%; Score 161; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY
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                                                                                                                                                                                                                            SMART; SM00217; WAP; 2.
PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
                                                                                                                                                                                                                                                                                                                                        WAP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14308 MW;
                                                                                                                   EMBL, U73004; AAC53047.1; -. EMBL, U88093; AAC53140.1; -. EMBL, U94341; AAC53394.1; -. HSSP, P19957; 2REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52.8%;
                                                                                                                                                                     MGD; MGI:109297; Slpi.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 2.
                                                                                                                                                                                                                WAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor.
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118
127
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26
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ID WAP3_PIG
AC Q29126;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
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"Purification and structure of caltrin-like proteins from seminal vesicle of the guinea pig.";
J. Biol. Chem. 255:6854-6853(1990).
-: FUNCTION: INHIBITS CALCIUM TRANSPORT INTO SPERMATOZOA.
-: PIWI GLYCOSYLATED.
-: SIMILARITY: CONTAINS I WAP-TYPE DOWAIN.
PIR; B35752; B35752.
HSSP; P19957; 2REL.
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Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                  WAP-3 PROTEIN.
8 X 6 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AQEPVKGP-VSTKPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pred. No. 7.1e-11;
11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45B0AFA582894D29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 160; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                      PRINTS; PRO0003; 4DISULPHCORE.
SMART; SM0017; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Pfam; PF00005; WAP; 1.
PRINTS; PR00003; 4DISULPHCORE.
SWART; SM00217; WAP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.6%;
                                                                                                                                                            EMBL; D50321; BAA08856.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Conservative
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                                                                                                                                                                                           HSSP; P19957; 2REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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CALU CAVPO
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MEDLINE=21638749; Pubbled=11780052;
MEDLINE=21638749; Pubbled=11780052;
MEDLINE=21638749; Pubbled=11780052;
MEDLINE=21638749; Pubbled=11780052;
MEDLINE=21638749; Pubbled=11780052;
MEDLINE=21638749; Pubbled=11780052;
MEDLINE: Startow K.F.; Bates K.N.; Beard D.M.; Beare D.M.;
Bassley O.P.; Bird C.P.; Blakey S.B.; Bridgeman A.M.; Brown A.J.;
Buck D.; Burrill W.D.; Blakey S.B.; Bridgeman A.M.; Brown A.J.;
MADLINE C.D.; Buller A.B.; Carder C.; Carter N.P.;
A. Coulson A., Coller R.E.; Connor R.E.; Corby N.R.;
A. Coulson A., Crankland J.A.; Fraser A.; French L.; Garner P.;
A. Blingron A.G.; Frankland J.A.; Fraser A.; French L.; Garner P.;
A. Mammond S.; Hante S.B.; Jekosch K.; Johnson C.M.; Johnson D.;
A. Kay M.P.; Kimberley A.M.; King A.; Knights A.; Laird G.K.; Lawlor S.;
A. Kay M.P.; Kimberley A.M.; King A.; Knights A.; Laird G.K.; Lawlor S.;
A. Marsh V.L.; Martin S.L.; McConnachie L.J.; McLay K.; McMurray A.A.;
A. Milne S.A.; Mistry D.; Moore M.J.F.; Mullikin J.C.; Nickerson T.;
A. Phillimore B.J.C.T.; Prathalingam S.R.; Plumb R.W.; Ramsay H.;
A. Phillimore B.J.C.T.; Prathalingam S.R.; Plumb R.W.; Ramsay H.;
A. Skuce C.D.; Smith M.L.; Scott C.E.; Sehra H.K.; Shownkeen R.; Sims S.;
                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning and expression of cDNA for human antileukoprotease from cervix uterus.",
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steller G., Brewer M.T., Thompson R.C.; "Isolation and sequence of a human gene encoding a potent inhibitor
                                                                                                                                                                                                                                                                          P03973; P07757; 23-007-1996 (Rel. 02, Created) 01-007-1996 (Rel. 12, Last sequence update) 01-007-1999 (Rel. 14, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) 4Antileukoproteinase 1 precursor (ALP) (HUSI-1) (Seminal proteinase inhibitor) (Secretory leukocyte protease inhibitor) (Mucus proteinase inhibitor) (MPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=87030258; PubMed=3533531;
Heinzel R., Appelhans H., Gassen G., Seemueller U., Machleidt W.,
Fritz H., Steffens G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates, Catarrhini; Hominidae, Homo.
                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Si-Tahar M., Merlin D., Sitaraman S., Madara J.L.; "Cloning and characterization of SLPI from human intestinal
                                                                                                                                                 7 GPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                            Score 158; DB 1; Length 55;
Pred. No. 5.3e-11;
8; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
           7FBABDB611A68399 CRC64;
                                                                                                                                                                                                                                                          132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 14:7883-7896(1986).
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87040761; PubMed=3640338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biochem. 160:61-67(1986).
55
6253 MW;
                                                    48.38;
                                                                       47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukocyte proteases.";
                                                                                         24; Conservative
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Parotid gland;
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
10
55 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelium.";
                                                                                                                                                                                                                                                              HUMAN
                 SEQUENCE
                                                        Query Match
                                                                                                                                                                                                                     KESULT 8
ALK1_HUMAN
 DOMAIN
                                                                                             Matches
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Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: MUCOUS FLUIDS.

DISBASE: THE PATHOLOGIES OF SEVERAL CHRONIC AND ACUTE DISEASES OF DISBASES. THE RESPIRATORY TRACT INVOLVE AN IMPALANCE BETWEEN THE PROTEASES OF CELLS INVOLVED IN INPLAMMATRY RESPONSES & THE INHIBITORS OF THESE PROTEASES. OF SATING OF SELLARATASIN THE LUNGS OF PATIENTS WHOSE LEVELS. OF ACTIVE ALPHA-1-ANTIPROTEASE ARE COMPROMISED BY GENETIC BACKGROUND, CIGARETTE SMOKING, AIR POLLUTANTS, OR A COMBINATION OF ALL THREE CAN RESULT SMOKING, AIR POLLUTANTS, ITS LOCK OF CLYCOSYLATION AND ITS STABILLTY MAKE THIS PROTEIN, ITS LOCK OF CLYCOSYLATION AND ITS STABILLTY MAKE THIS PROTEIN, ALCANO FOR CLYCOSYLATION AND ITS STABILLTY MAKE THIS PROTEIN A CANDIDATE FOR USE AS A THERAPEUTIC CHARACTER AND ADDITED ASSENTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bovine alpha-chymocrypsin.";
EMBO J. 7:345-351(1988).
-!- FUNCTION: ACID-STABLE PROTEINASE INHIBITOR WITH STRONG AFFINITIES
FOR TRYPSIN, GHYMOTRYPSIN, ELASTASE, AND CATHEPSIN G. MAY PREVENT
ELASTASE-MEDIATED DAMAGE TO ORAL AND POSSIBLY OTHER MUCOSAL
                                                                                                              "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88211544; PubMed=3366116; Gruetter M.G., Fendrich G., Huber R., Bode W.; ary crystal structure of the acid-stable proteinase inhibitor from human mucous secretions analysed in its complex with
                                                                                                                                                                                                                                                                                       SEQUENCE OF 26-132, AND SEQUENCE OF 26-65 FROM N.A. MEDLINE=86164996; PubMed=3485543; Sequellar U., Arnhold M., Fritz H., Wiedenmann K., Machleidt W., Heinzel R., Appelhans H., Gasen H.-G., Lottspeich F.; "The acid-stable proteinase inhibitor of human mucous secretions (HUSI-I, antileukoprotease). Complete amino acid sequence as revealed by protein and cDNA sequencing and structural homology to whey proteins and Red Sea turtle proteinase inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 26-52.

MEDLINE=91248412; PubMed=2039600;

MEDLINE=91248412; Ryle A.P.,

"Purification and characterization of elastase-specific inhibitor.

Sequence homology with mucus proteinase inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 26-132.
MEDLINE-86313644; PubMed=3462719;
Thompson R.C., Ohlsson K.;
"Isolation, properties, and complete amino acid sequence of human secretory leukccyte protease inhibitor, a potent inhibitor of leukocyte elastase.";
                                                                                                                                                                                                                          Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 83:6692-6696(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMBALANCES.
                                                                                                                                                                                                       TISSUE=Liver;
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EMBL; X04470; CAA28158.1; -.

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TRYPSIN INHIBITORY SITE (PROBABLE).
ELASTASE OR CHYMOTRYPSIN INHIBITORY SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88310901; PubMed=3136918;
Dear T.N., Ramshaw I.A., Kefford R.F.;
"Differential expression of a novel gene, WDNM1, in nonmetastatic rat
mammary adenocarcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EPVKGPVST--KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                                                                                                                                                                                                        TRYPSIN INHIBITORY DOMAIN.
ELASTASE INHIBITORY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      14326 MW; B62F3221E0903D90 CRC64;
                                                                                                                                                                                                                              ANTILEUKOPROTEINASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                        43.7%; Score 143; DB 1;
48.2%; Pred. No. 4.6e-09;
vative 4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AA.
                                                                                                                                                                                  SMART; SM00217; WAP; 2.
PROSITE; PS00317; 4 DISULFIDE CORE; 2.
Serine protease inhibitor; Repeat; Signal.
                                                                                                                                                                                                                                                                                                        (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WDNM1 protein precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                          WAP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Thymus;
MEDLINE=91207400; PubMed=2018519;
EMBL, AF114471; AAD19661.1; -. EMBL; AL015660; CAB64235.1; -. EMBL; BC020708; AAH20708.1; -. EMBL; X04502; CAA28187.1; -. EMBL; X04503; CAA28188.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer Res. 48:5203-5209(1988).
                                                                                                                                       InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 2.
PRINTS; PR00003; 4DISULPHCORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                               27; Conservative
                                                                                                                 Genew; HGNC:11092; SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Breast carcinoma;
                                                                                                                                                                          ProDom; PD001224; WAP;
                                                                                                                                                                                                                                       83
132
76
130
                                                                                                                                                                                                                                                                                                                 64
68
63
72
                                                  PIR, A01226, TIHUSP.
PIR, A25007, A25007.
PIR, A2541, A2541.
PIR, A25890, A25890.
PIR, S13455, S13455.
                                                                                                          HSSP; P19957; 2REL.
                                                                                                                                                                                                                                                                                                                                                                                                     132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                               35
43
51
57
89
96
                                                                                                                                                                                                                               26
26
33
31
45
45
                                                                                                                              MIM; 107285;
                                                                                                                                                                                                                                                                                  ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDNM RAT
                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P14730;
                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDNM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
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-!- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAP MACEU
                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9NOL8;
                                                                                                                                                                                                                    CHAIN
DOMAIN
                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
WAP MACEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         ς,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Epididymal protein BE-
                                   Biochem. Biophys. Res. Commun. 176:247-254(1991).
--- FUNCTION: INVOLVED IN THE METAGATIC POTENTIAL OF ADENOCARCINOMAS.
--- IN RAT. COULD HAVE PROTEINARS INHIBITING CAPACITY.
--- IN SAUE SPECIFICITY: SPLEEN, KIDNEY, BRAIN, LIVER, LUNG, AND CELL
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99201788; PubMed=10101572;
Fan H.-Y., Miao S.-Y., Wang L.-F., Koide S.S.;
"Expression and characterization of an epididymis-specific gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryotă, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
              "The WDNMI gene product is a novel member of the 'four-disulphide core' family of proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                   Score 101.5; DB 1; Length 74; Pred. No. 9.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                             12 KPGSCPIILIRCAMLNPPNR-----CLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                            29 KPGKCP-----KNPPRSIGTCVELCSGDQSCPNIQKCCSNGCGHVCKSP 72
                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                51802C70CDAF0521 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 29-123 FROM N.A., AND SEQUENCE OF 29-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-UUL-1998 (Rel. 36, Created)
16-UUL-1998 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Major epiddymis-specific protein 84 precursor
20) (WAP four-disulfide core domain protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 123 AA
                                                                                LINE RAT-2.
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                           WDNM1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND REVISION TO 29.
                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                            PIR; JH0390; JH0390.
HISSP, 19957; ZREL.
InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 1.
SMART; SM00217; WAP.
PROSITE; PS00317; 4 DISULIDE_CORE; 1.
Protease inhibitor; Signal.
                                                                                                                                                                                                 EMBL; X13309; CAA31688.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arch. Androl. 42:63-69(1999).
                                                                                                                                                                                                                                                                                                                                                     31.0%;
38.5%;
                                                                                                                                                                                                                                                                                                                                74 AA; 7740 MW;
                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
      ., Kefford R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Epididymis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Epididymis;
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WFD2 RABIT
Q28631;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                        TER
                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WFD2_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The gene for a novel member of the whey acidic protein family encodes three four-disulfide core domains and is asynchronously expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lactating mammary gland;
MEDLINE=20390063; PubMed=10801834;
Simpson K.J., Ranganathan S., Fisher J.A., Janssens P.A., Shaw D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
N' LINKED (GLCNAC. ...) (POTENTIAL).
M, 99F9A649CCBB5B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 PVTGTGADKPGVCPQL---SADLNCTQDCRADQDCAENLKCCRAGCSAICSIP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.7%; Score 100.5; DB 1
39.6%; Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 3 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  during lactation.";
J. Biol. Chem. 275:23074-23081(2000).
-!- FUNCTION: COULD BE A PROTEASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                          InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 2.
PRINTS; PR00003; 4DISULPHCORE.
Prodom; PD001224; WAP; 1.
SWART; SM00217; WAP; 2.
PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
Repeat; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whey acidic protein precursor (tWAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macropus eugenii (Tammar wallaby).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 N-12803 MW;
                                                                                                                                                                                                                           EMBL; U26725; AAA66525.2; -. HSSP; Q9N0L8; 1TWP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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123 AA;
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Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicholas K.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain,
MEDIARS=94010957; PubMed=8406507;
Legouls R., Cohen-Salmon M., del Castillo I., Levilliers J.,
Capy L., Mornon J.-P., Petit C.,
"Characterization of the chicken and quail homologues of the human gene responsible for the X-linked Kallmann syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: May be an adhesion-like molecule with anti-protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted. Localized at cell surface (By
                                                                                               69 N-LINKED (GLCNAC. . .) (POTENTIAL)
21133 MW; BF90B81DADBBESOD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 PVKAKPGRCPAVTGIC----PEKKSWFHTCQRDDQCKENKKCCSSACGRRCTNP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                                                                                                       30.7%; Score 100.5; DB 1; Length 191; 37.0%; Pred. No. 0.00026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 PVSTKPGSCPIILIRCAMLNPPNR-----CLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anosmin 1 precursor (Kallmann syndrome protein homolog).
                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FJJUN-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    676 AA
                                                                                                                                                                                                             WAP 1.
WAP 2.
WAP 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                              EMBL; AJ005356; CAB90357.1; -.
                                                                                         DB; 1TWP; 13-JAN-00.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 37.09
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                        126
175
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163
167
                                                                                                                                                                                                                                                                                                                                                                                                  191 AA;
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74
129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 EFLKYILSVKOGDCPAPEKASGFAAACV----ESCEADSECSGVKKCCSNGCGHTCQVP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 BPVKGPVSTKPGSCPI----ILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sippel A.E., "Comparison of the whey acidic protein genes of the rat and mouse."; Nucleic Acids Res. 12:8685-8697(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                   PROSITE; PS00317, 4 DISULFIDE CORE; 1.
Cell adhesion; Glycoprotein; Serine protease inhibitor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campbell S.M., Rosen J.M., Hennighausen L.G., Strech-Jurk U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Whey acidic protein precursor (Whey phosphoprotein) (WAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3FAC7ED82EA7E352 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
N-LINKED GLCNAC. ) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100.5; DB 1;
Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                          "CYSTEINE BOX".
 -! - SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
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                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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N-LINKED
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                                                                                                                               EMBL, L12144; AAA51435.1; -. PIR; B47222; B47222. INSSP; P19957; SEEL. InterPro; IPR003961; FN III. InterPro; IPR002221; WAF. Pfam; PF00041; fn3; 3. Pfam; PF00095; wap; 1. PRINTS; PR00003; 4DISULPHCORE. SMART; SM00060; FN3; 3.
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MEDLINE=85062841; PubMed=6095207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.7%;
ilarity 34.4%;
Conservative
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204
295
466
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676 AA;
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CARBOHYD
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                                                                                                                                                          -i - TISSUE SPECIFICITY: MILK-SPECIFIC; MAJOR PROTEIN COMPONENT OF MILK
    MEDLINE-82274212; PubMed-6896749;
Hennighausen L.G., Sippel A.E.;
"Comparative sequence analysis of the mRNAs coding for mouse and rat
                                                                                                                                                                                                                                                                                                                                                                                                             Dandekar A.M., Robinson E.A., Appella E., Qasba P.K.;
"Complete sequence analysis of cDNA clones encoding rat whey
phosphoprotein: homology to a protease inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 79:3987-3991(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
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2 AND 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHEY ACIDIC PROTEIN. WAP 1 (ATYPICAL).
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BY SHOSPHORYLATION
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                                                    Nucleic Acids Res. 10:3733-3744(1982).
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                                                                                                                                                                                                                                                                                                       EMBL; X01154; CAA25600.2; JOINED.
EMBL; X01155; CAA25600.2; JOINED.
EMBL; X01156; CAA25600.2; JOINED.
EMBL; J00802; AAA42340.1; --
EMBL; J00801; AAA42346.1; --
PIR; A01228; WYRT.
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                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted
                                                                                    MEDLINE=82275050; PubMed=6955785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14827 MW;
                                                                                                                                                                                                                                                                                                 EMBL; X01153; CAA25600.2; -.
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'40
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103
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                                                                                                                                                                                                                                                                                                                                                                                        046655; 1CJH.
SECUENCE FROM N.A.
                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SPECIES-Bovine; TISSUE=Mammary gland;
Kho Y.J., Lee D.Y., Choi Y.J., Baik M.G.;
Cloning and characterization of involution specific genes in bovine
                 Gaps
                                                                          70 KTPVNIEVQKAGRCPWNPIQMIAAGPCPKDNPCSIDSDCSGTMKCCKNGCIMSCMDPE 127
                                            6 KGPV8----TKPGSC----PILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090, 9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                   Morrison B.W., Leder P.;
"neu and ras initiate murine mammary tumors that share genetic markers generally absent in c-myc and int-2-initiated tumors.";
"Occogene 9:3417-3426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 KPGSCPIILIRCAMLNPP-----NRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 KPGAĆP-----KPPPRSFGTCDERĊTGDGSĊSĠNMKĊĊSNGĊĠHĀĊKPP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 96.5; DB 1; Length 74; Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: COULD HAVE PROTEINASE INHIBITING CAPACITY.
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                  24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42BDCAD5B330B3D3 CRC64;
37.9%; Pred. No. 0.00037; ive 6; Mismatches 24.
                                                                                                                                                                                                 01-10V-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WDNM1 PROTEIN.
                                                                                                                                                                 74 AA
                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=Mouse; STRAIN=FVB/N; TISSUE=Breast; MEDLINE=95060797; PubMed=7970700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMEL, AFIS9701, AAF75524.1; -...
HSSP, Q9N0L8; 1TWP.
MGD; MGILOFS06; EXPI.
InterPro; 1PR002221; WAP.
Pfam; PF00095; wap; 1...
PRINTS; PR000031; 4DISULPHCORE.
SMART; SM00217; WAP; 1...
PROSITE; PS00317; 4_DISULFIDE_CORE; 1...
Procease inhibitor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X93037; CAA63605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                 Mus musculus (Mouse), and
                    22; Conservative
                                                                                                                                                                                                                                                 WDNM1 protein precursor. WDNM1 OR EXPI
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 AA;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammary gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                      WDNM MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                        RESULT 14
WDNM MOUSE
                         Matches
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DB 1; Length 137;

30.0%; Score 98;

Query, Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: MILK-SPECIFIC; MAJOR PROTEIN COMPONENT OF MILK
                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 20-56 AND 93-132.
MEDLINE=98774264; PubMed=9513079;
Simpson K.J., Bird P., Shaw D., Nicholas K.R.;
"Molecular characterisation and hormone-dependent expression of the porcine whey acidic protein gene.";
J. Mol. Endocrinol. 20:27-35(1998).
                                                                                                                                                                                                                                                                                                                    TISSUE=Mammary gland, Masel A.M., Hall A., Bell K.T.; Masel A.M., Hall A., Bell K.T.; "Cloning and characterisation of the porcine whey acidic protein."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20144368; PubMed=10680116; Ranganathan S., Simpson K.J., Shaw D.C., Nicholas K.R.; The whey acidic protein family: a new signature motif and three-dimensional structure by comparative modeling."; J. Mol. Graph. Model. 17:106-113(1999).
-!- FUNCTION: COULD BE A PROTEASE INHIBITOR. MAY PLAY AN IMPORTANT ROLE IN MAMMARY GLAND DEVELOPMENT AND TISSUE REMODELING.
                                                                                                                       Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interro; 150005; wap; 2. Pfam; PF00095; wap; 2. PRINTS; PR00003; 4DISULPHCORE. SMART; SM00217; WAP; 2. PROSITE; PS00317; 4 DISULFIDE CORE; 2. PROSITE; Whey; Protease inhibitor; Repeat; Signal; 3D-structure. Milk; Whey; Protease inhibitor; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN REF. 1; AA SEQUENCE).; 7F7796493C0D98E0 CRC64;
                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-SER
                                                                          Whey acidic protein precursor (WAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                     3D-STRUCTURE MODELING OF 20-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13956 MW;
                                                                                                                                                                                                                                                                                                      SEQUENCE OF 17-132 FROM N.A.
STANDARD;
                                                                                                          scrofa (Pig)
           046655; 097559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
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DISULFID
CONFLICT
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29.2%; Score 95.5; DB 1; Length 132;

Query Match

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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REDILNB=21638749; PubMed=11780052;

RA Dones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F.; Bates K.M.; Beare D.M.,

RA Baseley O.P., Bird C.P., Blakey S.E., Bridgeman A.M.; Beare D.M.,

RA Buck D., Burrill W.D.; Butler A.P.; Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N.; Clark S.Y. Clee C.M.;

RA Chegg S., Cobley V.E., Collier R.E.; Connor R.E., Corby N.R.;

Coulson A., Coville G.J., Deadman R.P. Themi P.D., Dunn M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.;

RA Coulson A., Farakland J.A.; Fraeser A., French L., Howden P.J.;

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hammond S., Harley J.E., Heath P.D., Ho S., Holden J.L., Howden P.J.;

RA Hammond S., Harley J.E., Heath P.D., Ho S., Holden J.L., Howden P.J.;

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson D.,

RA Markh W.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Millimor B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Swann R.M., Sycamors N., Taylor R., Thomas D.W., Thorpe A.,

RA Phillimor B.J., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,

RA Tracey A., Tromans A.C., Vaudin M., Wallisy D.L., Williams L., Williams S.A.,

RA Hilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., 1111ams S.A.,

RA Rogers J.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                         72 PLLVPV-PKAGRCPWV---PAPLAPELCLEKNECSRDDQCRGNKKCCFSSCAMRCLDP 125
                                                                              4 PVKGPVSTKPGSCPIILIRCAMLNP----PNRCLKDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    014508; 096KJ1;
15-UUL-1998 (Rel. 36, Created)
15-UUN-2002 (Rel. 41, Last annotation update)
15-UUN-2002 (Rel. 41, Last annotation update)
Major epididymis-specific protein B4 precursor (HB4) (Epididymal
secretory protein B4) (MAP four-disulfide core domain protein 2)
WPDC2 OR HB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: POSSIBLE FUNCTION IN SPERM MATURATION.
-i- SUBCELLULAR LOCATION: Secreted (Potential).
-i- TISSUB SPECIFICITY: BETHHELIAL CELLES OF THE EPIDIDYMAL DUCT,
PREDOMINANTLY WITHIN THE DISTAL SECTIONS.
-i- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92153963; PubMed=1686187;
Kirchhoff C., Habben L., Ivell R., Krull N.;
A major human epididymis-specific cDNA encodes a protein with sequence homology to extracellular proteinase inhibitors.";
Biol. Reprod. 45:350-357(1991).
                                     22; Indels
          41.4%; Pred. No. 0.00067; tive 3; Mismatches 22
                                                                                                                                                                                                                                                       124 AA
                                24; Conservative
                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 414:865-871(2001)
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissum=Epididymis;
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                                                                                                                                                                                                                                                  WFD2 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                              Matches
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Legouis R., Hardelin J.-P., Levilliers J., Claverie J.-M., Compain S.,
Wunderle V., Millasseau P., le Paslier D., Cohen D., Caterina D.,
Bougueleret L., Delemarre-Van de Waal H., Lutfalla G., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of the X-linked Kallmann syndrome gene and its homologous pseudogene on the Y chromosome."; Nat. Genet. 2:305-310(1992).
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                               BY SIMILARITY.
SIMILARITY.
S- LLC (IN REF. 1).
S -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anosmin 1 precursor (Kallmann syndrome protein) (Adhesion molecule-like X-linked).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules."; Cell 67:423-435(1991).
                                                                                                                                               MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93265164; PubMed-1303284;
del Castillo I., Cohen-Salmon M., Blanchard S., Lutfalla G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92018217; PubMed=1922361;
Franco B., Guioli S., Pragliola A., Inceri B., Bardoni B.,
                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  16 KEGSCPQVNINFPQLGLCRDQCQVDSQCPGQMKCCRNGCGKVSCVTP 122
                                                                                                                                                                                                                                                                                                                                                                                                              12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSCG-MACFVP 56
                                                                                                                                                                                                                                                                                                                                  9536B00B385259AD CRC64;
                                                                                                                                                                                                                                                                                                                                                               Score 93; DB 1;
Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 680 AA.
                                                                                                                                        POTENTIAL
                                                                                                  SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 2.
                                                                                                                                                                  WAP 1.
                                                                                                                                                                             WAP 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAL1 OR KAL OR ADMLX OR KALIGI.
                                  AL031663; CAB37641.1; -.
                                                                                                                                                                                                                                                                                                                                     12993 MW;
                                                                                                                           Repeat; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                              Match 28.4%;
Local Similarity 40.4%;
les 19; Conservative (
         EMBL; X63187; CAA44869.1; -. EMBL; A18924; CAA01433.1; -.
                                                                       InterPro; IPR002221; WAP. Pfam; PF00095; wap; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                              HSSP, Q9N0L8; 1TWP.
Genew; HGNC:15939; WFDC2.
                                                                                                                                                      124
73
124
62
                                                                                                                                                                                                                                           1109
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                                                                                                                                                                                                                                                                                                                                     124 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                    EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i. PTM: N-glycosylated.
-i. DTM: N-glycosylated.
-i. DISEASE: Defects in KAL1 are a cause of Kal1mann syndrome (KAL1 OR KS), a genetic disorder that associates hypogonadotropic. hypogonadism and anosmia. In this disease, the normal embryonic migration of GNRH-synthesizing neurons from the olfactory placodes to the hypothalamic region as well as the axonal extension of olfactory neurons towards the forebrain are impaired.
-i. SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
-i. SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                              SEQUENCE OF 1-71 FROM N.A. MEDLINE=96069588; PubMed=7590336; Cohen-Salmon M., Tronche F., del Castillo I., Petit C.; Cohen-Salmon M., Tronche F., del Castillo I., Petit C.; Characterization of the promoter of the human KAL gene, responsible for the X-chromosome-linked Kallmann syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                              "Initial characterization of anosmin-1, a putative extracellular matrix protein synthesized by definite neuronal cell populations in the central nervous system.";
J. Cell Sci. 109:1749-1757(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hardelin J.-P., Levilliers J., Blanchard S., Carel J.-C., Leutenegger M., Pinard-Berrelletto J.-P., Bouloux P., Petit C.; "Heterogeneity in the mutations responsible for X chromosome-linked Kallmann syndrome.";
Tonlorenzi R., Carrozo R., Maestrini E., Pieretti M., Taillon-Miller P., Brown C.J., Willard H.F., Lawrence C., Persico N.G., Camerino G., Ballabio A.; A gene deleted in Kallmann's syndrome shares homology with neural cell adhesion and axonal path-finding molecules.";
                                                                                                                                                                                                                                                                                                                                   Soussi-Yanicostas N., Hardelin J.-P., del Mar Arroyo-Jimenez M.,
Ardouin O., Legouis R., Levilliers J., Traincard F., Betton J.-M.,
Cabanie L., Petit C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-linked Kallmann's syndrome.";
J. Clin. Endocrinol. Metab. 83:1650-1653(1998).
-!- FUNCTION: May be an adhesion-like molecule with anti-protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAKIANT KALI LYS-514, AND VARIANT VAL-534.
MEDLINE-98251583; PubMed-9589672;
Maya-Nunez G., Zenteno J.C., Ulloa-Aguirre A., Kofman-Alfaro S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'A recurrent missense mutation in the KAL gene in patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLÚLAR LOCATION: Secreted. Localized at cell surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT KAL1 LYS-267, AND VARIANT VAL-534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M97252, AAA59202.1; -.
EMBL, S60085; AAB20108.1; ALT_SEQ.
EMBL; X60299; CAA42841.1; -.
EMBL; X82034; CAA57554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93278384; PubMed=8504298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hum. Mol. Genet. 2:373-377(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR003961; FN III. InterPro, IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:6211; KAL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00041; fn3; 3.
Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                              Gene 164:235-242(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A40351; A40351.
PIR; S17982; S17982.
                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 308700; -.
                                                                                                                                                                                                                                                                                                                               PubMed=8832397;
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Beg O.U., von Bahr-Lindstrom H., Zaidi Z.H., Joernvall H.;

Beg O.U., von Bahr-Lindstrom H., Zaidi Z.H., Joernvall H.;

Beg O.U., son Bahr-Lindstrom H., Zaidi Z.H., Joernvall H.;

assessment of variations, internal repeat patterns, and relationships with neurophysin and other active polypeptides.";

Bur. J. Blochem. 159:195-201(1986).

-!- FUNCTION: COULD BE A PROTEASE INHIBITOR.

-: SUBCELLULAR LOCATION: Secreted.

-! TISSUE SPECIFICITY: MILK-SPECIFIC; MAJOR PROTEIN COMPONENT OF MILK
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                          PROSITE; PS00117; 4 DISULFIDE CORE; 1.
Cell adhesion; Glycoprotein; Serine protease inhibitor; Repeat;
Signal; Polymorphism; Disease mutation.
                                                                                                                                                               (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                          130 KOGDCPAPEKASGFAAACV----ESCEVDNECSGVKKCCSNGCGHTCQVPK 176
                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                  DB 1; Length 680;
                                                                                                                                                                                                                                                                                                                                        12 KPGSCPI----ILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
                                                                                                                                                                                                                                                                                                                     20, Indels
                                                                                                                                                                                                                                                                              5D6ACC9F14B5F5F8 CRC64;
                                                                                            FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
N-LINKED (GLCNAC...) (1)
                                                                                                                                                                                                                                         /FTIG=VAR 007721.

NN -> VR (IN REF. 4).

E -> K (IN REF. 3).

A -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Dromedary) (Arabian camel)
                                                                                                                                                                                                                                                                                                  Score 92.5; DB 1
Pred. No. 0.0055;
                                                                                                                                                                                                      007720
                                                                                                                                                                                                              E -> K (IN KAL1).
/FTId=VAR_012742.
                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                          N -> K (IN KAL1)
/FTId=VAR_007720
                                                                    ANOSMIN 1.
"CYSTEINE BOX".
                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 117 AA
                                                         POTENTIAL.
                                                                  ANOSMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, A24178, A24178.
HSSP, O46655, 1CJH.
InterPro; IPR002221, WAP.
Fam, PF00095, wap, 2.
PRINTS; PR00003, 4DISULPHCORE.
ProDom; PD001224; WAP; 1.
PRINTS; PR00003; 4DISULPHCORE.
SMART; SM00060; FN3; 4.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                76066 MW;
                                                                                                                                                                                                                                                                                                  28.3%;
                                                                                                                                                                                                                                                                                                           34.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whey acidic protein (WAP).
                                                                                                                                                                                                                                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                               514
                                                                                                                                                                                                                                534
                                                                                                                                                                                                                                                                      540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Camelus dromedarius
                                                                                                                                                                                                                                                                               680 AA;
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9838;
                                                                                                                                                                                                                                                   70
373
540
                                                                 21
21
130
181
286
403
                                                                                                                                                                                                              514
                                                                                                                                                                                                                                534
                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=Milk;
                                                                                                                                                                                                                                                                                                                                                                                                        WAP CAMDR
P09837;
                                                                                                                         DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                CARBOHYD
                                                                                                                                                                       CARBOHYD
                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                              JARIANT
                                                                                                                                                                                                                               VARIANT
                                                                                             DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                           VARIANT
                                                                 CHAIN
                                                                                    DOMAIN
                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                              WAP CAMDR
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95263176; PubMed=7744512;
MEDLINE=95263176; PubMed=7744512;
MEDLINE=95263176; PubMed=7744512;
MEDLINE=95263176; PubMed=7744512;
Pera I. , IVall R., Kirchhoff C.;
"Regional variation of specific gene expression in the dog epididymis as revealed by in-situ transcript hybridization.";
Int. J. Androl. 17:324-330(1994).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SUBCELLULAR ELOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: EPIDIDYMIS. HIGHEST LBVELS ARE FOUND IN THE CAUDA REGIONS. LOWER LEVELS IN THE DISTAL CAUDA. NOT DETECTED IN THE BFFERENT DUCTS.
-!- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=55263175; PubMed=7744511;
Ellerbrock K., Pera I., Hartung S., Ivell R.;
"Gene expression in the dog epididymis: a model for human epididymal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 EPV-----LKDGRCPWVQTPLTAKHCLEKNDCSRDDQCEGNKKCCFSSCAMRCLDP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Major epididymis-specific protein B4 precursor (CE4) (Epididymal secretory protein E4) (WAP four-disulfide core domain protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EPVKGPVSTKPGSCPIIL -- IRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 117;
                                     Se_inhibitor; Repeat; Phosphorylation.
54
11 WAP 1.
11 BY SIMILARITY.
40 BY SIMILARITY.
50 BY SIMILARITY.
50 BY SIMILARITY.
61 BY SIMILARITY.
62 BY SIMILARITY.
63 BY SIMILARITY.
64 BY SIMILARITY.
65 BY SIMILARITY.
66 BY SIMILARITY.
67 BY SIMILARITY.
68 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                      2D9BB6A5A37A921B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA
                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.00
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    27.7%; Score 90.5;
SMART; SM00217; WAP; 2.
PROSITE; PS00317; 4 DISULFIDE CORE; 2.
Milk; Whey; Protease inhibitor; Repeat
DOMAIN 9 54 WAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Int. J. Androl. 17:314-323(1994)
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HSSP; O46655; 1CJH.
InterPro; IPR002221; WAP.
PÉm; PR00095; wap; 2.
PRINTS; PR00003; 4DISULPHCORE.
                                                                                                                                                                                                                                                                                                                      12564 MW;
                                                                                                                                                                                                                                                                                                                                                                                           37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                         54
111
411
46
40
50
50
99
103
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                                                                                                                                                                                                                                                                                                                    117 AA;
                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 21; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Epididymis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9615;
                                                                                                CANFA
                                                                                             DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                           DISULFID
DISULFID
DISULFID
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DISULFID
SEQUENCE
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                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Nature 409:685-690(2001).
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPINLW1
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPPI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CETRAINCSTBL/63; TISSUE-Testis;

MEDLINE-21085660; PubMed=11217851;

RAWAN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawan J., Shinagawa A., Shibata K., Yomo H., Adachi J., Fukudishi Y., Konno H., Adachi J., Fukuda S., Arawawa T., Hara A., Fukunishi Y., Konno H., Kankawa T., Saito T., Okazaki Y., Golobori T., Bono H., Kashwawa T., Saito R., Ashburner M., Batalov S., Casavant T., Ashburner M., Radio I., Rochiwa H., Ashburner M., Batalov S., Casavant T., Ashburner M., Batalov S., Casavant T., Ashburner M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Auvenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Auvenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Auvenstein M.J., Bult C., Saya T., Sakamoto N., Nordone P., Ring B., Ringwald M., Razarelli J., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Runctional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Characterization of monkey and mouse Eppin, a protease inhibitor from
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c; TISSUE=Testis, and Epididymis;
Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                     MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4
                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Eppin precursor (Epididymal protesse inhibitor) (Serine protesse inhibitor-like with Kunitz and WAP domains 1).
                                                                                                                                                                                                                 .) (POTENTIAL).
                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                        DB 1; Length 124;
                                                                                                                                                                                                                                                                   Pred. No. 0.0042;
7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                    76 KEGSCPOVNTDFPQLGLCQDQCQVDSHCPGLLKCCYNGCGKVSCVTP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epididymis and testis.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           12 KPGSCPIILIRCAMLN-PPNRCLKDTDCPGIKKCCEGSCG-MACFVP 56
                                                                                                                                                                                                                       -LINKED (GLCNAC. . .) (PC
15AAF315BA13958C CRC64;
                                                                                                                                                                                                                    (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                       134 AA
                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                        26.9%; Score 88; 38.3%; Pred. No. (
                SMART; SM00217; WAP; 2.
PROSITE; PS00317; 4 DISULFIDE_CORE; 2.
Repeat; Signal; Glycoprotein.
                                                        POTENTIAL
                                                                                                                                                                                                                    N-LINKED
                                                                                   WAP 1.
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                               WAP 2
                                                                                                                                                                                                                               12951 MW;
     PD001224; WAP; 1.
                                                                                                                                                                                                                                                                      Local Similarity 38.3 es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                              124
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                               124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richardson R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                     EPPI MOUSE Q9DA01;
                                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                        DISULFID
                                                                                                                        DISULFID
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                      DISULFID
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                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                               SEQUENCE
     ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPINLW1
                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         EPPI_MOUSE
                                                                        CHAIN
                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             055925; Q9HD10; Q96SD7; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Eppin precursor (Epididymal protease inhibitor) (Serine protease inhibitor-like with Kunitz and WAP domains 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKGPVSTK---PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 VQGPSLADLLFPRRCPRFREECEH-QERDLCTRDRDCPKKEKCCVFNCGKKCLNPQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
-i- SUBCELLULAR LOCATION: Secreted (Potential).
-i- TISSUB SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
-i- SIMILARITY: CONTAINS 1 BPTI/KINITZ INHIBITOR DOMAIN.
-i- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score oc.
Pred. No. 0.0045;
Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFFEB63D4D4C427F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BPTI/KUNITZ INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PRO0759; BASICPTASE.
ProDom; PD000222; Kunitz_BPT1; 1.
SMART; SM00131; Ku1; 1.
SMART; SM0011; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
PROSITE; PS00280; BPT1 KUNITZ_1; 1.
PROSITE; PS50279; BPT1 KUNITZ_2; 1.
SGTINE protease inhibitor; SGTABL.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002223; Kunitz BPTI.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P31713; ISHP.
MGD; MGI:1922776; 1700024E17Rik.
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF346413; AAK31335.1; -.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK006296; BAB24514.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00014; Kunitz BPTI; 1. Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15470 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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RAY SEQUENCE FROM N.A.

RAY SEQUENCE FROM N.A.

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Back D., Burrill W.D., Butler A.D., Carder C., Carter N.D.,

RA Chapman J.C., Clamp M., Clark G., Clark L.M., Clark S.Y., Clee C.M.,

RA Coulson A., Coville G.J., Deadman R., Dhan M.D.,

RA Cliston A.G., Frankland J.A., Fraser A., French L., Dhun M.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garrer P.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Hammond S., Harley J.L., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

Lefvaslaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

Whitehead S.L., Whiteker P., Willey D.L., Williams L., Williams S.A.,

Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- ALTENATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTENATIVE SPLICING.
-!- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
-!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANT; SUVOLI; TATE; 1.

PROSITE; PS00210; 4 DISULFIDE_CORE; 1.

PROSITE; PS50279; BPTI_KUNITZ_1; 1.

Serine protease inhibitor; Signal; Alternative splicing.

SIGNAL 1 21

POTENTIAL.
                                                           SEQUENCE FROM N.A. (ISOPORM 1).
Stavrides G.S., Huckle E.J., Deloukas P.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
inhibitors expressed in the epididymis and testis."; Gene 270:93-102(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SM00131; KU; 1.
SMART; SM00217; WAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF286370; AAG00548.1; -. EMBL; AF286369; AAG00547.1; -. EMBL; AF286368; AAG00546.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL118493; CAB56343.1; -. AL031663; CAB37635.1; -. AL031663; CAC36265.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00014; Kunitz BPTI; 2.
Pfam; PF00095; wap; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:15932; SPINLW1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00974; 1BPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                               BY SIMILARITY.

BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Testis, and Epididymis;
Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Eppin precursor (Epidaywal protease inhibitor) (Serine protease inhibitor-like with Kunitz and WAP domains 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VKGPVSTK---PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 VQGPGLTDWLFPRRCPKIREECE-FQERDVCTKDRQCQDNKKCCVFSCGKKC 69
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- TISSUE SPECIFICITY: EXPRESSED IN EPIDIDYMIS AND TESTIS.
-!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 85; ____Pred. No. 0.0094;
                                           BPTI/KUNITZ INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.0%; Scor No. v.v. 40.4%; Pred. No. v.v. 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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Probom; PD000222; Kunitz_BPT1; 1.

SWART; SM00131; KU; 1.

PROSITE; PS00280; BPTI_KUNITZ_1; 1.

PROSITE; PS50279; BPTI_KUNITZ_2; 1.

Serine protease inhibitor; Signal.

SIGNAL
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InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                    133 AA; 15284 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF346414; AAK31336.1; -.
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Pfam; PF00095; wap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae, Macaca.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MAP Four-disulfide core domain protein 1 protein precursor (Prostate stromal protein ps20) (ps20 growth inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and expression of ps20 growth inhibitor. A novel by type 'four-disulfide core' domain protein expressed in smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Sprague-Dawley, TISSUE-Prostate;
MEDLINE-89136158; PubMed-9468514;
Larsen M., Ressler S.J., Lu B., Gerdes M.J., McBride L., Dang T.D.,
Rowley D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rowley D.R., Dang T.D., Larsen M., Gerdes M.J., McBride L., Lu B., "Purification of a novel protein (ps20) from urogenital sinus mesenchymal cells with growth inhibitory properties in vitro."; J. Biol. Chem. 270:22058-22065 (1995).

-: FUNCTION: Has growth inhibitory activity.

-: SUBCELLUIAR LOCATION: Secreted.

-: TISSUE SPECIFICITY: Vascular smooth muscle and prostate.

Periacinar ring.

-: SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                                  4;
                                                                                                                                                                                                                                5 VKGPVSTK---PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                             19 VOGPGLÍDWLFPRRCPTIREECE-FRERDVCTRHROCPDNKKCVFSCGKKC 69
                                                                                                                                                                    Score 85; DB 1; Length 133;
                                                                                                                                                                                                  25; Indels
                                                                                                                                      433AE946E39A35E9 CRC64;
         BYTI/KUNITZ INHIBITOR.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE OF 27-54, AND CHARACTERIZATION.
                                                                                                                                                                                    Pred. No. 0.0094;
                                                                                                                                                                                                                                                                                                                                             PRT; 212 AA
                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00317; 4 DISULFIDE CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scle.";
Biol. Chem. 273:4574-4584(1998).
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                                                                                                                                        15279 MW;
                                                                                                                                                                    26.0%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interPro; IPR002221; WAP.
                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                             STANDARD;
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SMART; SM00217; WAP; 1
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                        133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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SEQUENCE
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                                             DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Larsen M., Ressler S.J., Gerdes M.J., bu B., Byron M., Lawrence J.B., Rowley D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-UTN-2002 (Rel. 41, Created)
15-UTN-2002 (Rel. 41, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
15-UTN-2002 (Rel. 41, Last annotation)
15-UTN-2002 (Rel. 41, Last sequence)
15-UTN-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The WFDC1 gene encoding ps20 localizes to 16q24, a region of LOH in
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION. Has growth inhibitory activity (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
                                                                                                                                                                                  Length 212;
                                                                                                                                                                                                                             15; Indels
                                                                                                                                                                                                                                                                         8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                       2BB054DE9D8460A5 CRC64;
                                                                                                                                                                                    DB 1;
                                                                                                                                                                                  Score 81.5; DB :
Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY:
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN.
PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF169632; AAG21086.1; JOINED.
BMBL; RG028860, AA4128890.1; -
INTERPRO; IPR002221; WAP.
PÉGMI; PF00095; WAP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20424791; PubMed=10967136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamm. Genome 11:767-773 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF170446; AAG21086.1; -.
                                                                                                                                      23230 MW;
                                                                                                                                                                                    24.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 4-211 FROM N.A.
                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
91
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95
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92
87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            multiple cancers.";
                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                      212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
57
69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WFD1 MOUSE
Q9ESH5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
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                     DOMAIN
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SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         WFD1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FT
FT
FT
FT
SO
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Page 17

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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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TISSUE=Colon, Kidney, and Stomach;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human uterus.
        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: MILK-SPECIFIC; MAJOR PROTEIN COMPONENT OF MILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: NO PHOSPHATE OR CARBOHYDRATE BINDING COULD BE DETECTED;
HOWEVER, BOTH CHOLESTEROL AND TRIGLYCERIDE ARE ASSOCIATED WITH THE
MOUSE PROTEIN.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                      "Comparison of the whey acidic protein genes of the rat and mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=82196900, PubMed=6896234;
Hennighausen L.G., Sippel A.E.;
"Mouse whey acidic protein is a novel member of the family of 'four-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 256:11509-11516(1981).
-!- FUNCTION: COULD BE A PROTEACE IMHIBITOR. MAY PLAY AN IMPORTANT ROLE IN MAMMARY GLAND DEVELOPMENT AND TISSUE REMODELING.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piletz J.E., Heinlen M., Ganschow R.E.; "Blochemical characterization of a novel whey protein from murine
                                                                    11,
                                      Score 80.5; DB 1; Length 211;
Pred. No. 0.042;
6; Mismatches 15; Indels 11
                                                                                                                                                                                                                                                                                                                                                MEDLINE-85062841; PubMed-6095207;
Campbell S.M., Rosen J.M., Hennighausen L.G., Strech-Jurk U.,
Sippel A.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
 132 132 MISSING (IN REF. 2).
211 AA; 23079 MW; 605E7E6B0FC64FE5 CRC64;
                                                                                       8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                     61 PRTLPPGAC-----QATRCQADSECPRHRRCCYNGCAYAC 95
                                                                                                                                                                           WARP MOUSE STANDARD; PRT; 134 AA. PO1173; P70230; Q61023; 21-JUL-1986 (Rel. 01, Created) C-CT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Whey acidic protein precursor (WAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 2 WAP-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 12:8685-8697(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disulfide core' proteins.";
Nucleic Acids Res. 10:2677-2684(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=82052974; PubMed=6975276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X01157; CAA25604.1; -.
EMBL; X01158; CAA25604.1; JOINED.
EMBL; X01159; CAA25604.1; JOINED.
                                      24.6%;
                                                               14; Conservative
                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                     Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hennighausen L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=YBR;
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CONFLICT
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WFD1 HUMAN STANDARD; PRT; 220 AA.
Q9HC57; Q9HAU1;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
WAP four-disulfide core domain protein 1 protein precursor (Prostate strongal protein ps20) (ps20 growth inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20424791; PubMed-10967136;
Larsen M., Ressler S.J., Gerdes M.J., Lu B., Byron M., Lawrence J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Uterus;
Ong C.K., Ng C.Y., Lim K.B., Chan T.W.M.G., Huynh H.;
"Molecular cloning and characterization of the human ps20 protein in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowley D.R.;
"The WFDC1 gene encoding ps20 localizes to 16q24, a region of LOH in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 KGPVS---TKPGSCPIILIRCAMLNPP----NRCLKDTDCPGIKKCCEGSCGMACFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.3%; Score 79.5; DB 1; Length 134; ilarity 34.5%; Pred. No. 0.037; Conservative 4; Mismatches 27; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
0.037;
~heg 27; Indels
                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
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R -> S (IN REF 1).
C -> P (IN REF 2).
G -> V (IN REF 1).
G -> V (IN REF 1).
C -> P (IN REF 2).
C -> S (IN REF 2).
K -> Q (IN REF 2).
K -> Q (IN REF 2).
W, C12B2544877ECA80 CRC64;
                                                                                                                                                                                                                                                                                          WHEY ACIDIC PROTEIN
                                                                                                                                                                                                                                                  Milk; Whey; Protease inhibitor; Repeat; Signal.
                                                                                                                                                                                                                                                                                                      WAP 1 (ATYPICAL).
                                                                                                                                                                                                                             PROSITE; PS00317; 4_DISULFIDE CORE; 2.
EMBL; X01160; CAA25604.1; JOINED.
EMBL; V00856; CAA24224.1; -.
EMBL; U38816; AAA91321.1; -.
                                                          PIR; A01227; WYMS.
PIR; B23879; B23879.
HSSP, O46655; 1CJH.
MGD; MGI:98943; Wap.
InterPro; IPR002221; WAP.
Pfam; PP00095; Wap; 2.
PRINTS; PR00003; 4DISULPHCORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mamm. Genome 11:767-773 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14423 MW;
                                                                                                                                                                                                                                                                                   134
72
128
116
120
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                            DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rowley
                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Strausberg R.;

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InterPro;
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SEQUENCE
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                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  -!- FUNCTION: Has growth inhibitory activity (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
-!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts in positions 166 and 173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Devinoy E., Hubert C., Schaerer E., Houdebine L.M., Kraehenbuhl J.P.; "Sequence of the rabbit whey acidic protein cDNA."; Nucleic Acids Res. 16:8180-8180(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WAP FOUR-DISULFIDE CORE DOMAIN PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99301490; PubMed=2362817;
Thepot D., Devinoy E., Fontaine M.L., Hubert C., Houdebine L.M.;
"Complete sequence of the rabbit whey acidic protein gene.";
Nucleic Acids Res. 18:3641-3641(1990).
-!- FUNCTION: COULD BE A PROTEASE INHIBITOR.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
24.3%; Score 79.5; DB 1; Length 220;
Best Local Similarity 30.4%; Pred. No. 0.056;
Matches 14; Conservative 6; Mismatches 15; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K -> R (IN REF. 1).
8098EB9379F88CBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 PVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAP.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR002221; WAP.
Pfam; PF00095; wap; 1.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF169631; AAG16647.1; -.
EMBL, AF302109; AAG15263.1; ALT_FRAME.
EMBL, BC029159; AAH29159.1; -.
Genew; HGNC:15466; WFDC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whey acidic protein precursor (WAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Mammary gland;
MEDLINE=88335562; PubMed=3419910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
96
100
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104
217
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217 2
220 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 605322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAP RABIT
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its wolfised by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠.
س
-!- TISSUE SPECIFICITY: MILK-SPECIFIC; MAJOR PROTEIN CCMPONENT OF MILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 SAAGGSCRTPIIVPTPKAGRCPWVQAPMLSQLCEELSDCANDIECRGDKKCCFSRCAMRY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 STKPGSC--PILLI-----RCAMLNPP------NRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Egg white;
Kato. I., Tominaga N.;
Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists
of two tandem domains -- one Kunitz -- one of a new family.";
Fed. Proc. 38:832-832(1979).
-!- FUNCTION: THE FUNCTION THE SECOND ONE
INHIBITS SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
-!- SIMILARITY: CONTAINS 1 WAP-TYPE DOMAIN.
-!- CAUTION: AS THE PAPER ONLY INDICATES THE SPECIES AS "RED SEA TURTLE", THE SPECIES INDICATED HERE IS THEREFORE AN INFERENCE.
PIR; A01224; TITTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caretta caretta (Loggerhead).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Testudines; Cryptodira; Chelonioidea; Cheloniidae; Caretta.

NCBI_TaxID=8467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002221; WAP.
Pfam; PF00095; wap; 2.
ProDom; PD001224; WAP.
SMART; SM00217; WAP; 2.
PROSITE; PS00317; 4 DISULFIDE CORE; 2.
Milk; Whey; Protease inhibitor; Repeat; Phosphorylation; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 78; DB 1; Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 'o',
Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WAP 1 (ATYPICAL).
WAP 2 (ATYPICAL).
PHOSPHORYLATION (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 237 PHOSPHORYLATION (PROBABLE 127 AA; 13526 MW; 59DAD5FBFD2E2087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WHEY ACIDIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
10-CTL-2001 (Rel. 40, Last annotation update)
Chelonianin (Basic protease inhibitor) (RTPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.3%; Scc. 33.3%; Pred. No. v.c. 4; Mismatches
                                                           -!- PTM: EIGHT DISULFIDE BONDS ARE PRESENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00974; 6PTI.
InterPro; IPR002223; Kunitz_BPTI.
InterPro; IPR002221; WAP.
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X52564; CAA36798.1; -. EMBL; X07943; CAA30764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
121
?37
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PIR; S12586; S12586.
HSSP; 046655; 1CJH.
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P00993;
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34 AA; 3505 MW; 8F7D0B4C162C935A CRC64;

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SEQUENCE
                                                                                                                                 FBN2_HUMAN
                                               Matches
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                                                                                                                      RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Cucurbitales, Cucurbitaceae, Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Seed;
MEDLINE=20563490; PubMed=10801322;
Hernandez J. F., Gagnon J., Chiche L., Nguyen T.M., Andrieu J.-P.,
Heitz A., Trinh T., Pham T.T.C., Le Nguyen D.;
"Squash trypsin inhibitors from Momordica cochinchinensis exhibit an
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- PTM: THIS IS A CYCLIC PEPTIDE.
-1- MASS SPECTROMETRY: MW=3480.7; MW ERR=0.3; METHOD=Electrospray.
-1- SIMILARITY: BELONGS TO THE SQUASH FAMILY OF SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atypical macrocyclic structure.";
Biochemistry 39:5722-5730(2000).
-!- FUNCTION: INHIBITS TRYPSIN; PROBABLY PARTICIPATES IN A PLANT
DEFENSE MECHANISM.
                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                     22.8%; Score 74.5; DB 1; Length 110; 34.8%; Pred. No. 0.11; ive 4; Mismatches 15; Indels 1:
                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
REACTIVE BOND (TRYPSIN).
                                                                                                                                                                                                                                                                                                          63 RPGVCP-----KTSGPGICLHGCDSDSDCKEGQKCCFDGCGYIC 101
                                                                                                                                                                                                                                   269436243813418E CRC64;
                                                                                                                                                                                                                                                                                             12 KPGSCPIILIRCAMLNPPNRCL----KDTDCPGIKKCCEGSCGMAC 53
                                                                                                                  BPTI/KUNITZ INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                   Momordica cochinchinensis (Spiny bitter cucumber).
                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
Trypsin inhibitor I (MOGTI-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REACTIVE BOND.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                         34 AA
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InterPro; IPR000737; Squash.
Pfam; PF00299; squash; 1.
PRINTS; RN00299; SQUASHINHETR.
ProDom; PD003401; Squash; 1.
SWART; SM00286; PTI; 1.
SGAINE protease inhibitor.
ACT SITE
10 11 REACTIVE BON DISULFID 8 SIMILARIT DISULFID 8 25 BY SIMILARIT DISULFID 15 27 SIMILARIT DISULFID 15 21 33 BY SIMILARIT
                                                 SMART; SM00131; KU; 1.
SMART; SM00217; WAP; 1.
SMART; SS00317; 4 DISULFIDE CORE; 1.
PROSITE; PS00280; BFT KUNITZ_1; 1.
PROSITE; PS50279; BPT KUNITZ_1; 1.
Serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                          ProDom; PD000222; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, AND MASS SPECTROMETRY.
        Pfam; PF00095; wap; 1.
PRINTS; PR00003; 4DISULPHCORE.
PRINTS; PR00759; BASICPTASE.
 PF00014; Kunitz_BPTI; 1.
                                                                                                                                                                                                                                11916 MW;
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                                                                                                                                                                                                                                                                          16; Conservative
                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                110 AA;
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                                                                                                      Serine protease
DOMAIN 8
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ACT_SITE
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                                                                                                                                                         DISULFID
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Matches
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Am. J. Med. Genet. 92:7-12(2000).
-!- FUNCTION: STRUCTURAL. COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
-!- FUNCTION: STRUCTURAL. COMPONENT OF CONTAINING MICROFIBRILS REGULATE
THAT BINDS CALCIUM. FIBRILLIN-2-CONTAINING MICROFIBRILS REGULATE
THE EARLY PROCESS OF BLASTIC FIBER ASSEMBLY.
-!- DISEASE: DEFECTS IN FBN2 ARE THE CAUSE OF CONGENITAL CONTRACTURAL
ARACHNODACTYLY (CCA) (ALSO KNOWN AS BEALS SYNDROME). CCA IS
PHENOTYPICALLY SIMILAR TO MARFAN SYNDROME, BUT DOES NOT EFFECT THE
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91304567; PubMed=1852206;
Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M., Tsipouras P., Ramirez F., Hollister D.;
"Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.";
Nature 352:330-334(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
Eukoryota; Metazona; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS CCA HIS-1114.
MEDLINE=88407789; PubMed=9737771;
Babcock D., Gasner C., Francke U., Maslen C.;
"A single mutation that results in an asp-to-his substitution and partial exon skipping in a family with congenital contractual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94165150; PubMed=8120105; Zhang H., Apfelroth S.D., Hu W., Davis E.C., Sanguineti C., Bonadio J., Mecham R.P., Ramirez F.; "Structure and expression of fibrillin-2, a novel microfibrillar component preferentially located in elastic matrices."; J. Cell Biol. 124:855-863(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putnam E.A., Zhang H., Ramirez F., Milewicz D.M.; "Fibrillin-2 (FBN2) mutations result in the Marfan-like disorder, congenital contractural arachnodactyly."; Nat. Genet. 11:456-458(1995).
                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Godfrey M.;
"Two novel fibrillin-2 mutations in congenital contractural
   Score 67; DB 1; Length 34;
Pred. No. 0.28;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS CCA TYR-1252 AND SER-1433, AND VARIANT ILE-964 MEDLINE=96083599; Pubmed=7493032;
                                                                  10;
                                                                                                                       14 GSCPILLIRCAMLNPPNRCLKDTDCPGIKKC-CEGSCG 50
                                                                                                                                                           6 GVCPKIL-----QRCRRDSDCPGACICRGNGYCG 34
                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                        PRT; 2911 AA
                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS CCA PHE-1141 AND TRP-1252.
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20.5%;
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                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibrillin 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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15-JUN-2002
                                                              16;
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32.4%;
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   Local Similarity
es 22; Conserv
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1168
1184
1203
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2613
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                                                  EMBL, U03272; AAA18950.1; -.
EMBL; X62009; -; NOT_ANNOTATED_CDS.
PIR; S17063; S17063.
FIR; S31101; S31101.
HSSP; P35555; 1EMN.
Genew; HGNC:3604; FBN2.
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Pred. No. 14;
6; Mismatches 24; Indels 1
CALCIUM-BINDING.
CALCIUM-BINDING.
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                                                                                                                                              CALCTUM-BINDING.
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SIMILARITY.
SIMILARITY.
SIMILARITY.
EGF-LIKE 36, CG
EGF-LIKE 37, CG
EGF-LIKE 37, CG
EGF-LIKE 39, CG
EGF-LIKE 40, CG
EGF-LIKE 41, CG
EGF-LIKE 41, CG
EGF-LIKE 42, CG
EGF-LIKE 44, CG
EGF-LIKE 47, C
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EPVKGPVSTKPGSCPII--LIRCAMLNPPNRCLKDTDCPGIKKCCE------GSC----

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Trypsin inhibitor III (MCoTI-III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                         NCBI_TaxID=3674;
                                                                                                                                                                                                                                                            INHIBITORS.
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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ITR2_MOMCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                              TISSUE-Salivary gland;
MEDLINE-90172404; PubMed-1689777;
MEDLINE-90172404; PubMed-1689777;
MEDLINE-90172404; PubMed-1689777;
MEDLINE-90172404; PubMed-1689777;
MEDLINE-90172404; PubMed-10811, 1.;
The Balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structure split by many introns.";
The Balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structure split by many introns.";
J. Mol. Biol. 211:331-349(1990).
THE LARVAL THE LARVAL THESE. BALBIANI RING PROTEIN 3 COULD PLAY A ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS.
TISTACCELLULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THESE FROM FORMING WATER-INSOLUBLE FIBERS TOO EARLY.
THISSUE SPECIFICITY: SALIVARY GLAND.
TISSUE SPECIFICITY: SALIVARY GLAND.
2018 ECVALPGSCSPGTCQNLEGSFRC--ICPPGYEVKSENCIDINECDEDPNICLFGSCTNTP 2075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 PNTCE---CGCAQLNCPDNKKANKETCQCECKEVKKCNGGQVFCKDSCSCVC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1700;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN 21 1700 BALBIANI RING PROTEIN 3. SEQUENCE 1700 AA; 186145 MW; 34202B28521B0815 CRC64;
                                                                                                                                                                      01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Balbiani ring protein 3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB
Pred. No. 11;
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Pfam; PF03128; CXCXC; 71.
                                                                                                                                                        01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%;
32.7%;
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                                                                                                                                                                                                                       Chironomus tentans (Midge).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 32.7 tes 17; Conservative
                                                                                                                                   STANDARD;
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                                                                 2076 GGFQCLCP 2083
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                          -GMACFVP 56
                                                                                                                                                                                                                                                                              NCBI_TaxID=7153;
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16-OCT-2001
16-OCT-2001
                                                                                                                                 BAR3 CHITE
003376;
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P82410;
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Momordica cochinchinensis (Spiny bitter cucumber).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                   TISSUE=Seed;
MEDLINE=20263490; PubMed=10801322;
MEDLINE=20263490; PubMed=10801322;
Hernandez J.-F., Gagnon J., Chiche L., Nguyen T.M., Andrieu J.-P.,
Heitz A., Trinh T., Pham T.T.C., Le Nguyen D.;
"Squash trypsin inhibitors from Momordica cochinchinensis exhibit an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Momordica cochinchinensis (Spiny bitter cucumber).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Gaps
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Heitz A., Trinh T., Pham T.T.C., Le Nguyen D.,
"Squash trypsin inhibitors from Momordica cochinchinensis exhibit an
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFENSE MECHANISM.
-!- MASS SPECTROMETRY: MW-3379.6; MW ERR-0.5; METHOD-Electrospray.
-!- SIMILARITY: BELONGS TO THE SQUASH FAMILY OF SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                 atypical macrocyclic structure.";
Biochemistry 39:5722-5730(2000).
-!- FUNCTION: INHIBITS TRYPSIN; PROBABLY PARTICIPATES IN A PLANT
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Biochemistry 39:5722-5730(2000).
-!- FUNCTION: INHIBITS TRYPSIN; PROBABLY PARTICIPATES IN A PLANT
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
DSE13476B1A9AA6E CRC64;
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Pred. No. 0.53;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Trypsin inhibitor II (MCOTI-II)
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                                                                                                                                                                                       SEQUENCE, AND MASS SPECTROMETRY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P01074; 1BXJ.
InterPro; IPR000737; Squash.
Pfam; PP00299; squash, 1.
PRINTS; PR00293; SQUASHINHBTR.
ProDom; PD003401; Squash; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 21
11 23
17 29
30 AA; 3403 MW;
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MOD_RES 1 1 1
ACT_SITE 6 7
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EGF-LIKE 31, C
EGF-LIKE 32, C
EGF-LIKE 33, C
EGF-LIKE 34, C
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EGF-LIKE 36, C
EGF-LIKE 37, C
EGF-LIKE 38, C
EGF-LIKE 39, C
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EGF-LIKE 21, C
EGF-LIKE 23, C
EGF-LIKE 23, C
EGF-LIKE 24, C
EGF-LIKE 25, C
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EGF-LIKE 27, C
EGF-LIKE 28, C
TGFBP 5.
EGF-LIKE 29, C
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TGFBP 3.
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InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR0022221; Pibril-assoc.
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Fibrillin genes map to regions of conserved mouse/human synteny on mouse chromosomes 2 and 18.";
Genomics 18:667-672(1993).
-!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
-!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=95263670; PubMed=7744963;
Zhang H., Hu W., Ramirez F.;
Zhang H., Hu W., Ramirez F.;
Chang H., Hu W., Hu W., Ramirez F.;
Chang H., Hu W., Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 210-317 FROM N.A.
MEDLINE=94140368; PubMed-8307578;
Li X., Pereira L., Zhang H., Sanguineti C., Ramirez F., Bonadio J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
        -!- MASS SPECTROMETRY: MW=3453; MW ERR=0.2; METHOD=Electrospray.
-!- SIMILARITY: BELONGS TO THE SQUASH FAMILY OF SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                   Score 64; DB 1; Length 34; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
8F7D0B4C048BB93A CRC64;
                                                                                                                                                                                                                                                                                                                                                    14 GSCPIILIRCAMLNPPNRCLKDTDCPGIKKC-CEGSCG 50
                                                                                                                                                                                                                                                                                                                                                                                      6 GVCPKIL-----KKCRRDSDCPGACICRGNGYCG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 34
FBN2 MOUSE
TD FBN2 MOUSE
AC Q6155; Q63957;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-UNV-2002 (Rel. 41, Last annotation update)
DF Fibrillin 2 precursor.
GN FBN2 OR FBN-2.
                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                         REACTIVE BOND.
                                                         HSSP, P01074; 1BXJ.
InterPro; IPR000737; Squash.
Pfam; PF00029; Squash.
PRINTS; PR00293; SQUASHINHETR.
PRONOUN; P0003401; Squash; 1.
SWART; SW00286; PTI; 1.
PROSITE; PS00286; SQUASHINHETR.
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DISULED
21 33 BY SIMILARIT
DISULED
SEQUENCE 34 AA; 3477 MW; 8F7D0B4C048BB
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InterPro; IPR000152; Asx_hydroxyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L39790; AAA74908.1; -. EMBL; S69359; AACG0685.1; -. HSSP; P35555; 1EMN.
                                                                                                                                                                                                                                                                                         19.68;
                                                                                                                                                                                                                                                                                                            Local Similarity 39.5 ses 15; Conservative
                                                                                                                                                                                                                                                                                                         Similarity
                                                INHIBITORS.
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TGFBP 7.

EGF-LIKE 41, CALCIUM-BINDING.
EGF-LIKE 43, CALCIUM-BINDING.
EGF-LIKE 44, CALCIUM-BINDING.
EGF-LIKE 44, CALCIUM-BINDING.
EGF-LIKE 46, CALCIUM-BINDING.
EGF-LIKE 46, CALCIUM-BINDING.
EGF-LIKE 47, CALCIUM-BINDING.
BY SIMILARITY.
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EGF-LIKE 5.

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EGF-LIKE 6.

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CALCIUM-BINDING.

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EGF-LIKE 13.

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EGF-LI
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	,	10070 10070 10111
	12.00.11.11.00.11.11.00.11.11.00.11.11.00.11.11	17.61 17.61

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91016864; PubMed=2216744;

Cai F., Bourbonniere M., Tang D., Hu S.L., Weber J.M.;

Cai F., Bourbonniere M., Tang D., Hu S.L., Weber J.M.;

Nuclectide and deduced amino acid sequence of the bovine adenovirus type 7 proteinase.";

Nucleic Acids Res. 18:5567-5567(1990).

-! FUNCTION: THIOL PROTEAGE CLEAVING SPECIFIC GLY-ALA PEPTIDES IN A NUMBER OF VIRAL PRECURSOR PROTEINS (TERMINAL, IIIA, VI, VII, VIII, IIA AND MU) WHICH ARE REQUIRED FOR VIRION MATURATION. ALSO CLEAVES HOST CELLS CYTOSKELETAL KERATINS K7 AND K18.

-! CATALYTIC ACTIVITY: Cleaves proteins of the adenovirus and its host cell at two consensus sites: -Yaa-Xaa-Gly-Gly-|-Xaa- and -Yaa-Xaa-Gly-Ka-|-Gly- (in which Yaa is Met, Ile or Leu, and Xaa -Yaa-Xaa-Gly-Ka-|-Gly- (in which Yaa is Met, Ile or Leu, and Xaa
                                                                                                                                                                                                   2012 ECVALPGSCSPGTCQNLEGSFRC--ICPPGYEVRSENCIDINECDEDPNICLFGSCTNTP 2069
                                                                                                                                                           24; Indels 16; Gaps
                                                                                                                                                                                    3 EPVKGPVSTKPGSCPII--LIRCAMLNPPNRCLKDTDCPGIKKCCE-----GSC---- 49
                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Bovine adenovirus type 7 (Mastadenovirus bos7).
Viruses; dsDMa viruses, no RNA stage; Adenoviruse, Atadenovirus.
                                                                                                                                  Length 2907;
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY C5.
                                                                                                                                  DB 1;
                                                                                                                                                        7; Mismatches
                                     SIMILARITY.
SIMILARITY.
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            SIMILARITY. SIMILARITY.
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Pred. No. 29;
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30.9%;
                                                                                                                                                           21; Conservative
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1549
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1551
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1689
1696
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DISULFID
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ADEN_ADEB7
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MEDLINE=99252212; PubMed=10233982;
Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
Lintracisternal type A particle-mediated activation of the Notch4/int3
gene in a mouse mammary tumor: generation of truncated Notch4/int3
mRNAs by retroviral splicing events.";
J. Virol. 73:5166-5171(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Lung, and Testis;
MEDLINE-96281668; PubMed-8681805;
Uyttendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
UNotch4/int-3, a mammary proto-oncogene, is an endothelial
Cell-specific mammalian Notch gene.";
Development 122:2251-2259(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Rower D., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S., Rower L., Mahairas G., Qin S., Traicoff R., Zackrone K., Hood L., "Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Uyttendaele H., Ho J., Rossant J., Kitajewski J., "Vascular patterning defects associated with expression of activated Notch4 in embryonic endothelium.";
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97294599; PubMed=9150355;
Gallahan D., Callahan R.;
The mouse mammary tumor associated gene INT3 is a unique member of the NOTCH gene family (NOTCH4).";
Oncogene 14:1883-1890(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robbins J., Blondel B.J., Gallahan D., Callahan R.; "Mouse mammary tumor gene int 3: a member of the notch gene family transforms mammary epithelial cells."; J. Virol. 66:2594-2599 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                    NTC4 MOUSE STANDARD; PRT; 1964 AA.
P31695; Q62389; Q62390; O35442; Q9R1W9; O88314; O88316; Q9R1X0;
O1-JUL-1993 (Rel. 26, Created)
O1-MUV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
                                                 1;
19.1%; Score 62.5; DB 1; Length 202; 34.3%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21523956; PubMed=11518718;
Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
"Murine notch homologs (N1-4) undergo presenilin-dependent
                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
                                                                                                                                   92 LIKRSALSSPDKĊVKVIKNSQSVQCTĆAGSĆGLFC 126
                                                                                          20 LIRCAMLNPPNRCLK-DTDCPGIKKCCEGSCGMAC 53
                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21244657; PubMed=11344305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS, SEQUENCE FROM N.A
Query Match
Best Local Similarity 34.39
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                          embryonic development from 9.0 d.p.c.

PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a Cterminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNR-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called onch extracellular truncation (NEXT). This fragment is then cleaved by presentlin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: Phosphorylated.

DISBASE: Loss of the extracellular domain causes constitutive activation of the Notch protein, which leads to hyperproliferation of glandular epithelial tissues and development of mammary
                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart kidney, and at lower levels in the ovary and skeletal muscle. A very low expression is seen in the brain, intestine, liver and
                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcinomas.
--- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
--- SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
--- SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AB016771; BAA32281.1; ALT SEQ. AB016772; BAA32283.1; ALT_INIT. AB016773; BAA32284.1; ALT_INIT.
             Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002110; ANK.
InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR000561; BGF-like.
InterPro; IPR000742; BGF-2.
InterPro; IPR001881; BGF_Ca.
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                                                POST-TRANSLATIONAL PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M80456; AAB38377.1; -.
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U43691; AAC52631.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the membrane
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 proteolysis.";
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EGF-LIKE 20.
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(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                       NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4.
TRANSFORMING PROTEIN INT-3.
NOTCH EXTRACELLULAR TRUNCATION.
NOTCH INTRACELLULAR DOMAIN.
                                                                                                                                                    PROSITE; PS50081, ANK REPEAT; S.
PROSITE; PS50081, ANK REP REGION; 1.
PROSITE; PS00101, ANZ HYDROXYL; 11.
PROSITE; PS00118; EGF 12.
PROSITE; PS01186; EGF 2; 21.
PROSITE; PS01187; EGF CA; 9.
PROSITE; PS01187; EGF CA; 9.
PROSITE; PS01187; EGF CA; 9.
Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-11ke domain; Transcription regulation; Signal; Phosphorylation; Proto-oncogene.
                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIN/NOTCH 1.
LIN/NOTCH 2.
LIN/NOTCH 3.
ANK 1.
ANK 2.
ANK 3.
ANK 4.
                                                                                        PRINTS; PR01452; NOTCH.
SWART; SM00248; ANK; 5.
SMART; SM00179; EGF_CA; 11.
SWART; SM00001; EGF_Like; 15.
SWART; SM00004; NL; 2.
InterPro; IPR001438; EGF II.
InterPro; IPR000800; Notch.
                        Pfam; PF00008; EGF; 27.
Pfam; PF00008; ank; 6.
Pfam; PF00066; notch; 2.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.1%;
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1964
1443
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622
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686
724
762
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                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: HOMODIMER.
-!- INDUCTION: BY CADMIUM.
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                MYZA_MYTED STANDARD; PRT; 71 AA.

902635; Q09031;
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 41, Last annotation update)
15-UNW-2002 (Rel. 41, Last annotation update)
Metallothionein 20-III isoform A (MT-20-IIIA) (MT-I).

Mytilus edulis (Blue mussel), and
Mytilus galloprovincialis (Mediterranean mussel).

Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytillidae; Mytiloida;
MCBI_TaxID=6550, 29158;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94062828; PubMed=8243461;
Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
Kaegi J.H.R., Fothergill J.E.;
"Complete amino acid sequences of five dimeric and four monomeric
forms of metallothionein from the edible mussel Mytilus edulis.";
Eur. J. Biochem. 218:183-194(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 galloprovincialis.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
SEQUESTRATION OF TOXIC METAL IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ceratto N., Dondero F., Burlando B., Van de Loo J.W.H.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.0%; Score 62; DB 1; Length 71; 39.0%; Pred. No. 1.8; arive 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 0 BY SIMILARITY.
71 AA; 6899 MW; D4BFD9E599857657 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Metallothionein genomic DNA of the mussel Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PGPCNCI ------ETNVCICGTGCSG--KCCQ--CGDAC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate cluster; Cadmium.
INIT MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S39422; S39422.
InterPro; IPR003019; Metallthion.
InterPro; IPR001008; Mtllthion_mlsc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF199020; AAG28538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.galloprovincialis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00131; metalthio; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                    1152 ĠPQĆTCP 1158
                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=M.edulis;
  50 GMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viarengo A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MT2B MYTED
ID MT2B MYTED
AC P80258;
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Conservative
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                                                                                                                                                                                                                                                  Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7740;
                                                                                                                                                                                                                                                                                                                                                                                                         LPR BRALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amphioxus.
                                                                                                                                                                                                                                       Query Match
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VIROLOGY 200:400-408 (1995).

-!- FUNCTION: THIOL PROTEASE CLEAVING SPECIFIC GLY-ALA PEPTIDES IN A

-!- FUNCTION: THIOL PROTEASE CLEAVING SPECIFIC GLY-ALA PEPTIDES IN A

-!- FUNCTION: THIOL PRECURSOR PROTEINS (TERMINAL, IIIA, VI, VII, VIII,

NUMBER OF VIRAL PRECURSOR PROTEINS (TERMINAL, IIIA, VI, VII, VIII,

--- IIA AND MU) WHICH ARE REQUIRED FOR VIRION MATURATION. ALSO CLEAVES

--- GLLS CYTOSKELETAL KERATINS K7 AND K18.

--- CATALYTIC ACTIVITY: Cleaves proteins of the adenovirus and its

--- host cell at two consensus sites: -Yaa-Xaa-Gly-Gly-|-Xaa- and

--- Yaa-Xaa-Gly-Xaa-|-Gly- (in which Yaa is Met, Ile or Leu, and Xaa
                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vrati S., Boyle D., Kocherhans R., Both G.W.; "Sequence of ovine adenovirus homologs for 100K hexon assembly, 33K, pVIII, and fiber genes: early region E3 is not in the expected
                                                                                                                                                MEDLINE=94062828; PubMed=8243463;
Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
Mackay E.A., Fothergill J. B.;
"Regij J.H.R., Fothergill J.E.;
"Complete amino acid sequences of five dimeric and four monomeric
forms of metallothionein from the edible mussel Mytilus edulis.";
forms of metallothionein from the edible mussel Mytilus edulis.";
Li- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
SEQUESTRATION OF TOXIC METAL IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viruses, no RNA stage; Adenoviridae; Atadenovirus.
                                                                       Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenain (EC 3.4.22.39) (Endoprotease) (Late L3 23 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%; Score 62; DB 1; Length 71; 39.0%; Pred. No. 1.8; tive 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                   pfam; PF00131; metalthio; 1. —
PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate cluster; Cadmium.
SEQUENCE 71 AA; 6873 MW; D4BFD9FFB08577E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 PGPCNCI.----ETNVCICGTGCSG--KCCQ--CGDAC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is any amino acid).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C5.
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-101-thionein 20-111 isoform B (MT-20-IIIB)
Mytilus edulis (Blue mussel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 AA
                                                                                                                                                                                                                                                                                                                     PIR; $39422; $39422.
InterPro; IPR003019; Metallthion.
InterPro; IPR001008; Mtllthion_mlsc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95297141; PubMed=7778275;
                                                                                             Mytiloidea; Mytilidae; Mytilus.

    -!- INDUCTION: BY CADMIUM.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovine adenovirus type 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                          -!- SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=114430;
                                                                                                           NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=OAV287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                         SEQUENCE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
11s-UNN-2002 (Rel. 41, Last annotation update)
11s-UNN-2004 (Rel. 41, Last annotation update)
11s-UNN-2004 (Rel. 41, Last annotation (Rel. 41, Last annotation update)
11s-UNN-2004 (Rel. 41, Last annotation update)
11s-UNN-2005 (Rel. 41, Last annotation update)
11s-UNN-2005 (Rel. 41, Last annotation update)
11s-UNN-2006 (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine phosphate.

-!- SUBDANT: PROBABLE TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BOANS. THE ALPHA CHAINS CONTRIBUTE TO THE PORMATION OF THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN (BY SIMILARRIY).

-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
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-!- FUNCTION: THIS RECEPTOR BINDS TO THE INSULIN RELATED PEPTIDE AND HAS A TYROSINE-PROTEIN KIRAGE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                            HSRD.
HSRD.
HSRD.
HSROPS, COS.001; -. Peptlua...
InterPro; IPR000855; Peptluase CS; I.
AR PRINTS; PR0770; Peptidase CS; I.
AR PRINTS; PR0770; Peptidase CS; I.
BR ProDom; PD003705; Peptidase CS; I.
Ar SITE SS SS
BY SIMILARITY.
TO BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 LIKRSALNNSDRCITVERNTQSVQCTCAGSCGLFC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 LIRCAMLNPPNRCLK-DTDCPGIKKCCEGSCGMAC 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.8%; Score 61.5; 34.3%; Pred. No. 4.
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Interpro; IPR000719; EMk_Dkinase.
Interpro; IPR003961; FN III.
Interpro; IPR003962; FNIII_repeat.
Interpro; IPR002104; FNIII_Like.
Interpro; IPR002101; FNIIII_Like.
Interpro; IPR001245; Tyr_pkinaseII.
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HSSP; P06213; 1IRK.
                                                                                                                                                                                                                                       EMBL; U40839; AAA84980.1; -.
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Pfam; Fruuval; fn3; 3.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF000757; Furin-like; 1.

DR Pfam; PF001030; Recep_L_domain; 2.

DR PRINTS; PR00109; TYRKINASE.

DR PRODOM; PD0000001; Euk pkinase; 1.

DR SMART; SM00261; FU; 1.

SMART; SM00219; TYRKC; 1.

R SMART; SM00219; TYRKC; 1.

R SMART; SM00219; TYRKC; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00101; PROTEIN KINASE TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INSULIN-LIKE PEPTIDE RECEPTOR, ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 GSCPIILIRCAMLNPPN-----RCLKDTDCPGI-----KKC------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSULIN-LIKE PEPTIDE RECEPTOR, BETA
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(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            013403, 015854;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Trefoil factor 2 precursor (Spasmolytic polypeptide) (SP).
TPF2 OR SML1.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
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PHOSPHORYLATION (AUTO-) (B PLINKED (GLCNAC...) (PC N-LINKED (GLCNAC...) (PC N-LI
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Pred. No. 23
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1363 AA;
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TFF2_HUMAN
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: STOMACH.
-!- SIMILARITY: CONTAINS 2 P-TYPE (TREFOIL) DOMAINS.
-!- DATABASE: NAME=ALIAS Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infoblogen.fr/services/chromcancer/Genes/TFF2ID264.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                Tomasetto C., Rio M.C., Gautier C., Wolf C., Hareuveni M., Chambon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFNB10 locus using 34 novel microsatellite markers, genomic structure,
                                                                                                                  "hSP, the domain-duplicated homolog of pS2 protein, is co-expressed with pS2 in stomach but not in breast carcinoma."; EMBO J. 9:407-414(1990).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=20408883; PubMed=10950923;

MEDLINE=20408883; PubMed=10950923;

Metronhofer M., Guipponia M., Barras C., Rossier C., Shibuya K.,

Wattenhofer M., Guipponia M., Barras C., Rossier C., Shimizu N.,

Wang J., Kawasaki K., Asakawa S., Minoshima S., Shimizu N.,

Antonarakis S., Bonne-Tamir B.,

"Refined localization of autosomal recessive nonsyndromic deafness
"Refined localization of autosomal recessive nonsyndromic deafness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: INFIBITS GASTROINTESTINAL MOTILITY AND GASTRIC ACID
SECRETION: COULD FUNCTION AS A STRUCTURAL COMPONENT OF GASTRIC
MUCUS, POSSIBLY BY STABILIZING GLYCOPROTEINS IN THE MUCUS GEL
THROUGH INTERACTIONS WITH CARBOHYDRATE SIDE CHAINS (BY
SIMILARITY).
                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-27224512; PubMed=9070946;
Seib T., Blin N., Hilgert K., Seifert M., Theisinger B., Engel M., Dooley S., Zang K.D., Welter C.;
The three human trefoil genes TFF1, TFF2, and TFF3 are located within a region of 55 k on chromosome 21q22.3.";
Genomics 40:200-202(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and exclusion of six known genes in the region."; Genomics 68:22-29(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
TREFOIL FACTOR 2.
P-TYPE 1.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                  MEDLINE=90151615; PubMed=2303034;
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EMBL, U47291; AABOS397.1; JOINED.
EMBL, AB038162; BAB13730.1; -.
EMBL, S12371, S12371.
HSSP, P01359, 1PCP.
Genew; HGNC:11756; TFF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, X51698, CAA35995.1; -.
EMBL, U47292, AAB05397.1; -.
EMBL, U47289; AAB05397.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000519; P trefoil.
Pfam, PF00088; trefoil; 2.
PRINTS; PR00680; PTREFOIL.
SMART; SM00018; P; 2.
PROSITE; PS00025; P_TREFOIL; 2.
NCBI_TaxID=9606;
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                                                                                                    Lathe R.;
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DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=94150718; PubMed=7906398; MEDIINE=94150718; PubMed=7906398; Milson R., Ainscough R., Anderson K., Baynes C., Berks M., Milson B., Ainscough R., Anderson K., Copner J., Cooper J., Durkin R., Favello A., Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Liatreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Simston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Wateston R., Wateston R., Wainstock L., Wilkinson-Sproat J.,
BY SIMILARITY.

BY SIMILARITY.

MGRRDAQLIAALLYUGLCA -> RHGTARRPAPGSAPRPGA

MC (IN REF. 1).

K -> N (IN REF. 1).
                                                                                                                                                                                                         Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.2~\mathrm{Mb} of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durbin R.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; a (shown here) and b; may be produced by alternative splicing.
-!- SIMILARITY: TO CHITIN-BINDING MOTIFS.
                                                                                                                                                                                                         16;
                                                                                                                                                          Score 61; DB 1; Length 129; Pred. No. 3.7;
                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                      10 STKPGSCPIILIRCAMINPPNRCLKDTDC--PGI--KKCCEGSCGMACF 54
                                                                                                                                                                                                                                                                                               23 SEKPSPC----QCSRLSPHNR----INCGFPGITSDQCFDNGC---CF 59
                                                                                                               6A296A11AD9CCC5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               194504; P34505; P34506; P90907; P31504; P31504
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1246 AA.
                                                                                                                                                                                                            6; Mismatches
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WormPep; K04H4.2b; CE19968.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR002899; WR1/EB.
                                                                                                                    129 AA; 14284 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z27078; CAA81587.1; -. EMBL; Z27078; CAA81588.1; -.
                                                                                                                                                                 18.7%;
                                                                                                                                                                                 36.7%;
                                                                                                                                                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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118
19
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PIR; S40993; S40993.
PIR; S40994; S40994.
HSSP; P10968; 2CWG.
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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    DISULFID
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                                                 CONFLICT
                                                                                            CONFLICT
                                                                                                                    SEQUENCE
                                                                                                                                                            Query Match
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STQRCDLHTLCPPDFTCSLSGACKCKININCPGDGTVPETSCQ
SASHUDHCPSSSHKCTLLNKEHFACCYSPGLVVBGGVTAEV
SSECPIGGSVEVDPRFGTSCRYSLQCPSPYFCNQRGQ -> 0
                                                                                                                                                                                                                                                                                  DSDINSTINPSQPETIKIKNNYKKSNSSKKHRKPKKKDVDP
LSDPLLQNDFPIGPPGYGFPEHLSNLDEVLIRAQGDGECPA
GLHCDTAINLCCPLLLPLTDPKNPKKRKTERRKQKQDGNEM
                                                                              ANCTSDEDCPTTFKCYQGCCKLAVCPRSLTAVKFTCKTQYH
CRANEHCFFGGCCPKTIBLAVIKSQVLTMSKDNEHTKETEK
LIIGDCEVDTRVKKCDIDIICPEMSECVDGICCKQPPKARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
11-Ypin inhibitor I (MCTI-I).
Momordica charantia (Bitter gourd) (Balsam pear).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                              ITPTPTRTTEPPKLRCLSSNTDEVNSLGGASSSSATCGGTN
                                                                                                                                                   GNGLMALSIPVHCSLSDDCPIASRCEYGKCCPFLSESADST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hara S., Makino J., Ikenaka T.; "Amino acid sequences and disulfide bridges of serine proteinase inhibitors from bitter gourd (Momordica charantia LINN.) seeds."; J. Biochem. 105:88-92(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                     EASANFPDSDPARFSSYSCGCMG -> VG (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61; DB 1; Length 1246;
Pred. No. 24;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 1; Length 30;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                               1246 AA; 130610 MW; 4FA1A17D3F9606C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D5E1344365E34E9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 CPIILIRCAMLNPPNRCLKDTDCPGIKKC-CEGSCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REACTIVE BOND.
                                                                                                                                                                                                                                                                  (IN ISOFORM B)
SWART; SM00494; ChtBD2; 1.
SWART; SM00289; WR1; 14.
Hypothetical protein; Alternative splicing.
VARSPDIC 166 529 ITPTPTRTTEPPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JX0057; JX0057.
HSSP, P01074; IBXJ.
InterPro; IPR000737; Squash.
Pfam; PF00299; squash; 1.
PRINTS; PR00293; SQUASHINHBTR.
PRODOM; PD003401; Squash; 1.
PROSITE; PS00286; PTI; 1.
PROSITE; PS00286; SQUASH_INHBITOR; 1.
                                                                                                                                                                                                                                                                                                                                                                               ISOFORM B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=89291812; PubMed=2738047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 CTSDEDCPTTFKCYQGCCKLA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%;
38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           18.7%;
47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3413 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 CLKDTDCPGIKKCCEGSCGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=seed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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P10294;
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ITR1 MOMCH
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RESULT 46
ZAN MOUSE
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-!- INDUCTION: BY CADMIUM.
-!- SIMILARITY: BELONG TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
PIR; S39420; S39420.
InterPro; IPR003019; Metallthion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Digestive gland;
MEDLINE-99206055; PubMed=10190057;
MAEDLINE-99206055, PubMed=100057;
MAEDLINE-99206055, White K.N., Lovejoy D.A.;
"Cloning and characterization of metallothionein cDNAs in the mussel Mytilus edulis L. digestive gland.";
                                                                                                                                                                                                  MEDLINE=94062828; PubMed=8243463; Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E., Kaegi J.H.R., Fothergill J. D.E.; "Complete amino acid sequences of five dimeric and four monomeric forms of metallothionein from the edible mussel Mytilus edulis."; Eur. J. Blochem. 218:183-194(1993).

-i- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR SEQUESTRATION OF TOXIC METAL IONS.
                                                                 P80251; P80257;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metallochionein 20-1 isoforms A and B (MT-20-IA and MT-20-IB).
Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida; Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete amino acid sequences of five dimeric and four monomeric forms of metallothionein from the edible mussel Mytilus edulis."; Eur. J. Biochem. 218:183-194(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94062828; PubMed=8243463;
Mackay E.A., Overnell J., Dunbar B., Davidson I., Hunziker P.E.,
Kaegi J.H.R., Fothergill J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            66 66 S -> A (IN MT-20-IB).
71 AA; 6944 MW; 4FD275FE34E81654 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PGPCNCI------BTNVCICGTGCSG--KCCR--CGDAC 29
                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00131; metalthio; 1.
PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate cluster; Cadmium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metallothionein 20-II (MT-20-II)
Mytilus edulis (Blue mussel)
4 CPRIL-----KQCKRDSDCPGECICMAHGFCG 30
                                                            71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.3%; Score 60; DB 139.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                      Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 39.0° tes 16; Conservative
                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                   -:- SUBUNIT: HOMODIMER
                                                         MT21 MYTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYTED
                                                                                                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                              MT21 MYTED
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Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                -!- INDUCTION: BY CADMIUM.
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD.
-i- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
-i- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE ZONA PELLUCIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Species diversity in the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Diochem. Physiol. 122C:287-296(1999).
FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR SEQUESTRATION OF TOXIC METAL IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.3%; Score 60; DB 1; Length 71; 39.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 AA; 6887 MW; 4FD275FE39857654 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PGPCNCI-----ETNVCICGTGCSG--KCCR--CGDAC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00131; metalthio; 1.
PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate cluster; Cadmium.
1N1T_MET 0 0 0 0 0 SEQUENCE 71 AA, 6887 MW; 4FD275FE39857654 C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAN MOUSE STANDARD, PRT, 5376 AA. 088799; O08647, 16-072-2001 (Rel. 40, Last sequence update) 16-071-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S39421; S39421.
InterPro; IPR003019; Metallthion.
InterPro; IPR001008; Mtllthion_mlsc.
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MEDLINE=98123114; PubMed=9452463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97271566; PubMed=9126492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 4864-5376 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ005456; CAA06553.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                             -!- SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gao Z., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zonadhesin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE OF 2-75 FROM N.A.
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                 DOMAIN
                            DOMAIN
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                                                                                                                                                                                                                                      DR PEAM; PRO0094; vwr_U.

DR PEAM; PRO10949; vwd; 4.

PEAM; PRO10959; NAM; 3.

PEAM; PRO12445; TIL1; 25.

DR PEAM; PRO12445; TIL1; 25.

DR PEAM; PRO12445; TIL1; 25.

DR SWART; SM00174; POLN; 11.

DR SWART; SM00174; VWC; 17.

DR SWART; SM00116; VWC; 17.

DR SWART; SM00116; VWC; 17.

DR PROSITE; PS00102; EGF_1; 1.

DR PROSITE; PS001040; WAM 1; FALSE_NEG.

DR PROSITE; PS00040; MAM 1; FALSE_NEG.

DR PROSITE; PS00060; MAM 1; FALSE_NEG.

DR PROSITE; PS00060; MAM 2; 3.

DR PROSITE; PS00060; MAM 2; 3.

DR PROSITE; PS00060; MAM 2; 3.

DR PROSITE; PS00060; MAM 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (MUCIN-LIKE DOMAIN).
DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS. DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2). SIMILARITY: CONTAINS 3 MAM DOMAINS. SIMILARITY: CONTAINS 25 VWFD DOMAINS. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                        ZONADHESIN.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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InterPro; IPR000561; EGF-like.
InterPro; IPR0005698; MAM domain.
InterPro; IPR002919; TIL Cysrich.
InterPro; IPR00319; TIL Cysrich.
InterPro; IPR003107; VWF_D.
InterPro; IPR001107; VWF_D.
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Bukaryota; Metazoa, Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Eisenia.
NCBI_TAXID=6396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-41.

Gruber C., Dallinger R., Hunziker P., Gehrig P., Berger B.,
Stuerzenbaum S.,
"(cd)-metallothionein from Eisenia foetida: evidence for
posttranalational processing to a functional one-domain protein.";
Submitted (FEB-1999) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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(POTENTIAL)
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39.0%; Pred. No. 1e+02;
tive 1; Mismatches 12; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 CAMLNPPN----RCLKDTDCPG-----IKKCCEGSCGMAC 53
VWFD 25. (PARTIAL).
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                                                                                                                                                                                                                                                                                                        (GLCNAC.
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                                                                 EGF-LIKE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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les 16; Conservative
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NCBI TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                        521 -CFKP 524
                                                                                                                                                                                                                                                                                                      52 ACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (hNotch4).
                                                                                                                                                                                                                                                                                                                                                                                                                         NTC4 HUMAN
                                                                                                                                         SEQUENCE
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NTC4_HUMAN
                                                                                                                                                                                                          Matches
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
Sturzenbaum S.R., Guppy L., Morgan A.J., Kille P., "Metallothionein isolated from the common brandling worm Eisenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                              SUBMITTED (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 59.5; DB 1; Length 75; 51.9%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical zinc metalloproteinase T04G9.2 (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   FDE2C30BA606494B CRC64;
                                                                                              -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: POSTERIOR ALIMENTARY CANAL.
-!- INDUCTION: BY CADMIUM.
                                                                                                                                                                                                                                                                                              EMBL, AJ236886, CAA15423.1; -.
InterPro, IPR001396, Echnd Metthion4.
PRINTS, PR00873; MTECHINOIDEA.
Metal-binding; Metal-thiolate cluster; Cadmium.
                                                                                                                                                                                                                                                                                                                                                                                   A -> Q (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; M12.UPA; -.
MORMPED; T04G9.2; CE04883.
InterPro; IPR001506; Astacin.
InterPro; IPR001589; Prenyl site.
InterPro; IPR00139; Shrr.
InterPro; IPR000130; Zn MTpeptdse.
Pfam; PF01400; Astacin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 RCLKDTDCPGIKK-CC----EGSCGMA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 RCLKSECLPGCKKLCCADAEKGKCGNA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 75 AA; 7411 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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CONFLICT
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                                   foetida.
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463 ÖKPVTQPIQPLPPVPPLPPTTPEDCEDLRVDCLVLVSQRYCKISQNF--MKSYCAKSCGF 520
                                                                                                                                                                                                                                                                 18.2%; Score 59.5; DB 1; Length 621; 27.7%; Pred. No. 20; Live 7; Mismatches 27; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gray G.E., Mann R.S., Mittaiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
"Human ligands of the Notch receptor.";
Am. J. Pathol. 154:785-794(199)
-!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jaggedl. Jagged2 and Deltal to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and
                                                                                                                                                                                                                                                                                                                                                         2 QEPVKGPVS-----TKPGSCPIILIRCAMINPPNRCLKDTDCPGIKKCCEGSCGM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T., Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.; Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3."; Gene 189:235-244(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
SMART; SM00254; ShKT; 3.

SMART; SM00235; ZnMc; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

Hypothetical protein; Hydrolase; Metalloprotease; Zinc.

Hypothetical protein; Hydrolase; Metalloprotease; Zinc.

ZINC (CATALYTIC) (BY SIMILARITY).

SF BY SIMILARITY.

("ATALYTY: "PV SIMILARITY).
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Miyagawa T., Tokunaga K., Hojho H.;
"Human notch4 gene variant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             099466; 000306; 099940; 099458; 094388; 09UI19; 09UIJ0; 15-UNW-2002 (Rel. 41, Last sequence update) 15-UNN-2002 (Rel. 41, Last annotation update) Neurogenic locus notch homolog protein 4 precursor (Notch 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow, and Heart;
MEDLINE=288360031; PubMed=9693032;
Li L., Huang G, M., Banta A.B., Deng Y., Smith T., Dong P.,
Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood
Scaloning, characterization, and the complete 56.8-kilobase
sequence of the human NOTCH4 gene.";
Genomics 51:45-58(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                       621 AA; 68584 MW; A98D3721C8ADE489 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 2003 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10079256;
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                                                                                                                                                                                                                                                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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PROSITE; PS00010; ASX HYDRCAIL, --
PROSITE; PS00022; EGF_1; 28.
R PROSITE; PS01186; EGF_2; 21.
R PROSITE; PS01187; EGF_2; 21.
R PROSITE; PS01187; REPORT; ANK repeat; EGF-like domain;
RM Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
RM Triplet repeat expansion; Alternative splicing.
F SIGNAL 24 2003 NOTCH PROTEIN HOMOLOG 4.
TOTAL 25 2003 NOTCH PROTEIN HOMOLOG 4.
                                                                                                                                                                                                                                                                                                                                               EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 6.
EGF-LIKE 6.
EGF-LIKE 7.
EGF-LIKE 7.
EGF-LIKE 9.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9.
CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 10.
EGF-LIKE 11.
EGF-LIKE 12.
EGF-LIKE 12.
EGF-LIKE 13.
EGF-LIKE 14.
EGF-LIKE 14.
EGF-LIKE 15.
EGF-LIKE 16.
EGF-LIKE 17.
EGF-LIKE 17.
EGF-LIKE 18.
EGF-LIKE 18.
EGF-LIKE 18.
EGF-LIKE 19.
EGF-LIKE 19.
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SMART; SM00179; EGF_CA; 42.
SMART; SM00019; EGF_Ilke; 4.
PROSITE; PS000010; ASX. HYDROXYL; 43.
PROSITE; PS01026; EGF_1; 2.
PROSITE; PS01186; EGF_2; 38.
PROSITE; PS01187; EGF_CA; 43.
Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain; Repeat; Signal; Multigene family.
SIGNAL.
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                         1105 SPKPGFPP----RCACLSGYGGPDCLTPPAPKGCGPPSPCIVNGSCSETTGLGGPGFRCS 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CD-1; TISSUE=Kidney;

STRAIN-CD-1; TISSUE=Kidney;

OCA K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;

SUBMITCEG (ARR-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS

THAT BINDS CALCIUM. FIBRILLIN-IO-CONTAINING MICROFIBRILS PROVIDE

LONG-TERM FORKE BRARING STRUCTURAL, SUPPORT.

FIBRILLIN-I MOLECULES OR WITH OTHER COMPONENTS OF THE

MICROFIBRILS (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 47 EGF-LIKE DOMAINS.

-!- SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROFEIN DOMAINS.
                                                                                                                                                                      ----- 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-95130561; PubMed=7829516;

MIN W., Germiller J., Sanguineti C., Smiley E., Pangilinan T.,

Pereira L., Ramirez F., Bonadio J.;

"Primary structure and developmental expression of Fbn-1, the mouse
fibrillin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                           DB 1; Length 2003;
                                                                                                                                       Indels
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                                                                                                      Score 59.5; DB
Pred. No. 51;
5; Mismatches
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InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF Ca.
InterPro; IPR002212; Fibril-assoc.
Pfam; PP00008; EGF; 46.
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EMBL, U22493; AAA4217.1; -.
HSSP, P35555; IAPU.
MGD; MGI:95489; Fbn1.
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Conservative
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MBDLINE=93300909; PubMed=7686164;
MBDLINE=93300909; PubMed=7686164;
Bristow J., Tee M.K., Gitelman S.E., Mellon S.H., Miller W.L.;
"Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene overlapping P450c21B.";
J. Cell Biol. 122:265-278(1993).
                                                                                                                                                              1976 ECVLDPGKCAPGTCQNLDGSYRC--ICPPGYSLQNDKCEDIDECVEPPICALGTCSNTE 2033
                                                                                                     Gaps
                                                                                                                                      3 EPVKGPVSTKPGSCPII--LIRCAMLNPPNRCLKDTDCPGIKKCCE-----GSC---- 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Assembly of Baskin D., Faust J., Loretz C., Ahearn M.E., Banta A., Schwartzell S., Smith T.M., Spies T., Hood L.; Sequence determination of 300 kilobases of the human class III MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Feetal adrenal gland;
MEDLINE=97081760; PubMed=8923003;
Speek M., Barry F., Miller W.L.;
Alternate promoters and alternate splicing of human tenascin-X, a gene with 5' and 3' ends buried in other genes.";
Hum. Mol. Genet. 5:1749-1758(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schalkwijk J., Zweers M.C., Steijlen P.M., Dean W.B., Taylor G.,
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MEDLINE=96015044; PubMed=8530023;
Tee M.K., Thomson A.A., Bristow J., Miller W.L.;
Tee M.K., Thomson A.A., Bristow J., Miller W.L.;
Sequences promoting the transcription of the human XA gene
overlapping P450c21A correctly predict the presence of a novel,
adrenal-specific, truncated form of tenascin-X.";
Genomics 28:171-178(1995).
                                                                                                     26; Indels 16;
                                                               18.0%; Score 59; DB 1; Length 2871; 27.5%; Pred. No. 78; tive 8; Mismatches 26; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           TENX HUMAN STANDARD; PRT; 4289 AA. p22105; PT8230; PT8210; PT8210; PT821; 0.08424; Q9UMG7; 01-MUG-1991 (Rel. 19, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-UM-2002 (Rel. 41, Last annotation update) Tenascin-X precursor (TN-X) (Hexabrachion-like). TNX OR XB OR HXBL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00022; EGF 1; 18.
PROSITE; PS0116; EGF 2; 19.
PROSITE; PS0116; EGF 2; 19.
Glycoprotein; Cell adhesion; Repeat; EGF-like domain; Coiled coil; Extracellular matrix; Alternative splicing; Signal;
                                                                                                                                                                                                    SIMILARITY: CONTAINS 19 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 32 FIBROMSETIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
SIMILARITY: THERE ARE TWO GENES FOR TN-X: TNXA AND THXE. THE ARE PWO GENES FOR TN-X: TNXA AND THXE. TNXA IS
PARTIAL GENE WHICH CAN SOMETIMES RECOMBINE WITH TNXB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
TENASCIN-X.
EGF-LIKE 1 (INCOMPLETE).
EGF-LIKE 2.
EGF-LIKE 4.
EGF-LIKE 5.
EGF-LIKE 5.
                                                                                                                                                                                                                                                                                                                                      EMBL, U89337; AAB47488...

EMBL, AF019413; AAB67981.1; ---

EMBL, X13782; CAAA7100.1; ---

EMBL, V13782; CAAA7100.1; ---

EMBL, U2488; AAB41287.1; ---

EMBL, U2488; AAA41287.1; ---

EMBL, U25696; AAA450889.1; ---

EMBL, M25813; AAA35884.1; ---

EMBL, M25813; AAA3588.1; ---

EMBL, M25813; EMPLOGED, EMP
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SIGNAL 1 23
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DISULFID
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                                         4
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Stomach, and Pancreas;
MEDLINE=90151615; PubMed=2303034;
Tomasetto C., Rio M.C., Gautier C., Wolf C., Hareuveni M., Chambon P.,
                                                                                         681 EEP---PASACPGGCGPRELCRAGQCVCVEGFRGPDCAIQTCPG-----DCRGRGECHD 731
                                         Gaps
                                                                2 QEPVKGPVSTKPGSC-PILLIR------CAMLNPPNRCLKDTDCPGIKKCCE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                     "hSP, the domain-duplicated homolog of pS2 protein, is co-expressed with pS2 in stomach but not in breast carcinoma."; EMBO J. 9:407-414(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taupin D., Bei H., Hocker M., Wang T., Podolsky D.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INHIBITS GASTROINTESTINAL MOTILITY AND GASTRIC ACID
SECRETION. COULD FUNCTION AS A STRUCTURAL COMPONENT OF GASTRIC
MUCUS, POSSIBLY BY STABILIZING GLYCOROTEINS IN THE MUCUS GEL
THROUGH INTERACTIONS WITH CARBOHYDRATE SIDE CHAINS (BY
                                                                                                                                                                                                                                                                                                                                   Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                         24;
            18.0%; Score 59; DB 1; Length 4289; 31.7%; Pred. No. 1.1e+02; ive 4; Mismatches 15; Indels 2
                                                                                                                                                                                                            TFF2 MOUSE STANDARD; PRT; 129 AA. 003404; 008913; 01-0CT-1994 (Rel. 30, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-UNN-2002 (Rel. 41, Last annotation update) 15-Trefoil factor 2 precursor (Spasmolytic polypeptide) (SP). TFF2 OR SML1 OR SP. Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLUTAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: STOMACH AND PANCREAS.
-!- SIMILARITY: CONTAINS 2 P-TYPE (TREFOIL) DOMAINS.
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TREFOIL FACTOR 2.
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P-TYPE 2.
BY SIMILARITY.
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Pfam; PF00088; trefoil; 2.
PRINTS; PR00680; PTREPOIL.
SMART; SM0018; P. 2.
PROSITE; PS00025; P_TREFOIL; 2.
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                                          20; Conservative
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MGD; MGI:1306805; Tff2.
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                                                                                                                                               732 GSC 734
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30-MAY-2000 (Rel. 39, Last sequence update)
30-CCT-2010 (Rel. 40, Last amnotation update)
Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
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"The putative acetyl-CoA synthetase gene of Cryptosporidium parvum and a new conserved protein motif in acetyl-CoA synthetases.";
J. Parasitol. 82:423-427(1996).
-I. CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
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                                                                                                                                                                      DB 1; Length 129;
                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
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                                                                                                                                25A37794199175D4 CRC64;
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MEDLINE=96237870; PubMed=8636846;
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                                                                                                                                14172 MW;
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37.88;
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Matches 17; Conservative
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                                                                                                                                                                                                                    Conservative
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                                                                                                                                129 AA;
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Q27549;
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                                                                                                                                                                                                                                                                                                                                                                                         JUSCELLULAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: EXPRESSED MAINLY IN BRAIN, WHERE IT IS MOST
ABUNDANT IN THE CEREBELLUM, CEREBRAL CORTEX AND THE OCCIPITAL
POLE; LOW EXPRESSION IN THE PUTAMEN AND THE THALAMUS. ACCORDING TO
REF.1, FOUND IN SPINAL CORD, TESTIS, LIVER, KIDNEY AND PANCREAS
WITH DETECTABLE LEVELS IN PLACENTA, LUNG AND HERRT. ACCORDING TO
REF.2, EXPRESSED IN THE PROSTATE, OVARY, THYROID AND SPLEEN, BUT
NOT FOUND IN KIDNEY, LIVER, LUNG, SKELETAL MUSCLE, BONE MARROW AND
                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sortilin-related receptor precursor (Sorting protein-related receptor containing LDLR class A repeats) (SorLA) (SorLA) (Low-density lipoprotein receptor relative with 11 ligand-binding repeats) (LDLR relative with 11 ligand-binding repeats) (LDLR
                                                                                                                                                                        Morwald S., Yamazaki H., Bujo H., Kusunoki J., Kanaki T., Seimiya K., Morisaki N., Nimpf J., Schneider W.J., Saito Y.,
"A novel mosaic protein containing LDL receptor elements is highly conserved in humans and chickens."

Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: THE PROPEPTIDE REMOVED IN THE N-TERMINUS MAY BE CLEAVED BY
                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FURIN OR HOMOLOGOUS PROTEASES.
SIMILARITY: CONTAINS 5 BNR REPEATS.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 11 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000561; EGF-like.
InterPro; IPR003961; FN III.
InterPro; IPR003962; Fn III.
InterPro; IPR002860; GH BNR.
InterPro; IPR00213; LDL recept A.
InterPro; IPR00033; Ldl recept A.
PF00041; fn 3; 5.
                                                                                                                                                      TISSUE=Brain;
MEDLINE=97301565; PubMed=9157966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00057; ldl_recept_a; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y08110; CAA69325.1; -. EMBL; U60975; AAC50891.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:11185; SORL1.
                                                                                      Homo sapiens (Human)
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                                                                                                                                         SEQUENCE FROM N.A.
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PROSITE; PS01186; EGF 2; 1.

PROSITE; PS01209; LDLRA 1; 10.

PROSITE; PS50068; LDLRA 2; 11.

Endocytosis; Receptor; Transmembrane; EGF-like domain; Repeat;

Glycoprotein; LDL; Lipid transport; Cholesterol metabolism; Signal.

SIGNAL
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LUL-RECEPTOR CLASS A 2.

LUL-RECEPTOR CLASS A 3.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 5.

LUL-RECEPTOR CLASS A 6.

LUL-RECEPTOR CLASS A 6.

LUL-RECEPTOR CLASS A 7.

LUL-RECEPTOR CLASS A 9.

LUL-RECEPTOR CLASS A 9.

LUL-RECEPTOR CLASS A 10.

LUL-RECEPTOR CLASS A 10.

LUL-RECEPTOR CLASS A 11.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 4.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 1.

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FIBRONECTIN TYPE-III 5.
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BNR 5.
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Pfam; PF00058; Idl_recept_b;
Pfam; PF02012; BNR; 5.
                                                             PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00261; LDLRECEPTOR.
                                                                                                                        SMART; SM00181; EGF; 1.
SMART; SM00060; FN3; 5.
SMART; SM00192; LDLa; 11.
SMART; SM00135; LY; 5.
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Venta P.J., Li J., Yuzbasiyan-Gurkan V., Brewer G.J., Schall W.D.; "Complete sequence of the structural gene for canine von Willebrand factor and identification of a mutation causing Scottish terrier von Willebrand's disease.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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Matches 17; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              -!- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
-!- SIMILARITY: CONTAINS 3 VWFA DOMAINS.
-!- SIMILARITY: CONTAINS 3 VWFD DOMAINS.
-!- SIMILARITY: CONTAINS 4 VWFD DOMAINS.
-!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
-!- SIMILARITY: SOME, TO SILKWORM HEMOCYTIN.
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IMPORTANT IN THE MAINTENANCE OF HOMEOSTASIS, IT
PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A
NONCOVALENT COMPLEX WITH COAGULATION FACTOR VIII AT THE SITE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular matrix; Signal.
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BY SIMILARITY.
VON WILLEBRAND FACTOR.
VWFD 1.
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PROSITE; PS01225, CTCK 2; 1.
PROSITE; PS50234; VWPA; 3.
PROSITE; PS01208; VWPC; 3.
Blood coagulation; Platelet; Glycoprotein; 1
Plasma, Hemostasis; Repeat; Cell adhesion; SIGNAL
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                                                                                           VASCULAR INJURY (BY SIMILARITY).
SUBUNIT: MULTIMERIC (BY SIMILARITY).
TISSUE SPECIFICITY: BLOOD.
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InterPro; IPR000004; SapB.
InterPro; IPR0002919; TIL_Cysrich.
InterPro; IPR001007; VWF A.
InterPro; IPR001007; VWF D.
InterPro; IPR001846; VWF D.
Pfam; PF000007; Cys_knot; 1.
Pfam; PF000092; Vwa; 3.
Pfam; PF00093; Vwa; 3.
Pfam; PF00094; Vwa; 4.
Pfam; PF00094; Vwa; 4.
Pfam; PF00094; Vwa; 3.
Pfam; PF00094; Vwa; 3.
Pfam; PF00094; Vwa; 3.
Pfam; PF00094; Vwa; 4.
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EMBL; L16903; AAA30903.1; -.
EMBL; AF099154; AAD04919.1; -.
EMBL; U66546; AAB93766.1; -.
HSSP; P04275; 1AUQ.
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SMART; SM00216; VWD; 4.
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                                                                                                                                                                                                                                                                   MEDLINE=9121855; PubMed=2065077;
Roesijadi G., Vestling M.M., Murphy C.M., Klerks P.L., Fenselau C.C.;
"Structure and time-dependent behavior of acetylated and
non-acetylated forms of a molluscan metallothionein.";
Biochim. Biophys. Acta 1074:230-236(1991).
-!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
SEQUESTRATION OF TOXIC METAL IONS.
-!- INDUCTION: BY CADMIUM.
-!- FIM: THIS MT OCCURS IN BOTH ACETYLATED AND NON-ACETYLATED FORMS.
-!- FIM: THIS MT OCCURS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.
                                                                                                                                                                      MEDLINE=89372898; PubMed=2774559;
Roesijadi G., Kielland S., Klerks P.;
"Purification and properties of novel molluscan metallothioneins.";
Arch. Biochem. Biophys. 273:403-413(1989).
                                                                                      "Primary structure of molluscan metallothioneins deduced from PCR-amplified cDNA and mass spectrometry of purified proteins."; Biochim. Biophys. Acta 1074:371-377(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Frog adenovirus 1.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Siadenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenain (EC 3.4.22.39) (Endoprotease) (Late L3 23 kDa protein).
                                SEQUENCE FROM N.A.
MEDILME=91363394; PubMed=1888750;
Unger M.E., Chen T.T., Murphy C.M., Vestling M.M., Fenselau C.,
Roesijadi G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001008; Mtllthion_misc.
Pfam; PF00131; metalthio; 1.
PRINTS; PR00875; MTMOLLUSC.
Metal-binding; Metal-thiolate cluster; Cadmium; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.6%; Score 57.5; DB 1; Length 74; 35.4%; Pred. No. 5.6; tive 2; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 SCPIILIRCAMLNPPNRCLKDTDCPGIKKCC----EG--SCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 SCPATGCKC---GPGCKCGDDCKCAGCKVKCSCTSEGGCKCGEKCTGP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6364DFB4046E205E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLATION (PARTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, PS5949, IDME.
InterPro, IPR003019; Metallthion.
InterPro, IPR001008; Mtllthion_mlsc.
                                                                                                                                                                                                                                            SEQUENCE OF 1-24, AND ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X59862; CAA42522.1; -.
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PIR; S17156; S17156.
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es 17; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                              SEQUENCE OF 1-27.
       NCBI_TaxID=6565;
                                                                                                                                                                                                                                                            TISSUE=Gill
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Q9IIH4;
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MOD RES
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Eukaryota, Metazoa, Mollusca, Bivalvia, Pteriomorphia, Ostreoida,
Ostreoidea, Ostreidae, Crassostrea.
                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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Pred. No. 99;
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Best Local Similarity 40.0
Matches 18; Conservative
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           Davison A.J., Wright K.M., Harrach B.;
Davison A.J., Wright K.M., Harrach B.;
Phylogenetic position of an amphibian adenovirus.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIOL PROTESE CLEAVING SPECIFIC GLY-ALM PEPTIDES IN A NUMBER OF VIRAL PRECURSOR PROTEINS (TERMINAL, IIIA, VI, VII, VIII, NUMBER OF VIRAL PRECURED FOR VIRION MATURATION. ALSO CLEAVES HOST CELLS CYTOSKELETAL KERATINS K7 AND K18.
-!- CATALYTIC ACTIVITY: Cleaves proteins of the adenovirus and its host cell at two consensus sites: -Yaa-Xaa-Gly-Gly-|-Xaa- and -Yaa-Xaa-Gly-Axaa-Gly-(in which Yaa is Met, Ile or Leu, and Xaa is any amino acid).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Low-density lipoprotein receptor-related protein 2 precursor (Megalin)
(Glycoprotein 330).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moestrup S.K., Cui S., Vorum H., Bregengaard C., Bjorn S.E.,
Norris K., Gliemann J., Christensen E.I.;
"Evidence that epithelial glycoprotein 330/megalin mediates uptake of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G., "Complete cloning and sequencing of rat gp330/'megalin,' a distinctive member of the low density lipoprotein receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Indels
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InterPro; IRR000855; Peptidase_C5.
Pfam; PP00770; Peptidase_C5; 1.
PRINTS; PR007705; Peptidase_C5; 1.
Pydrolase; Thiol protease, Late protein.
ACT SITE 54 BY SIMILARITY.
ACT_SITE 71 71 BY SIMILARITY.
ACT_SITE 71 121 BY SIMILARITY.
SCOUTENCE 204 AA; 23222 MW; 91DC0B01544577A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729(1994).
                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY C5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 ILKSTALTKPSRCIKLVKSKEAVQCTCSAACGLFC 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley; TISSUE=Kidney;
MEDLINE=95024033; PubMed=7937880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95386696; PubMed=7544804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF224336; AAF86933.1; -.
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ID _LRP2_RAT
AC P98158;
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           SOUTH THE TRANSPORT OF 
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                                                                                                                                                                             MEDLINE=94172242; PubMed=7510321;
A Zheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,
Zheng G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,
Andres G., McCluskey R.T.;
Andres G., McCluskey R.T.;
I. "Organ distribution in rats of two members of the low-density
I proprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
II proprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
II proprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
II proprotein receptor gene family, gp330 and LRP/alpa 2MR, and the
II proprotein RAPD! ",
II Histochem Cytochem 42:331-542(1944).
II JACTOREM ACTIVATOR-PLASMINOGEN, EXTRACELLULAR MATRIX COMPONENTS,
IL COMPLEX, APOLIPOPROTEIN E-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
I COMPLEX, APOLIPOPROTEIN B-ENRICHED BETA-VLDL, LIPOPROTEIN LIPASE,
IL COMPLEX, APOLIPOPROTEIN UPTAKE OF POLYBASIC DRUGS SUCH AS
APPORTININ, AMINOGLYCOSIDES AND POLYMYXIN B.
C -1- SUBJUIT: PORMS A MULTIMERIC COMPLEX TOGETHER MITH A RECEPTOR-
ASSOCIATED PROTEIN (RAP).
C -1- SUBJUIT: PORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-
ASSOCIATED PROTEIN (RAP).
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-1. TISSUE SPECIFICITY: EPITHELIAL CELLS OF KIDNEY GLOMERULUS AND PROXIMAL TUBULE, LUNG, EPIDIDYMIS, YOLK SAC, AMONG OTHERS.
-1. SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS A DOMAINS.
-1. SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
-1. SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
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PROSITE; PS001186; BGF_1; 1.
PROSITE; PS01186; BGF_2; 8.
PROSITE; PS01187; EGF CA; 3.
PROSITE; PS01209; LDLRA_1; 31.
PROSITE; PS0068; LDLRA_2; 36.
ROSITE; PS0068; LDLRA_2; 36.
ROSITE; PS0068; LDLRA_2; 37.
ROSITE; PS0068; LDLRA_2; 27.
ROSITE; 
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LDL.RECEPTOR CLASS A 3.
LDL.RECEPTOR CLASS A 4.
LDL.RECEPTOR CLASS A 5.
LDL.RECEPTOR CLASS A 6.
LDL.RECEPTOR CLASS A 6.
LDL.RECEPTOR CLASS A 7.
EGF-LIKE 1.
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InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR0001651; EGF-like.
InterPro; IPR001081; EGF Ca.
InterPro; IPR001083; LDL_recept_A.
InterPro; IPR001033; Ldl_recept_A.
Pfam; PF00057; ldl_recept_a; 36.
Pfam; PF00058; ldl_recept_b; 33.
PRINTS; PR00261; LDLRECEPTOR.
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                                            Clin. Invest. 96:1404-1413(1995).
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SMART; SM0135; LY; 35.
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polybasic drugs.";
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CALCIUM-BINDING (POTENTIAL).
CLASS B 35.
CLASS B 37.
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      LDL-RECEPTOR CLASS A 35.
LDL-RECEPTOR CLASS A 36.
EGF-LIKE 14.
EGF-LIKE 15. CALCIUM-BINDING (POTENT
LDL-RECEPTOR CLASS B 35.
LDL-RECEPTOR CLASS B 36.
LDL-RECEPTOR CLASS B 37.
EGF-LIKE 16.
EGF-LIKE 16.
SH9-BINDING (POTENTIAL).
SH3-BINDING (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M3KA_HUMAN STANDARD; PRT; 954 AA.
002779; 012761; 014871;
01-FEB-1994 (Rel. 28, recated)
30-MAY-2000 (Rel. 39, Last sequence update)
115-JUM-2002 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)
(Mixed lineage kinase 2) (Protein kinase MST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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Pred. No. 1.7e+02;
1; Mismatches 18; Indels 5
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Dorow D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
Sutherland G.R., Simpson R.J.;
"Complete nucleotide sequence, expression, and chromosomal localisation of human mixed-lineage kinase 2.";
Eur. J. Blochem. 234:492-500(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURNCE FROM N.A.

TISSUE=Brain;
MEDLINE=95249256; PubMed=7731697;
Katoh M., Hirai M., Sugimura T., Terada M.;
"Cloning and characterization of MST, a novel (putative) serine/threonine kinase with SH3 domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 244-480 FROM N.A.
TISSUB=Colon epithelium;
MEDLINE=93238756; PubMed=8477742;
Dorow D.S., Devereux L., Dietzsch E., de Kretser T.;
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|GTCQPTQFRC----PDHRCISPLYVCDGDKDCADGSDEAGC 1184
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2 BY SIMILARITY.
405 LEUCINE-ZIPPER 1 (BY SIMILARITY).
440 LEUCINE-ZIPPER 2 (BY SIMILARITY).
464 SRL -> AV (IN REF. 2).
480 LKLERGGSHISLPSGF -> AQAAGRRQPHQPALML (IN REF. 2).
471 G -> S (IN REF. 2).
471 G -> S (IN REF. 2).
807 G -> R (IN REF. 2).
818 V -> A (IN REF. 2).
818 V -> A (IN REF. 2).
818 V -> A (IN REF. 2).
819 V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50002; SH3; 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
"Identification of a new family of human epithelial protein kinases containing two leucine/isoleucine-zipper domains.";

Eur. J. Biochem. 213:701-710(1993).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLE.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE KINASE SUBFAMILY.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches 13; Indels
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Pfam; PP00068; Pkinase; 1.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00306; SH3; 1.
SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                   EMBL, X90846; CAA62351.1; -. EMBL; Z48615; CAA88531.1; -. PIR; S32468; S32468. HSSP; P11362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 34.9%;
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.48;
                                                                                                                                                                                                                                                                                          Genew; HGNC:6849; MAP3K10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
112
125
222
405
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954 AA;
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BINDING
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 60
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28 AA

PRT;

IEL1 MOMCH STANDARD; 1 P10296; 01-MAR-1989 (Rel. 10, Created)

IEL1 MOMCH

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-!- SUBDULT: MONOMER.
-!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
-!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAIN SUPPLIED DOMAIN THIN CLUSTER A OF THE ALPHA DOMAIN AND ARE CORDINATED VIA CYSTEINYL THIOLATE BIDGES TO 11 CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
Elastase inhibitor I (WCIL-I).
Momordica charantia (Bitter gourd) (Balsam pear).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; wagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              MEDLINE=89291812; PubMed=2738047; Makino J., Ikenaka T.; Makino J., Ikenaka T.; Makino J., Ikenaka T.; Mamino acid sequences and disulfide bridges of serine proteinase inhibitors from bitter gourd (Momordica charantia LINN.) seeds."; J. Biochem. 105:88-92(1989).
J. Biochem. 105:88-92(1989).
INHIBITORS...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metallothionein IB gene.";

Mol. Cell. Biol. 6:2149-2157 (1986).

-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE

-RESIDUES THAT BIND VARIOUS HEAVY METALS; THESE PROTEINS ARE

TRANSCRIPTIONALLY REGULATED BY BOTH HEAVY METALS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87064506; PubMed=3785191;
Heguy A., West A., Richards R.I., Karin M.;
"Structure and tissue-specific expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
961C63D22C74FEC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AA.
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RDSDCLAQCICVDGHCG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 CPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REACTIVE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART, SM00286, PTI, 1.
PROSTIE, PS00286, SQUASH_INHIBITOR, 1.
Serine procease inhibitor.
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    PIR, JX0059; JX0059.
HSSP, P01074; 1CTI.
InterPro; IPR000737; Squash.
Pfam, PF00299; squash; 1.
PRINTS; PR00293; SQUASHINHBTR.
ProDom; PD003401; Squash; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.3%;
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27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                            NCBI_TaxID=3673;
                                                                                                                                                                                                                                TISSUE-Seed;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
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MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Gaps
                                                                                                                                                                                                                                                              PRINTS; PRO0860; MTVERTEBRATE.
PROSITE; PSO0203; METALLOTHIONEIN VRT; 1.
Metal-binding; Metal-thiolate cluster; Zinc; Copper; Cadmium;
Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56.5; DB 1; Length 61; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                          ACETYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 TTGGSC----ACA----GSCKCKECKCTSCKKCCCSCCPVGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 TKPGSCPILLIRCAMLNPPNRC-LKDTDCPGIKKCCEGSCGMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.
Bacteria, Chlamydiales, Chlamydiaceae, Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-05bable 50S ribosomal protein L25.
RPLY OR CT799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   CLUSTER B.
CLUSTER B.
CLUSTER B.
CLUSTER B.
CLUSTER B.
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CLUSTER A.
                                                                                                                                                                                                                              Metllthion_vert.
                                                                                                                                                EMBL; M13484; AAA36331.1; JOINED.
                                                                                                                                                                                                                  InterPro; IPR003019; Metallthion.
InterPro; IPR000006; Metllthion v
                                                                                                                              EMBL; M13485; AAA36331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.3%;
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                                                                                                                                                                                       Genew; HGNC:7394; MT1B.
                                                                                                                                                           PIR; A25244; A25244.
HSSP; P02795; 2MHU.
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AA;
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                                                                                                                                                                                                       MIM; 156349; -
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or send an email to license@isb-sib.ch).
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Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Brooks K., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle L.J., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Androry P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
Altherford K., Rutter S., Saunders D., Geeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Arylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Woldward J., Volckaert G., Aert R., Roben J., Grymonprez B.,
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Ber P., Zimmermann W., Wedder H., Wambutt R., Hurnelle B.,
Goffeu A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Calibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
A Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                            Science 282:754-759(1998).
-!- FUNCTION: BINDS TO THE 5S RRNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L25P FAMILY OF RIBOSOMAL PROTEINS.
                                                                         "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             و
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Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHCI-2DPAGE; 084805; -..
InterPro; IPR001021; Ribosomal_L25.
Ffam; Pf01386; Ribosomal_L25p; 1.
TIGRPAMS; TIGR00731; ctc_TL5; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
SEQUENCE 185 AA; 20439 MW; 0E88BBE105B71547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 RDVRLNIPIRCINTVDCVGVKLGGSLRQVIRCIRVVCKPKDIVP 143
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 RCAMLNPPNRCLKDTDCPGIK-----KCCEGSCGMACFVP
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15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C3F10.05c in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.3%; Score 56.5; DF
31.8%; Pred. No. 15;
:ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001352; AAC68394.1; -.
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                                                                                                                Chlamydia trachomatis.
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       RAPARATA PRAPA PRA
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RESULT 65

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                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A conotoxin with novel cysteine framework from Conus betulinus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                              1;
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 TKPGSCPILLIRCAMLNPPNRCL-----KDTDCPGIKKCCEGSCGMACFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 TSVGCLLLVIVFLNLVVPTSACRAEGTYCENDSQC-CLNECCWGGCGHPCRHP 57
                                                                                                                                                                                                                                                                                                                         DB 1; Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conus betulinus (Beech cone).
Eukaryota, Metazoa, Mollusca, Gastropoda, Caenogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 56; DB 1; Length 70; r; Pred. No. 7.8; 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                         17.3%; Score 56.5; DB 1; Length 3: 34.2%; Pred. No. 24; Live 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    south China sea.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Secreted (Potential)
                                                                                                                                                                                                                                                                        11 protein.
326 AA; 37867 MW; 7D88277601A571BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F6575A2E830AD903 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                                                                                                                                                                                                                       164 PTRGVVVLEDWINPLLSERCKLLLQSELCNQDSYDCPG 201
                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONOTOXIN BETX.
                                                                                                                                                                                                                                                                                                                                                                                                  4 PVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDT-DCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurotoxin; Toxin; Signal; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cleavage on pair of basic residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF208661; AAF23167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.58;
                                                                                                                                                                                                                                                  EMBL; Z69369; CAA93303.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 AA; 7900 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 34.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conotoxin BeTX precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Venom duct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=89764;
                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CX2X CONBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fan C.-X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 64
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/GITR-D; ARE PRODUCED BY ALTERNATIVE SPLCING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nocentini G.,
"Identification of a soluble human GITR splicing (hGITR-D).";
"Identification of a soluble human GITR splicing (hGITR-D).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBD datebases.
-!- FUNCTION: RECEPTOR FOR THYSPIS. SEEMS TO BE INVOLVED IN
INTERACTIONS BETWEEN ACTIVATED T LYMPHOCYTES AND ENDOTHELIAL CELLS
AND IN THE REGULATION OF T CELL RECEPTOR-MEDIATED CELL DEATH.
MEDIATED NF-KAPPA-B ACTIVATION IN THE TRAFZ/NIK PATHWAY.
-!- SUBUNIT: BINDS TO TRAFI (THY RECEPTOR-ASSOCIATED FACTOR 1), TRAFZ,
AND TRAF3, BUT NOT TRAFS AND TRAF6.
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L., Liu D., Wang S.-X., Kwon B.S.; "Identification of a novel activation-inducible protein of the tumor
            09Y5U5, 09S851, Q9NYJ9,
16-OCT-2001 (Rel. 40, Last sequence update)
16-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 18 precursor
(Gluccorticoid-induced TNFR-related protein) (Activation-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR."; Curr. Biol. 9:215-218(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEUKOCYTES AND WEAKLY IN SPLEEN.
-!- INDUCTION: UPPREGULATED IN PERIPHERICAL MONONUCLEAR CELLS AFTER ANTIGEN STIMULATION/LYMPHOCYTE ACTIVATION.
-!- SIMILARITY: CONTAINS 3 THPR-CYS REPEATS.
                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                         Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T., Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D., Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     necrosis factor receptor superfamily and its ligand."; J. Biol. Chem. 274:6056-6061(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=T-cell;
MEDLINE=99156876; PubMed=10037686;
PRT;
                                                                                                                                                                                                                                                                                                             TISSUE=Bone marrow;
MEDLINE=99175482; PubMed=10074428;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF125304; AAD22635.1; -. EMBL; AF117297; AAD19694.1; -. EMBL; AF241229; AAF63506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF241229; AAF63506.1;
Genew, HGNC:11914; TNFRSF18.
MIM; 603905; -.
                                                                                                                                           INFR family receptor).
INFRSF18 OR GITR OR AITR.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted (isoform 2)
                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Thymus;
  TR18 HUMAN
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2
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TWER-CYS 2.

TWER-CYS 2.

TWER-CYS 3.

TWER-CYS 3.

TWER-CYS 3.

TWER-CYS 3.

TWER-CYS 3.

TWER-CYS 4.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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TO CRACK CONTROLLENDED CONTRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAPQAAGALRSALGRALLPWQQKWVQEGGSDQRPGPCSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=90311312; PubMed=2164210;
Plowman G.D., Whitney G.S., Neubauer M.G., Green J.M., McDonald V.L.,
Todaro G.J., Shoyab M.;
"Molecular cloning and expression of an additional epidermal growth
factor receptor-related gene.";
Proc. Natl. Acad. Sci. U.S.A. 87:4905-4909(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGPCRRERETQSWPPSSLAGPDGVGS (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QEPVKGP-----VSTKPGSCPILLIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGM 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 ORPIGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEECCSEWDCMCVQP--EFHCGD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-UIN-2002 (Rel. 41, Last annotation update)
Receptor protein-tyrosine kinase erbB-3 precursor (EC 2.7.1.112)
(C-erbB3) (Tyrosine kinase-type cell surface receptor HER3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.A., "Isolation and characterization of ERBB3, a third member of the ERBB/epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumors."; Proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
                                                                                                                                                    TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.1%; Score 56; DB 1; Length 241; 25.8%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches 30; Indels
                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
SMART; SM00208; TNFR; 1,
PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQCMWPRE -> K (IN REF. 2).
90DC3B4AA7E82CBE CRC64;
                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1342 AA.
                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90083234; PubMed=2687875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.89
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                          Receptor, ........Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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163
184
184
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115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERB3 HUMAN
P21860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 AC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 PC 85
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DISULFID
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REPEAT
REPEAT
REPEAT
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                                                                                                                                                 CHAIN
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                                                                                                                                                                                          (POTENTIAL).

-- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND SECRETED (SHORT PORM).

-- ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AND A SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

-- ITSSUES PRESCRIFICITY: EPITHELIAL TISSUES AND BRAIN.

-- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITH THE SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

-- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RESIDUES AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF PHOSPHATIDYLINGSITOL 3-KINASE (BY SIMILARITY).

-- DISEASE: OVEREXPRESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.

-- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR PROTEIN-TYROSINE KINASE ERBB-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ransferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                             Biochem. Biophys. Res. Commun. 192:1189-1197(1993).
-!- FUNCTION: BINDS AND IS ACTIVATED BY NEUREGULINS AND NTAK.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                               MEDLINE=93282822; PubMed=7685162;
Katoh M., Yazaki Y., Sugimura T., Terada M.;
"c-erbB3 gene encodes secreted as well as transmembrane receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00261; FU; 3.
SMART; SM00261; FU; 3.
SMART; SM00201; FU; 3.
SMART; SM00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; FALSE NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; 11.
Transmembrane; Glycoptotein; Multigene family; Receptor; Signal; Transmembrane; Glycoptotein; Wintigene family; Receptor; Signal;
                                                                                                                                                                tyrosine phosphate.
-!- SUBUNIT: HETERODIMER WITH EACH OF THE OTHER ERBB RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IRR000494; EGFR L domain.
InterPro; IPR000119; Buk pkinase.
InterPro; IPR001245; Furin-like.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; pkinase; I.
Pfam; PF00069; Pkinase; I.
Pfam; PF001005; Rurin-like; I.
ProDom; PD000001; Euk_pkinase; I.
[3] SEQUENCE FROM N.A. (SHORT FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M29366; AAA35790.1; -.
EMBL; M34309; AAA35979.1; -.
EMBL; S61953; AAB2695.1; -.
PIR; A36223; A6223.
HSSP; P11362; 1FGK.
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Transferase, Tyloc...
Alternative splicing...
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MEDLINE=92381036; PubMed=1512259;

MEDLINE=92381036; PubMed=1512259;

A Robbrock A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,

Robbrock A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,

Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.;

"Cloning and functional expression of Dfurin2, a subtilisin-like

T proportorin processing enzyme of Drosophila melanogaster with multiple

T repeats of a cysteine motifi.";

J. Biol. Chem. 267:17208-17215(1992).

L. FUNCTION: FURNI IS LIKELY TO REPRESENT THE UBIQUITOUS ENDOPROTEASE

CLEAVAGE AT THE RX(K/R) R CONSENSUS MOTIF (BY SIMILARITY).

CLEAVAGE AT THE RX(K/R) R CONSENSUS MOTIF (BY SIMILARITY).

CLEAVAGE AT THE RX(K/R) R CONSENSUS MOTIF (BY SIMILARITY).

C. -- CATALYTIC ACTIVITY: Release of macure proteins from their component C3 and von Willebrand factor from their
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N-LINKED (GLCNAC. . .) (POTENTIAL).
ELSGGVYIEKNDKLCHMDTIDMRDIVRDRDAEIVVEDNGR.
SC -> GQFPRVPSGLIPQFAQDWYLLDDDPRLLTLSASSK.
VPVTLAAV (IN SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Perrygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophildae, Drosophila.

NCBI_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. FURIN SUBFAMILY.
                                                                                                                                                                                                               (POTENTIAL).
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01-APR-1993 (Rel. 25, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
Furin-like protease 2 precursor (EC 3.4.21.75) (Furin 2).
                                                                                                                                                                                                                                                                                                                                                                                                           7201E7F66CA374BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                     (IN SHORT ISOFORM)
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Best Local Similarity 33.3
Matches 15; Conservative
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSSP; Q99405; 1MPT.
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RESULT 68 FBN1\_HUMAN

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SEQUENCE OF 1-912 FROM N.A.
TISSUB=Placenta, and Fibroblast;
MEDLINE=94010947; PubMed=7691719;
Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;
"Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure and alternatively spliced exons at the 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96144829; PubMed=8568869;
Knott V., Downing A.K., Cardy C.M., Handford P.A.;
"Calcium binding properties of an epidermal growth factor-like domain
pair from human fibrillinies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee B., Godfrey M., Vittale E., Hori H., Mattei M.-G., Sarfarazi M., Tsipouras P., Ramirez F., Hollister D.W.; "Linkage of Marfan syndrome and a phenotypically related disorder to two different fibrillin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION.
MEDLINE=91317849; PubMed=1860873;
Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.D.,
"Purification and partial characterization of fibrillin, a cysteine-
rich structural component of connective tissue microfibrils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Solution structure of a pair of calcium-binding epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y., "Partial sequence of a candidate gene for the Marfan syndrome."; Nature 352:334-337(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98031893; PubMed=9362480;
Yuan X., Downing A.K., Knott V., Handford P.A.;
"Solution structure of the transforming growth factor beta-binding
protein-like module, a domain associated with matrix fibrils.";
                                                                                                                                  Bukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                        Pangilinan T., Bonadio J., "Genomic organization of the sequence coding for fibrillin, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D., Handford P.A.;
                                                                                                                                                                                                                                                       Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
                                                   (Rel. 29, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                            defective gene product in Marfan syndrome.";
Hum. Mol. Genet. 2:961-968(1993).
       PRT; 2871 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 266:14763-14770(1991).
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MEDLINE=91304567; PubMed=1852206;
                                                                                                                                                                                                                       TISSUE=Placenta;
MEDLINE=93372860; PubMed=8364578;
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     STANDARD;
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Cell 85:597-605(1996).
                                                                                      Fibrillin 1 precursor
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=9606;
                                      01-JUN-1994
                                                                   15-JUN-2002
                                                                                                      OR FBN
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MEDITARE 97169383; PubMed=9016526; Collod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J., Godfrey M., Hayward C., Kartunen L., Milewicz D., Peltonen L., Richards R.I., Wang W., Junien C., Bolleau C.; Markan Database (second edition): software and database for the analysis of mutations in the human FBNI gene."; Nucleic Acids Res. 25:147-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307. MEDLINE=33250834; PubMed=1301946; Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.; "Clustering of fibrillin (FRN1) missense mutations in Marfan syndrome patients at cysteine residues in BGF-like domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hewett D.R., Lynch J.R., Smith R., Sykes B.C.,
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disrupt calcum binding of the epidermal growth factor-like module.",
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                                                    alleles result in a lethal phenotype.";
Am. J. Hum. Genet. 55:1083-1091(1994).
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J. Clin. Invest. 94:709-713(1994).
    VARIANTS MFS GLY-217 AMD ARG-2627.
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P04429;
13-AUG-1987 (Rel. 05, Created)
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Best Local Similarity 26.69
Matches 17; Conservative
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HSTN_VIBCH
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                                                                                                                                                                                                                                                                                                      SPECIES - Cholerae, STRAIN-NRT36; MEDLINE=90382953; PubMed=2205577; Ogawa A., Kato J.I., Watanabe H., Nair B.G., Takeda T.; Ogawa A., Kato J.I., Watanabe H., Nair B.G., Takeda T.; Cloning and nucleotide sequence of a heat stable enterotoxin gene from vibrio cholerae non-Ol isolated from a patient with traveler's
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                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666, 674;
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MEDLINE-91257548; PubMed-2044934;
Arita M., Honda T., Miwatani T., Takeda T., Takao T., Shimonishi
"Purification and characterization of a heat-stable enterotoxin o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heat-stable enterotoxin ST precursor (Nonagglutinating cholera
vibrios ST) (NAG-ST) (Non Ol-ST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEMS Microbiol. Lett. 63:105-110(1991).
-!- SIMILARITY: BELONGS TO THE HEAT-STABLE ENTEROTOXIN FAMILY.
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PROSITE; PS00273; ENTEROTOXIN H_STABLE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=V.cholerae; STRAIN=Serovar non-O1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Infect. Immun. 58:3325-3329(1990)
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                                                                                                                                                    Vibrio cholerae, and
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HSTO_VIBCH
ID HSTO_VIBCH
AC Q07425;
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                                                                                                                                               STRAINSEL TOT Inbba GP156 / Serotype O1;
MEDLINE=94066893; PubMed=8246823;
Ogawa A., Takeda T.;
"The gene encoding the heat-stable enterotoxin of Vibrio cholerae is flanked by 123-base pair direct repeats.";
Microbiol. Immunol. 37:607-616 (1993).
-! SIMILARITY: BELONGS TO THE HEAT-STABLE ENTEROTOXIN FAMILY.
-! CAUTION: THIS TOXIN IS ONLY EXPRESSED IN SOME VIBRIO STRAINS. MOST SEROTYPE-O1 STRAINS DO NOT EXPRESS THIS TOXIN.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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Pred, No. 9.7:
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01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annoration update)
Trefoil factor 2 precursor (Spasmolytic polypeptide) (SP).
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BY SIMILARITY.
HEAT-STABLE ENTEROTOXIN STO.
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heat-stable enterotoxin STO precursor (Ol-ST)
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BY SIMILARITY.
BY SIMILARITY.
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Pfam; PF02048; Enterotoxin HS; 1.
PROSITE; PS00273; ENTEROTOXIN H_STABLE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 KDTDCPGIKK-----CCEGSCGMACF 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::||||:|||45 ENEECPFIKQVDENGNLIDCCEICCNPACF 74
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L03220; AAA16516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.0%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8742 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poxin; Enterotoxin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 36.7 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01559; 1ETN.
                                                                                                                            IIJ
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                           Vibrio cholerae
                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFF2 RAT
Q09030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FF2 RAT
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
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Jeffrey G.P., Oates P.S., Wang T.C., Babyatsky M.W., Brand S.J.; "Spasmolytic polypeptide: a trefoil peptide secreted by rat gastric mucous cells.";

TISSUE-Antrum, MEDLINE-94131228; PubMed-8299900;

Gastroenterology 106:336-345(1994).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
FUNCTION: INHIBITS GASTROINTESTINAL MOTILITY AND GASTRIC ACID SECRETION. COULD FUNCTION AS A STRUCTURAL COMPONENT OF GASTRIC MUCUG, POSSIBLY BY STABILIZING GIYCOPROTEINS IN THE MUCUS GEL THROUGH INTERACTIONS WITH CARBOHYDRATE SIDE CHAINS.
SUBCELLULAR LOCATION: SECRETED THE DIGESTIVE TRACT, WHERE IT WAS FOUND PREDOMINANTLY IN THE STOWAGE WITH HIGHEST EXPRESSION IN THE AWNRUM. IT IS SECRETED PREDOMINANTLY FROM ANTRAL MUCOUS CELLS INTO THE LUMEN OF THE GASTROINTESTINAL TRACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel androgen-regulated gene, PMEPA1, located on chromosome 20q13 exhibits high level expression in prostate."; Genomics 66:257-263(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPGSCPIILIRCAMLNPPNRCLKDTDCPGIKK-----CCEGS--CGMA-CFVP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 KPSPC----RCSRMTPSNR--KNCGFPGITSDQCFNLGCCFDSSVAGVPWCFHP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Segawa T., Sesterhenn I.A., McLeod D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                096909; 090103; 096872;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transmembrane prostate androgen-induced protein (Solid tumor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               005D0848F64F92D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                         TREFOIL FACTOR 2.
P-TYPE 2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 15;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.0%; Score 55.5;
                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=20334621; PubMed=10873380;
                                                                                                                                                                                                                                                                                                HSSP; P01359; 1PCP.
InterPro; IPR000519; P_trefoil.
Pfam; PF00088; trefoil; 2.
PRINTS; PR00680; PTREFOIL.
                                                                                                                                                                                                                                                                                                                                                                              TREFOIL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                              Repeat, Growth factor, Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14077 MW;
                                                                                                                                                                                                                                                                                       EMBL; M97255; AAA19025.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TMEPAI OR PMEPA1 OR STAGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 34.5
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu L.L., Shanmugam N., Se
Moul J.W., Srivastava S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              23
129
121
121
127
58
57
69
107
                                                                                                                                                                                                                                                                                                                                                               SMART; SM00018; P; 2.
PROSITE; PS00025; P_T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMEP HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
DISULFID
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09-833799-13b.rsp

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MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashuret J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard D.M.,
RA Baseley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Bacaley O.P., Butler A.B., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Clington A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gvilliam R.H., Hall R.E.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gvilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.N.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Marsh V.L., Martin S.L., McCommachie L.J., McLay K., McMurray A.A.,
RA Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,
RA Swann R.M., Sycamore N., Taylor R., Thomas D.W., Thorpe A.,
RA Mintehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Mintheed S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHRLWGVNSTAAAAAGONVSCTCNCKRSLFQSMEIT ->
MA (IN ISOFORM 2).
6103473561AE08DA CRC64;
            Rae F.K., Hooper J.D., Nicol D.L., Clements J.A., characterization of a novel gene, STAG1/PMEPA1, upregulated in renal cell carcinoma and other solid tumors.";
Mol. Carcinog. 32:44-53(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -: SUBUNIT: Interacts with the WW domains of NEDD4 (By similarity).
-: SUBCELLULAR LOCATION: Type 1b membrane protein (Potential).
-: ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WW-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- INDUCTION: By androgen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 8-287 FROM N.A. (ISFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL035541; CAB55862.1; -.
EMBL; BC015918; AAH15918.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransmembrane; Alternative splicing.
MEDLINE=21453682; PubMed=11568975;
                                                                                                                                      MEDLINE=21638749; PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF305616; AAL16781.1; -.
EMBL; AF305426; AAL09357.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF224278; AAF86322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 AA; 31609 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew, HGNC:14107; TMEPAI.
MIM; 606564; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
63
287
161
232
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in ovary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rogers J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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REPUINE-21638749; PubMed=1780052; RAND 3/.

REDIURE-21638749; PubMed=1780052; RAND BOLOUKAS P., Matthews L., Backley C.L., Balcoukas P., Matthews L.P., Babbage A.K., Bacquley C.L., Bancos M., Stavrides G., Almeida J.P., Babbage A.K., Bacquley C.L., RADONE M., Stavrides G., Almeida J.P., Babbage A.K., Bacquley C.L., RADONE M., Barl C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RADONE D. Burrill W.D., Butler A.P., Carder C., Carter N.P., Coulson A., Collier R.E., Connor R.E., Corby N.R., Coulson A., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhanm P.D., Garrier P., RADONE A., Collier G.J., Deadman R., Dhanm P., Garrier P., RADONE A.G., Frankland J.A., Fraser A., Hall R.E., RADONE A.G., Hunt A.R., Hunt S.E., Holden J.L., Howden P.J., RAMMOND S., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., RADONE A.M., King A., Khights A., Laird G.K., Lawlor S., RAMINE S.M., Mistry D., Mocomachie L.J., McLay K., McCourray H.A., Mistry D., Mocomachie L.J., McLay K., McCourray H., Ramsay H., RADONE B.J.C.T., Parathalingem S.R., Plumb R.W., Ramsay H., RADONE B.J.C.T., Parathalingem S.R., Plumb R.W., Rownkeen R., Sims S., Ryknee C.D., Smith M.L., Soderlund C., Steward C.A., Shownkeen R., Sims S., Race C.D., Smith M.L., Soderlund C., Thomas D.W., Thorpe A., Race C.D., Smith M.L., Taylor R., Taeey A., Tromans A.C., Vaudin M., Walli M., Wallis J.M., Thorpe A., Porers J.
                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MIGHT ACT AS AN E3 UBIQUITIN-PROTEIN LIGASE, OR AS PART
-!- GOF THE E3 COMPLEX, WHICH ACCEPTS UBIQUITIN FROM SPECIFIC E2
UBIQUITIN-CONJUGATING ENZYMES, SUCH AS UBEZL3/UBCM4, AND THEN
TRANSFERS IT TO SUBSTRATES.
-!- SUBUNIT: INTERACTS WITH BETA-I-TYPE (PRKCB1) AND ZETA-TYPE PROTEIN
KINASE C (PRKCZ) AND WITH UBEZL3. FORMS HOMODIMERS IN VITRO (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence and comparative analysis of human chromosome 20.";
                                                                                                            20; Indels 17; Gaps
                                                                                 -----CP-----GIKKCCE 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                            UT13 HUMAN STANDARD; PRT; 500 AA.

OBENNO; 055623; Q9BYM9;

16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ubiquitin conjugating enzyme 7 interacting protein 3 (Hepatitis VireX X-associated protein 4) (HBV associated factor 4).

Homo sapiens (Human)
DB 1; Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
17.0%; Score 55.5; D
29.7%; Pred. No. 28;
tive 8; Mismatches
                                                                                     4 PVKGP--VSTKPGSCPIILIRCAMLNPPNRCLKDTD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 3).
                        Best Local Similarity 29.7 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 414:865-871(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                           220 GSGG 223
                                                                                                                                                                                47 GSCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.;
           Query Match
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                                                                                                                                                                                                                                                                                                               U7I3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALSLTRAVAGGDEQVAMKCAIWLAEQRVPLSVQLKPEVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKQQQQEGNYLQHVQLDQRS -> GVPAGHHPQQPGGGLL
         ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1/RBCK1 (SHOWN HERE), 2/RBCK2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TODI -> MGTATPDGREDQE (IN ISOFORM 3 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ubl conjugation pathway; Zinc-finger; Coiled coil; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLH (IN ISOFORM 2 AND ISOFORM 4).
MISSING (IN ISOFORM 2 AND ISOFORM 4).
7492E03EB2E9CE4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 45;
3; Mismatches 15; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 QEPGRGQPDAVPEPPVGWQCP----GCTFINKPTR-----PGCEMCC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEPVKGPVSTKP----GSCPIILIRCAMINPPNRCLKDTDCPGIKKCC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ictalurid herpesvirus 1 (Channel catfish virus) (CCV). Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANBP2-TYPE.
COILED COIL (POTENTIAL)
                     AND 4; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
-!- PTM: PHOSPHORYLATED (BY SIMILARITY).
-!- SIMILARITY: CONTAINS I UBIQUITIN-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS I RING-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS I BOX-TYPE ZINC FINGER.
-!- SIMILARITY: CONTAINS I RANBP2-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
56 kDa serine protease (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B BOX-TYPE.
B BOX-LIKE-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UBIQUITIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.0%; Score 55.5; 30.0%; Pred. No. 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RING-TYPE
                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50053; UBIQUITIN 2; 1.
PROSITE; PS50119; ZF BBOX; FALSE NEG.
PROSITE; PS501199; ZF RANBP2 1; 1.
PROSITE; PS50199; ZF RANBP2 2; 1.
PROSITE; PS500199; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                         InterPro; IPR000626, Ubiquitin.
InterPro; IPR0001315; Znf Bbox.
InterPro; IPR001315; Znf RanGDP.
InterPro; IPR001841; Znf RanGDP.
Pfam; PF00097; Zf-C3HC4; 1.
Pfam; PF000641; Zf-RanBP; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                   EMBL, U67322, AAD00162.1, -.
EMBL, AL121747, CAC17516.1; -.
EMBL, AL121747, CAC28311.1; -.
EMBL, AL121747, CAC28312.1; -.
EMBL, BC000983, AAH00833.3, -.
Genew, HGNC.15864, C20orf18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56381 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 30.04
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 AA;
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Q00139;
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ZN_FING
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.

NCBI_TaxID=3661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wieczorek M., Otlewski J., Cook J., Parks K., Leluk J., Wilmowska-Pelc A., Polanowski A., Wilusz T., Laskowski M. Jr., Wilmowska-Pelc A., Polanowski A., Wilusz T., Laskowski M. Jr., squash family of serine proteinase inhibitors. Amino acid sequences and association equilibrium constants of inhibitors from squash, summer squash, aucchini, and cucumber seeds."; Biochem. Biophys. Res. Commun. 126:646-652(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SIMILARITY).
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01-MAY-1992 (Rel. 22, Last annotation update)
Trypsin inhibitors IV and III (CMII-IV and CMII-III).
                                                                                                                                                                                                    Davison A.J.; "Channel catfish virus: a new type of herpesvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 İVLVDGVATGSPNALVTDFDCRPGMKHCGVCQQLISGSTG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 IILIRCAMLNPPNRCLKDTDC-PGIKKC--CE----GSCG 50
                                                                                                                                                                                                                                                                  Virology 186:9-14(1992).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AA
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Prodom; PE01043; P; PARTIAL.
Prodom; PE000136; SÜBTILASE_ASP; FALSE_NEG.
PROSITE; PS00137; SUBTILASE_HIS; FALSE_NEG.
PROSITE; PS00138; SUBTILASE_SER; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002884; P domain.
InterPro; IPR000209; Peptidase_S8.
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MEDLINE=85149300; PubMed=3977882;
                                                                                                                                  STRAIN=Auburn 1;
MEDLINE=92087490; PubMed=1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 AA; 55984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Created)
Ictalurid Herpes-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M75136; AAA88150.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase, Serine protease.
ACT SITE 334 334
SEQUENCE 518 AA; 55984 MA
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MEROPS; S08.UPA; -.
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                                                                                                   FROM N.A.
                                  NCBI_TaxID=10401;
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                                                                                                                                         MEDLINE=92118901; PubMed=1731946; Krishnamoorthi R., Gong Y., Lin C.-L.S., Vandervelde D.; Krishnamoorthi R., Gong Y., Lin C.-L.S., Vandervelde D.; Krishnamoorthi R., Gong Y., Lin C.-L.S., Saquence-specific proton assignments and secondary structure of reactive-site hydrolyzed Cucurbita maxima trypsin inhibitor III."; Biochemistry 31:898-904 (1992).

INHIBITORS.

INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                    Nowak K., Slominska A., Polanowski A., Wieczorek M., Wilusz T.; "Trypsin inhibitor III from squash seeds (Gucurbita maxima), its reactive site and amino acid sequence."; Hoppe-Seyler's Z. Physiol. Chem. 362:1017-1019(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.8%; Score 55; DB 1; Length 32; 38.9%; Pred. No. 5.3; tive 3; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       CMTI-IV.
CMTI-III.
REACTIVE BOND.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
OFS91120B0137512 CRC64;
Hoppe-Seyler's Z. Physiol. Chem. 364:93-95(1983).
                                                                                                                                                                                                                                                                      PIR; A01313; TIPU3.
PIR; S07156; S07156.
HSSP; POLO74; ICTI.
InterPro; IPR000737; Squash.
Pfam; PF00299; squash.
ProDom; PD000391; SQUASHINHBTR.
ProDom; PD003401; Squash. 1.
SWART; SM00286; PTI; 1.
PROSTE; PS00286; SQUASH INHIBITOR; 1.
CHAIN
                                         TISSUE=Seed;
MEDLINE=82005824; PubMed=7275008;
                           PRELIMINARY SEQUENCE (CMT-III).
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Matches 14; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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A08105 Synthetic A
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A703181 Homon sapi
Z93016 Human DNA s
AF036687 Caenorhab
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AC084528 Caenorhab
AX403457 Sequence
AY037803 Homo sapi
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                                 AXO69252 Sequence 101502 Sequence 3 AX32839 Sequence AX334507 Sequence AX334507 Sequence AX334507 Sequence AX335376 Sequence AX335376 Sequence AX33560 Human mRNA AX01489 Sequence ACO708 Homo sapi ALO35660 Human SLPT A08111 Synthetic A A08110 Synthetic A A08010 Synthetic A A0800285 Sus scrof
                                                                                                                                                                                                                                                                                                                                                                                       L10920 Chicken KAL
AJ223217 Bos tauru
AJ23218 Bos tauru
AX334505 Sequence
AX335289 Sequence
AX35639 Sequence
AX35639 Sequence
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AL591512 Mouse DNA
AB076019 Tribolodo
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AL596122 Mouse DNA
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synthetic construct
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Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D.
Polypeptides and polypeptide analogues with inhibitory activity
gaginst human elastase
Patent: EP 0402068-A 29 12-DEC-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
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PAT 21-AUG-1995
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attificial sequences.

(bases 1 to 206)
Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D.
Polypeptides and polypeptide analogues with inhibitory activity
paginst human elastase
Patent: EP 0402068-A 27 12-DEC-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
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                                                                                artificial sequences.

(bases 1 to 206)

(thristophers,E., Schroder,J.M., Pioli,D., Wiedow,O. and Edge,M.D. Polypeptides and polypeptide analogues with inhibitory activity against human elastase
Patent: EP 0402068-A 28 12-DEC-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  artificial sequences.

1 (bases 1 to 347)

Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D. Polypeptides and polypeptide analogues with inhibitory activity against human elastase
Patent: EP 04020668-A 30 12-DEC-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
Location/Qualifiers
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TITLE
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Homo sapiens

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 434)

Wang, T. and Dillon, D.C.

Compositions and methods for therapy and diagnosis of head/neck and
lung squamous cell carcinoma

Patent: WO 0065053-A $ 02-NOV-2000,

CORIXA CORPORATION (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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antileukoproteinase; elafin; elastase inhibitor; proteinase
inhibitor; psoriasis; SKALP; transglutaminase substrate.
Homo sapiens.
                                  21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
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AX041087.
AX041087.1 GI:11340657
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09-833799-13B (1-57) x A31089 (1-347)
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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu 20
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//taaslation="WRASSFLIVVFLIAGTLVLEAAVTGVPVKGQDTVKGRVPFNGQ
/PVKGQDVSVKGQDFVKRQDFVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
KCCEGSCGMACFVPQ"
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          Molhuizen, H.O., Alkemade, H.A., Zeeuwen, P.L., de Jongh, G.J., Wieringa, B. and Schalkwijk, J. SKALP/elafin: an elastase inhibitor from cultured human teratinocytes. Purification, cDNA sequence, and evidence for transglutaminase cross-linking J. Biol. Chem. 268 (16), 12028-12032 (1993)
                                                                                                                                                              Direct Submission
Submitted (20-NOV-1992) Molhuizen H.O.F., Academic Hospital,
Dermatology, Nijmegen, The Netherlands, 6500 HB
Location/Qualifiers
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/product="skin-derived antileukoproteinase"
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/db_xref="GI:28712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="skin-derived antileukoproteinase"
/function="proteinase inhibitor"
142 c 119 g 115 t
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/clone_lib="HL1110b Clonetech"
/ 4.78
| partial
/citation=[1]
3. 356
/function="proteinase inhibitor"
/citation=[1]
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Mismatches:
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AX397178
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Matches:
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Gaps:
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/db_xref="taxon:9606"
/clone="pGESKA"
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synthetic construct
artificial sequences.

1 (bases 1 to 504)
Christophers,E., Schroder,J.M., Pioli,D., Wiedow,O. and Edge,M.D.
Christophers,E., Schroder,J.M., Pioli,D., Wiedow,O. and Edge,M.D.
applyreptides and polypeptide analogues with inhibitory activity
against human elastase
Patent: EP 0402068-A 31 12-DEC-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                        King, G.E., Meagher, M.J., Xu, J. and Secrist, H. Compositions and methods for the therapy and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 199
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/organism="synthetic construct"
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CORIXA CORPORATION (US)
Location/Qualifiers
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DNA fragment from patent EP0402068.
A31090
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/db_xref="taxon:9606"
_105 c 139 g 120
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| 152 c 120 g
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Contact: MGC help desk
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HUMELAFIN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
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Submitted (23-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
158 GCGCAAGACCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 217
                                                            199 GCGCAAGAGCCAGTCAAAGGTCCACTACACTAAGCCTGGCTCCTGCCCCATTATCTTG 258
                                               40
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                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
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                                                                                                  41 ileiysiysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                                                                                                                                                   1 (bases 1 to 571)
Sager, R., Zou, Z., Lee, S. Whan. and Tomasetto, C. Laure.
Cancer diagnosis using nucleic acid hybridization
Patent: US 5688641-A 14 18-NOV-1997,
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                  Sequence 14 from patent US 5688641.
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167 c 130 g
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Homo sapiens
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Best Local Similarity:
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 19 Row: d Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505786. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAH10952.1"
| Ma_xxfe="d1:15012095"
| /translation="WRASSFLIVVPLIAGTLVLEAAVTGVPVKGQDTVKGRVPFNGQ
| ppvkGQvSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
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                                                 CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadangesystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="Similar to protease inhibitor 3, skin-derived
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Homo sapiens (library: lambda EMBL) DNA, clone lambda hI-G1.
Homo sapiens
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/db xref="taxon:9606"
/db xref="MGC:13613 IMAGE:4083155"
/tissue type="Brain, glioblastoma"
/clone_lib="NIH_MGC_57"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Sequence 4153 from Patent WO0194629.
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/db_xref="071:219615"
/translation="MRASSFLIVVVFLIAGTLVLEAAVTGVPVKGQDTVKGRVPFNGQ
DPVKQQVSVKQQDKYKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
KCCGGSCGMACFVPQ"
                                                                                         Hirose, S.
Direct Submission
Submitted (01-SEP-1992) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; Ookayama, Meguro-ku,
Tokyo 152, Japan (Tel:03-3726-1111(ex.2226), Fax:03-3729-0335)
Submitted (01-SEP-1992) to DDBJ by:
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Primary structure of the human elafin precursor preproelafin deduced from the nucleotide sequence of its gene and the presence of unique repetitive sequences in the prosegment Biochem. Biophys. Res. Commun. 185 (1), 240-245 (1992)
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/db_xref="taxon:9606"
/clone_lib="lambda_EMBL"
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Tokyo Institute of Technology
Ookayama, Meguroku
Tokyo 152
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/product="elafin"
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                           1. .2309
/organism="Homo sapiens"
/db_xref="taxon:9606"
a 537 c 603 g 572
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_537 c 603 g
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AX333644.
AX333644.1 GI:18124363
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Alignment Scores:
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KEYWORDS
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/product=alafin_precursor"
/product=alafin_precursor"
/protein_id="AAA36483.1"
/db_xref="G1:190338"
/tb_xref="G1:190338"
/tb_xref="G1:100"
/t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Characterization and gene sequence of the precursor of elafin, an elastese-specific inhibitor in bronchial secretions Am. J. Respir. Cell Mol. Biol. 8 (4), 439-445 (1993) 93236929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 2309)
Sallenave, J.M. and Silva, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            j98. .401
join(517. .595,1453. .1727)
/function="elastase-specific proteinase inhibitor"
/note="elafin has been sequenced at the protein level;
pre-elafin has not; its existence is assumed from its
molecular weight (PAGE analysis); putative"
                                                                                                                                                                                                       1554 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 1613
                                                                                                                                                                                                                                                                                                                     20
                                                                                                                                                                                                                                                                                 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                   1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
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                                                                                                                                                                                                                                                                                                                                                                                               41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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L10343
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/tissue_type="placenta"
/tissue_lib="EMBL-3 (from Clontech)"
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  Mismatches:
Indels:
Gaps:
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                                                                                                           09-833799-13B (1-57) x AX334316 (1-2309)
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537 c
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/number=1
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Homo sapiens
Best Local Similarity:
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BASE COUNT 595
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                             Query Match:
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PRI 23-JUL-1993
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| protein_id="Anaba5371.1"
| db_xref="GI:29981"
| translation="MRASSFLIVVPFLIAGTLVLEAAVTGVPVKGQDTVKGRVPFNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
KCCEGSCGMACFVPQ"
                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear PRI 23-JUL-195
pre-elafin=elastase-specific inhibitor [human, placental, Genomic, 5309 nt].
589717
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Am. J. Respir. Cell Mol. Biol. 8 (4), 439-445 (1993)
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Sallenave, J.M. and Silva, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="pre-elafin"
join(517. :595,1453. :1727)
/gene="pre-elafin"
/note="elastase-specific inhibitor; This sequence comes
                                                                                                                                                                              GenBank staff at the National Library of Medicine created this entry [NCBI glabbag 130251] from the original journal article. This sequence comes from Fig. 4.
Location/Qualifiers
                                                                                                                                                                                                                                  21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                      1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLu
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join(398. .595,1453. .1727,1962. .2119)
517. .1727
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Conservative:
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Indels:
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                                                            Indels:
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                                                                                                                  09-833799-13B (1-57) x HUMPREELAS (1-2309)
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Homo sapiens
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                                          Best Local Similarity:
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Best Local Similarity:
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8476637
                  Percent Similarity:
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ACCESSION VERSION

KEYWORDS

SOURCE

DEFINITION

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human.

ORGANISM

Sehra, H.

AUTHORS

JOURNAL

COMMENT

FEATURES

REFERENCE

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Note="Charlie2 repeat: matches 3534, .3727 of consensus"
14238. .14548
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note="LIMA8 repeat: matches 4484. .6153 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1MC4 repeat: matches 7650. .7849 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSg/x repeat: matches 136. .308 of consensus"
                                                                                     /note="L1MB1 repeat: matches 5294. .6159 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1M4b repeat: matches -263. .330 of consensus"
21634. .21829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MER74A repeat: matches 248. .557 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1M4 repeat: matches 3850. .3998 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="MER20 repeat: matches 109. .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1M3e repeat: matches 22. .1826 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="LTR16B repeat: matches 2. .461 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L2 repeat: matches 2329, .2497 of consensus"
6548. .6731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="L2 repeat: matches 2021. .2087 of consensus"
8286. .6466
                                                                                                                    2001. .2042

1001e="21 copies 2 mer ta 83% conserved"

2072. .3376

100te="L1 repeat: matches 5193. .5300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="HERVL repeat: matches 4. .2665 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1 repeat: matches 4299. .4610 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MLT2B repeat: matches 1. .444 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1. .312 of consensus"
1294. .4592
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MER20 repeat: matches 7. .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluSx repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="HAL1 repeat: matches 1501. .1692 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="30 copies 2 mer ct 75% conserved" 4492. .17136
                                                                                                                                                                                                                                                                                                                              /note="18 copies 2 mer at 80% conserved" complement(2469. .2951)
                                                                                                                                                                                                                                                                  copies 2 mer ta 84% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="19 copies 2 mer gt 94% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="FLAM_A repeat: matches 1.589. .10634
                         note="match: STS: Em:HS211D12S"
                                                                                                                                                                                                                                                                                                                                                                                          'note="match: GSS: Em:AQ809877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="match: GSS: Em:AQ386436"
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14337. .14396
complement (1. .100)
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                                                                                                                                                                                                                            /note="16 com
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   misc_feature
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Direct Submission

Direct Submission

Submitted (129-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Nov 27, 2000 this sequence version replaced gi:10198636.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
requests: clonered of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone name. Note that the
variation annotation may not be found in the sequences with
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw.; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
and paper database can be found at
http://www.sanger.ac.uk/FGP/Chr20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/FGP/Chr20
IMPORTANT: This sequence is not the entire insert of clone
RP1-172H20 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP1-10112 is at 100 in this sequence. The true right end of clone RP1-21012 is at 28594 in this sequence. The true right end of clone RP1-21012 is at 100 in this sequence. This true right end of clone RP1-21012 is at 100 in this sequence. This requence was made to resolve all sequenced all regions were either double-stranded or sequenced noted all regions were either double-stranded or sequenced or sequenced by at least one plasmid subclone and the assembly was confirmed by restriction digest.
RP1-17H20 is from the library RPC1-1 constructed by the group of Pleter de Jong. For further details see
http://www.accept.corg.uccept.corg.uccept.corg.uccept.corg.uccept.corg.uccept.corg.uccept.corg.uccept.corg.uccept.corg.uccept.corg
                                                                                                                                                                                                                                                                                                                                                                                                                         HSJ172H20 99747 bp DNA linear PRI 07-APR-2001 Human DNA sequence from clone RPI-172H20 on chromosome 20q12-13.12 Contains SEMG1 and SEMG2 genes for semenogelin I and II, the Pl3 gene for protease inhibitor 3, skin-derived (SKALP), ESTs, STSs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                  1554 GCGCAAGAGCCAGTCAAAAGGTCCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 1613
                                                                                                                                                          21 IleargCysalaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
   1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu 20
                                                                                                                                                                                                                                                                                                     1674 Archaghaerecrerendaneecrerrecessaresecrerrecerecens 1724
                                                                                                                                                                                                                                         41 IleLysLysCysCluGlySerCysGlyMetAlaCysPheValProGln 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; PI3; SEMG1; SEMG2; SKALP.
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/map="q12-13.12"
/clone="RP1-172H20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete sequence.
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VECTOR: pCYPAC2.
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.122 of consensus"

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31730. 31886
/note="LiM1 repeat: matches 859. 987 of consensus"
31209. 34261
/note="LiM3 repeat: matches 859. 1833 of consensus"
34232. 34942
/note="LiM1 repeat: matches 1560. 2657 of consensus"
34941. 36117
/note="Li repeat: matches 3935. 5142 of consensus"
36118. 36412
/note="Allulo repeat: matches 9. 292 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #6081. .46114

**Mocte="17 copies 2 mer to 82% conserved"

#6492. .46761

#6828. .46915

/note="LIME repeat: matches 5521. .5793 of consensus"

#6828. .46915

/note="LIME3A repeat: matches 5300. .5388 of consensus"

#6916. .47210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13119. 45775
note="LIPA15 repeat: matches 3467. 6157 of consensus"
18840. 45956
note="LIME repeat: matches 5530. 5647 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17211. 47769
/note="LIME3A repeat: matches 5388. 5937 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L1 repeat: matches 4912, .5038 of consensus" 37434. .37469

Note="L1P repeat: matches 2850. .2885 of consensus" 83377. .39183

Note="L1M4C repeat: matches 1312. .1666 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J2261. 42088 "note="LiPA15 repeat: matches 671. .3485 of consensus" 12057. .43098 "note="LiPA5 repeat: matches 5104. .6143 of consensus" note="LiPA5 repeat: matches 5104. .6143 of consensus"
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match: ESTs: Em:AA527557 Em:AA583567 Em:AA582866"
                                                                                      /note="LTRi6A repeat: matches 201. .378 of consensus" 27612 .27639 /note="14 copies 2 mer ac 100% conserved" /note="L1036 repeat: matches 202. .531 of consensus" 28959 .29336
'note="L1M4b repeat: matches 330. .524 of consensus"
                                                                                                                                                                                                                                 7.000 matches 469. .859 of consensus" 29337. .2971

7.00te="THEIC repeat: matches 1. .371 of consensus" 29712. .31317

/note="THEIC-internal repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L1 repeat: matches 2905. .3780 of consensus" 7299. .37425
                                           /note="Alusx repeat: matches 1. .309 of consensus" 25460. .25629
                                                                                                                                                                                                                                                                                                                                                                                       31318. .31729
| note="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluSq repeat: matches 1. .305 of consensus"
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19535. .51104
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join(49537. .49615,50475. .50749)
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8638. 48679
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Length: Matches: Conservative:

5.78e-26 327.00 100.00%

Percent Similarity:

Pred. No.:

CDS

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linear PAT 28-JUL-1999
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                                                                                                   50576 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 50635
                                                                                                                                                                       Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
1 (bases 1 to 8598)
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Ishima,Y., Okawa,N., Yoshida,M., Amagaya,S. and Kaji,A. Elafin derivative
Patent: US 734014-A 3 31-MAR-1998;
Location/Qualifiers
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Sequence 3 from patent US 5734014.
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                                                         09-833799-13B (1-57) x HSJ172H20 (1-99747)
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JP 1998127292-A/1.
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Pichia pastoris
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Best Local Similarity:
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ELAFINS-EXPRESSION VECTOR AND PRODUCTION OF ELAFINS BY UTILIZING
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                                                    Pichia pastoris
JP 1998127292-A/1
19-M2-1998
31-OCT-1996 JP 1996304233
TANIXAMA MITSUE, YAMAMOTO TAKASHI, OKAWA NORIYUKI, PI
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FT /note='native Pichia elafin'.
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Ishima,Y., Okawa,N., Yoshida,M., Amagaya,S. and Kaji,A.
Blafin derivative
Patent: US 5734014-A 5 31-MAR-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      /product='improved Pichia elafin'
949. .1203
1204. .1374
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/clone='pPIC9/ELF25L'
949. .1377
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Matches:
Conservative:
Mismatches:
Indels:
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                        Patent: JP 1998127292-A 1 19-MAY-1998;
TSUMURA & CO
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/organism="Pichia pastoris"
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(Cl2P21/02,Cl2R1:84);
strandedness: Double;
topology: Linear;
hypothetical: No;
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ACCESSION
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Ishima,Y., Okawa,N., Yoshida,M., Amagaya,S. and Kaji,A.
Elafin derivative
Patent: US 5734014-A 7 31-MAR-1998;
Location/Qualifiers
1.177
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Sequence 11 from patent US 5688641.
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/organism="unknown"
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/organism="Bos taurus"
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/gene="bTrappin-2"
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Zeeuwen, P.L., Hendriks, W., de Jong, W.W. and Schalkwijk, J. Identification and sequence analysis of two new members of the SKALP/elafin and SPAI-2 gene family. Biochemical properties of the transglutaminase substrate motif and suggestions for a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Boinae, Bos.

1 (bases 1 to 573)
Zeeuwen, P. L. J. M.
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**Michinga, B. and Schalkwijk, J.
**SKALF/elafin: an elastase inhibitor from cultured human keratinocytes. Purification, cDNA sequence, and evidence for transglutaminase cross-linking J. Biol. Chem. 268 (16), 12028-12032 (1993)
                                                                                                                                                                                                                                                                                                                                                                                 1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
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                                                                                    1 (bases 1 to 321)
Sager, R., Zou,Z., Lee,S.Whan. and Tomasetto,C.Laure.
Cancer diagnosis using nucleic acid hybridization
Patent: US 5688641-A 11 18-NOV-1997;
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158 c 145 g 107 t
                                                                                              Accelerated evolution in inhibitor domains of porcine elafin family
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PVKGQDPVKGQDPVKGQEPVKGQDPVKGQDPVKRQGRIGGPLLTKPGSCPRVLIRCAM
MNPPNRCLRDAQCPGVKKCCEGSCGKTCMDPQ"
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (sites)
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4 (bases 1 to 573)
Tamechika, I., Itakura, M., Saruta, Y., Furukawa, M., Kato, A.,
Tachibana, S. and Hirose, S.
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Direct Submission
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QGPVRGKDQVKGQGPVKGQDLGKSQDPVKAQLPDKGQDLGKGEDSVKGQDPFKAQLPD
KLQDPVKAQPAIKRLILLTKPGSCPRILIRCLMVNPPNRCLSDAQCPGLKKCCEGFCG
                       Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                            Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of technology, Department of Balogoitaal Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1771 CAAGATCCAGTGAAAGCCCAACCTGCAATCAAACGTCTAATCTTACTCACCAAGCCTGGC 1830
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Tamechika,I., Itakura,M., Saruta,Y., Furukawa,M., Kato,A.,
Tachibana,S. and Hirose,S.
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Conservative:
Mismatches:
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join(629. .710,1541. .1962)
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/organism="Sus scrofa"

/b_xref="taxon:9823"

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/clone="lambda WAP-1"
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/note="SINE (PRE-1)"
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/note="TG repeat"
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/product="elafin"
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/number=2
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/number=1
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                                                                                                     Hirose, S.
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/product="elafin (trappin-2)"
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IRCMMVNPPNRCLSDAQCPGVKKCCEGFCGKECLNPR"
                                                                                                                                                                                                                                                     AB003281 1128 bp DNA linear MAM 26-MAY-1999
Phacochoerus aethiopicus gene for elafin (trappin-2), partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-APR-1997) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Phacochoerus.
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                               1891 GATGCTCAGTGCCCAGGGCTCAAGAAGTGCTGTGAAGGCTTTTGCGGGAAGGCCTGTATG 1950
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35 AspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMetAlaCysPhe
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Phacochoerus aethiopicus DNA.
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Pig mRNA for elafin family member protein, complete cds.
D50322
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                                                                                                                                                                                                                         Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of rechnology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mall:shiroseapio:titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                              Sus scrofa cDNA to mRNA, clone:WAP-5.
Sus scrofa
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="WAP-5"
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/note="PCR primer"
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/note="PCR primer"
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/product="unnamed"
97. .447
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CEGFCGKDCMDPK"
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Submitted (23-FBB-1996) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(B-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
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Tamechika, I., Itakura, M., Saruta, Y., Furukawa, M., Kato, A., Tachibana, S. and Hirose, S.
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Purutani,Y., Kato,A., Yasue,H., Alexander,L.J., Beattie,C.W. and
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On Apr 29, 1997 this sequence version replaced gi:1209380.
Sequence updated (21-Apr-1997).
Location/Qualifiers
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Sus scrofa gene for elafin homolog, exon2, partial cds.
D83668
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Journal of Biological Chemistry (1996) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elafin homolog; elastase inhibitor.
Sus scrofa DNA, clone_lib:PCR product.
Sus scrofa
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/product="elafin homolog"
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<1. .208
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/note="exon2 part"
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/number=2
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MAM 26-MAY-1999
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373. .555
/product="elafin homolog"
/function="elastase specific inhibitor"
/function="elastase specific inhibitor"
/note="Mature protein has a characteristic
disulfide-linked structure called four disulfide core or
WAP motif"
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Pecari tajacu gene for trappin, partial cds.
AB003283
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/db_xref="taxon:9829"
<212..675
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/protein_id="BAA77827.1"
/db_xref="GI:4887642"
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/note="PCR primer"
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Accelerated evolution in inhibitor domains of porcine elafin family
                  KGQDPVKGQDLVKGQDPVKAQLPDKGQDLVKGQDPVKGQDPVKDQDPVKAELAVRRLV
LPRRKPGFCPMIKIRCALFNPPNRCLTDAGCPGARKCCIGSCGKACLNPVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 15-DEC-1998
/translation="RPKGQGTKKGHALIKGQDPVRGQGPVKGQDPVKAQLPDKGQDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zeeuwen, P.L., Hendriks, W., de Jong, W.W. and Schalkwijk, J. Identification and sequence analysis of two new members of the SKALP/elafin and SPAI-2 gene family. Biochemical properties of the transglutaminase substrate motif and suggestions for a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-JAN-1998) Zeeuwen P.L.J.M., Dermatology, University Hospital Nijmegen, PO BOX 9101, 6500 HB Nijmegen, THE NETHERLANDS 2 (bases 1 to 270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ223215.1 GI:2764783
proteinase inhibitor; putative; sTrappin-2 gene; transglutaminase
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Macaca mulatta mRNA for putative sTrappin-2 protein, partial.
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Tachibana,S. and Hirose,S.
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Zeeuwen, P.L.J.M.
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MAM 14-APR-2000
   Direct Submission
Submitted (21-APR-1997) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (Dases 1 to 483)

Kuroki,J., Hosoya,T., Itakura,M., Hirose,S., Tamechika,I.,
Yoshimoto,T., Ghoneim,M.A., Nara,K., Kato,A., Suzuki,Y.,
Furukawa,M. and Tachibana,S.
Cloning, characterization, and tissue distribution of porcine S
a protein with a transglutaminase substrate domain and the WAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697 CGCTGCCTTGGATTCTTCTCCGTTGCCCGCTGGCCAATCCCTCTAACAAGTGTTGGAGA 756
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                                                                                                                               /organism="Phacochoerus aethiopicus"
/db_xref="taxon:85517"
<203. .828
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95403443
Hirose, S.
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partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phacochoerus aethiopicus DNA.
Phacochoerus aethiopicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Phacochoerus.
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transglutaminase cross-linking
J. Biol. Chem. 268 (16), 12028-12032 (1993)
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BGGPGVWCHZILLIGQDPVKGQDPVKGQDPVKGQDLVKSQDLVKSQDFVKAELPDIGQD
VVKGHEPVEGQDPVNAQLPDKVQDPVKAQPAVPGRFLLSKRGHCPRILFRCPLSNPSN
KCWRDYDCPGVKKCCEGFCGKDCLYPK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA containing a sequence encoding Na+, K+-ATPase inhibitory peptide (SPAI:sodium ion, potassium ion ATPase inhibitory peptide). E06782
        Submitted (27-SEP-1993) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726, Pax:045-924-5824)
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/db xref="taxon:9823"
/cbll.line="NM538"
/clone lib="lambdaEMBL3 SP6/T7"
join(DI7754.1:1. .82,1. .482)
/note="preproSPAI-2"
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                                                                                               Submitted (27-Sep-1993) to DDBJ by:
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/protein_id="BAA04603.1"
/db_xref="GI:1054617"
                                                                                                                               Department of Biological Sciences
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                                                                                                                                             Tokyo Institute of Technology
4259 Nagatsuta-cho, Midori-ku
Yokohama, Kanagawa 226
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   Direct Submission
                                                                                                                Shigehisa Hirose
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Sus scrofa cell_line:NM514 cDNA to mRNA, clone_lib:lambda gt10.
Sus scrofa
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, Suina; Suid.

Jubana,S.

Jubana
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D83667 D17753
D83667.1 GI:1304046
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_192 c 182 g
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/organism="Sus sp."
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Tamechika, L., Itakura, M., Saruta, Y., Furukawa, M., Kato, A., Tachibana, S. and Hirose, S. Accelerated evolution in inhibitor domains of porcine elafin family
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ERGPGPVWCHZILDIGQDPVKGQDPVKGQDPVKGQDLVKSQDBVKAELPDIGQD
VVKGHEPVBGQDPVMAQLPDKVQDPVKAQPAVPGRFLLSKRGHCPRILFRCPLSNPSN
KCWRDYDCPGVKKCCEGFCGKDCLYPK"
                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                  Sus scrofa DNA, clone_lib:EMBL SP6/T7 clone:lambda WAP-2.
Sus scrofa
                                                                                                                                                                                 J. Biol. Chem. 271 (12), 7012-7018 (1996)
96215132
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join(629. .710,1552. .2033)
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/db_xref="GI:1228060"
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/clone="lambda WAP-2"
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/note="SINE (PRE-1)"
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/product="SPAI-2"
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/number=2
                     D50320.1 GI:1228059
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3 (bases 1 to 3782)
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/number=2
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Yoshimoto,T., Ghoneim,M.A., Nara,K., Kato,A., Suzuki,Y.,
Furukawa,M. and Tachibana,S.
Cloning, characterization, and tissue distribution of porcine SPAI,
a protein with a transglutaminase substrate domain and the WAP
                                                                                                                                                                         Direct Submission
Submitted (21-FEB-1996) Shigehisa Hirose, Tokyo Institute of Submitted (22-FEB-1996) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; Ookayama, Meguro-ku, Tokyo 152, Japan (Tel:81-3-3726-1111, Fax:81-3-3729-0335) On or before Mar 17, 1999 this sequence version replaced g1:2078450, g1:1054611, g1:2077950.
D17753:Submitted (27-Sep-1993) to DDBJ by:Shigehisa Hirose.
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                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/db xref="taxon:9823"
/cell_line="NM514"
/clone_lib="lambda gt10"
61. .624
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/product="proSPAI-2"
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/product="SPAI-2"
722
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Hirose, S.
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/translation="MRSRSFLVLVAVFLICETLVAQRPEKIRGPKGGGQDPVEGQDQD
KGGGPVKVEILDIGQDLVKRPDPVKGQDPVKGQDLVKSQDPVKAELPDIGQDVVKGHD
PVEGQDPVNAQLPDKVQDPVKAQPPVQGRLLHYKPGLCPWIFLRCPLPKPPNKCWRDS
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Matches:
Conservative:
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/db_xref="taxon:10116"
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/note="PCR primer"
                                                               15. .77
375. .557
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97. .561
/number=2
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D50323
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Tamechika, I., Itakura, M., Saruta, Y., Furukawa, M., Kato, A.,
Tachibana, S. and Hirose, S.
Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furutani, Y., Kato, A., Yasue, H., Alexander, L.J., Beattie, C.W. and
                                                                                                                                                                                               1842 CAAGATCCAGTCAAAGCCCAACCTGCAGTCCCAGGTCGATTCCTTCTCTTTAAGCGTGGC 1901
                                                                                                                                                                                                                                                    1962 GATTATGACTGTCCAGGGGTCAAGAAGTGCTGTGAAGGCTTTTGCGGGAAGGATTGTTTG 2021
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                                                                                                                                                                                                                                                                                              35 AspThrAspCysProGlyIleLysLysCysCluGlySerCysGlyMetAlaCysPhe 54
                                                                                                                                                                2 GinGluProValLysGlyPro------ValSerThrLysProGly 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evolution of the trappin multigene family in the Suidae J. Biochem. 124 (3), 491-502 (1998)
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/produce="elafin family member protein"
/protein id="BAA08858.1"
/db_xreff="GI:1864016"
                 3782
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                  Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elafin family member protein.
Sus scrofa cDNA to mRNA, clone:WAP-4.
Sus scrofa
                                                                                Indels:
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'note="PCR primer"
                                                                                                                                 09-833799-13B (1-57) x PIGWAPB (1-3782)
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490 pmRNA linear ROD 29-AUG-1999 complete cds.
AF178426
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Song.X., Zeng.L., Jin,W., Thompson,J., Mizel,D.E., Lei,K.,
Billinghurst,R.C., Poole,A.R. and Wahl,S.M.
Secretory leukocyte protease inhibitor suppresses the inflammation and joint damage of bacterial cell wall-induced arthritis
J. Exp. Med. 190 (4), 535-542 (1999)
9380355
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Song,X.-y. and Zeng,L.
Subrect Submission
Submitted (17-AUG-1999) Oral infection & Immunity Branch, National
Institute of Dental & Craniofacial research, 9000 Rockville Pike,
Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                    444 TTTTTACGTTGCCCGTGCCCAAACCCTGCTAACAAATGTTGGAGAGATTCTCACTGCCCA 503
                                                              384 GCCCAACCTCCAGTCCAAGGTCGATTACTTCACTATAAGCCTGGCCTCTGCCTTGGATT 443
1 AlaGlnGluProValLysGlyPro---ValSerThrLysProGlySerCysProllelle 19
                                                                                                                                    20 LeulleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysPro 39
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LKLEKPECGTDWECPGKQRCCQDTCGFKCLNPVPIRGPVKKKPGRCVKFQGKCLMLNP
PNKCQNDGQCDGKYKCCEGMCGKVCLPPV"
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/db_xref="G1:3132274"
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RAGLPFKRGLCPRVRIHCNLWNPPNQCWRDAHCPGAKKCCEGFCGKTCMNPR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-FEB-1998) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:+81-45-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                                                                                                                                                                                                                                               4 ProValLysGlyProValSerThrLysProGlySerCysProllelleLeulleArgCys 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Furutani,Y., Kato,A., Yasue,H., Alexander,L.J., Beattie,C.W.
              /product="secretory leukocyte protease inhibitor"
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Location/Qualifiers
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codon start=1
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Hippopotamus amphibius gene for trappin, partial cds.
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Mammalia, Eutheria, Cetartiodactyla, Hippopotamidae, Hippopotamus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-APR-1997) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
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                                                                                                                                                                                                                                                                                    129 CAAGACCCAGTCAAAGGACAAGATGTAGTCGTAGCACAAAGACCGAGCCGGACTTCCATTC 188
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Evolution of the trappin multigene family in the Suidae
J. Biochem. 124 (3), 491-502 (1998)
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Mismatches:
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/note="PCR
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37. .>329
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JOURNAL
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304 ATGATGCTTAACCCTCCCAATGTCTGCCAGAGGGACGGGCAGTGTGACGGCAAATACAAG 363
       5 ValLysGlyProValSerThrLysProGlySerCysProllelleLeuIleArgCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/cell_line="ras-transformed 3T3 cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="serine protease inhibitor"
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MMU88093
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/product="antileukoproteinase"
/protein_id="haAa63446.1"
/db_xref="GI:164320"
/translation="WAPWAPEGAENALKGGACPPRKIVQCLRYEKPKCTSDWQCPDKK
KCCRDTCAIKCLNPVAITNPVKVKPGKCPVVYGQCMMLNPPNHCKTDSQCLGDLKCCK
                                                                                                                                                                                                                                                                                                                                                           MAM 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
I (Bases I to 600)
Farmer,S.J.; Fliss,A.E. and Simmen,R.C.
Complementary DNA cloning and regulation of expression of the messenger RNA encoding a pregnancy-associated porcine uterine protein related to human antileukoproteinase
Mol. Endocrinol. 4 (8), 1095-1104 (1990)
                                                                                                                                                                           435 GAGTGCTCCACATTAAATCCCCCAAAACGGTGTTTGAGAGATGCTCAGTGCCCAAGGAAC 494
                                                                                                                                                                                                         22 ArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlylle 41
                                                                                                                                                2 GlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeuIle
                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                        PIGALP

Porcine antileukoproteinase mRNA, complete cds. M57446
M57446.1 GI:164319
antileukoproteinase.

Porcine uterus. CDNA to mRNA, clone pALP.
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28
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                                       Conservative:
Mismatches:
Indels:
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/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone="pALP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="uterus"
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/gene="ALP"
           6.64e-10
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/codon start=1
/product=*secretory leukocyte protease inhibitor"
/produci=*secretory leukocyte protease inhibitor"
/prodein id="AAC53140.1"
/db xref="G1:1945383"
/translation="WKSCGLLPFTVLiALGILAPWTVEGGKNDAIKIGACPAKKPAQC
LKLEKPOCRTDWECPGKGCQDACGSKCVNPVPIRKPVWRKPGRCVKTQARCMMLNP
LKLEKPOCRTDWECPGIGGKVCLPPM"
179 c 177 g 158 t
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Mus musculus secretory leukocyte protease inhibitor mRNA, complete
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 671)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zithik,R.J., Zhang,J., Kashem,M.A., Kohno,T., Lyons,D.E., Wright,C.D., Rosen,E., Goldberg,I. and Hayday,A.C.
The cloning and characterization of a murine secretory leukocyte procease inhibitor cDNA
Biochem. Biophys. Res. Commun. 232 (3), 687-697 (1997)
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Submitted (31-JAN-1997) Internal Medicine, Yale University, 333 Cedar Street, New Hayen, CT 06520, USA
Location/Qualifiers
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                                             284 Argercaacceccaarcacracaagacagacagecagracergagracrraaarac 343
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24
                                                                                                                                                       25 MetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCys 44
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 67 Row: j Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755573. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MKSCGLLPFTVLLALGILAPWTVEGGKNDAIKIGACPAKKPAQC
LKLEKRQCRTDWECPEKQRCCODACGSKCVNPVPIRKPVWRKPGRCVKTQARCWMLNP
WVCQRDGGKYKCCEGTGKVCLPPM"
242 c 233 g 214 t
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                                                                                                                                                               Chordata, Craniata, Vertebrata, Buteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                        Direct Submission
Submitted (23-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ProvalLysGlyProvalSerThrLysProGlySerCysProllelleLeulleArgCys 23
Mus musculus, secretory leukocyte protease inhibitor, clone MGC:41142 IMAGE:1513866, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/product="secretory leukocyte protease inhibitor"
                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
CDNA Library Preparation: Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Mammary gland, lactating mouse"
/clone_lib="Soares_mammary_gland_NMLMG"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="MGC:41142 IMAGE:1513866"
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Mismatches:
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|db_xref="G1:20306996"
|db_xref="LocusID:20568"
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                                                                  BC028509.1 GI:20306995
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                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 894)
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                                                                                                                                         Mus musculus
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                                                                                                                   house mouse.
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DEFINITION
                                                                                                                                       ORGANISM
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                                                                                                                                                          ROD 29-OCT-1997
                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutleleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 682)
Abe, T., Tominaga, Y., Kikuchi, T., Watanabe, A., Satoh, K., Watanabe, Y. and Nukiwa, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MKSCGLLPFTVLLALGILAPWTVEGGKNDAIKIGACPAKKPAQC
LKLEKPQCRTDWECPGKQRCCQDACGSKCVNPVPIRKPVWRKPGRCVKTQARCMMLNP
PNVCQRDGQCDGKYKCCEGICGKVCLPPM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Abe,T., Tominaga,Y., Kikuchi,T., Watanabe,A., Satoh,K., Watanabe,Y. and Nukiwa,T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROD 07-AUG-2002
                                                                                                                                                   MMU94341
Mus musculus secretory leukoprotease inhibitor mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-MAR-1997) Department of Respiratory Oncology and Molecular Medicine, Institute of Development, Aging and Cancer, Tohoku University, 4-1 Seiryomachi, Aoba-ku, Sendai 980-77, Japan Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial pneumonia causes augmented expression of the secretory leukoprotease inhibitor gene in the murine lung Am. J. Respir. Crit. Care Med. 156 (4 Pt 1), 1235-1240 (1997)
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245 CCCATTCGCAAACCAGTGTGGAGAAGACTGGGAGGTGCGTCAAAACTCAGGCAAGATGT 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="secretory leukoprotease inhibitor"
/protein_id="AAC53394.1"
/db_xref="GI:1945451"
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/strain="B6CBA [C57Black/6 x CBA]"
/db_xref="taxon:10090"
/tissue_type="lung"
14..409
                                                        364 recreteredegiararerereseaaagrereceeeee 402
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Matches:
Conservative:
              44 CysCysGluGlySerCysGlyMetAlaCysPheValPro 56
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Chen, D.H., Xu, X.P., Bagchi, M.K. and Bagchi, I.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Function="serine protease inhibitor"
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAD34035.1"
/db_xref="GI:4929549"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 g
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                                                                                           AF151982.1 GI:4929548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="SLPI"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="SD"
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60.38%
52.83%
49.08%
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                                                              mRNA, complete cds.
                                                                                                                               Rattus norvegicus.
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                                                                                                                                              Rattus norvegicus
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Best Local Similarity:
Query Match:
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RESULT 43
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                AF151982
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/db_xref="G1:1763263"
/db_xref="G1:1763263"
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LKLENPQCRTDWECPGKQRCCQDACGSKCVNPVPIRKPVWRKPGRCVKTQARCMMLNP
PNVCQRDGGCDGKYKCCEGIGGKVCLPPM"
297 c 288 g 252 t
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                                                                                                                                                                                             Mus musculus secretory leukocyte protease inhibitor mRNA, complete
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Jin,F.Y., Nathan,C., Radzioch,D. and Ding,A.
Secretory leukocyte protease inhibitor: a macrophage product induced by and antagonistic to bacterial lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527 ATGATGCTTAACCCTCCCAATGTCTGCCAGAGGGACGGGCAGTGTGACGCCAAATACAAG 586
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                24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlylleLysLys 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1123)
Ding.A., Jin.F.-Y. and Nathan, C.F.
Direct Submission
Submitted (01-00T-1996) Medicine, Cornell University Medical
College, 1300 York Ave. Box 57, New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="secretory leukocyte protease inhibitor"
                                                                                                                                                                              linear
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Mismatches:
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                                                                                                                 587 TGCTGTGAGGGTATATGTGGGAAAGTCTGCCTGCCCCCG 625
                                                                               44 CysCysGluGlySerCysGlyMetAlaCysPheValPro 56
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/cell_line="RAW 264.7"
/cell_type="macrophage"
447. .842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Mus musculus"
                                                                                                                                                                              1123 bp
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Mus musculus
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Best Local Similarity:
Query Match:
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JOURNAL
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LKREKPECSTDWGCPGKQRCCQDTCGFKCLNPVPIRGPVKKPGRCLKFQGKCLMLNPP
NKCQNDGQCDGKYKCCEGMCGKVCLPPV"
ARIDIUME ROD 01-JUN-1999 MRNA linear ROD 01-JUN-1999 ARIUN STATUS SECRETORY leukocyte protease inhibitor (SLPI)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-MAY-1999) Center for Biomedical Research, The Population Council, 1230 York Avenue, New York, NY 100021, USA Location/Qualifiers
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/product="secretory leukocyte protease inhibitor"
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elafin family member protein.
Sus scrofa DNA, clone_lib:EMBL SP6/T7 clone:lambda WAP-3.
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40 GlylleLysLysCysCluGlySerCysGlyMetAlaCysPheValProGln 57

20 LeulleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysPro 39

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Tachibana, S. and Hirose, S.
Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                    Direct Submission
Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(B-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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/note="SINE (PRE-1)"
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/product="unnamed"
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951 c 1131 g
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3 (bases 1 to 3670)
Hirose, S.
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AB042257 464 bp mRNA linear ROD 30-OCT-2001 Cavia porcellus mRNA for caltrin-like protein II, complete cds. AB042257
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RHPPNKCTSDYDCPKPQKCCPGYCGKQCYQPE"
                                                                                                                                               Cavia porcellus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                         Coronel, C.E., San Agustin, J. and Lardy, H.A. Purification and structure of caltrin-like proteins from seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (26-APR-2000) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Bioscience; Nagatudacho4259 Midori-ku,
Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:81-45-924-5726,
Fax:81-45-924-5824)
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/codon_start=1
/product="codouct":
/protein_id="BAB70710.1"
/db_xref="GI:16519355"
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                                                                                                                             Cavia porcellus tissue_lib:seminal vesicle cDNA to mRNA.
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J. Biol. Chem. 265 (12), 6854-6859 (1990)
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/db_xref="SWISS-PROT:P22075"
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/db xref="taxon:10141"
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Matches:
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Evolution of caltrin-like protein
Unpublished
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Furutani, Y. and Hirose, S.
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Page 24

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REMERING.

RATCHERS.

RAINTAYD.M. Addans.C., Adio-Oducla, B., Ali-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are J.R., Ayele, M., Banks, T., Barbaria, J., Bewies, S., Brieva, M., Brown, R., Brown, M., Bryant, N.D., Boule, S., Brieva, M., Brown, R., Brown, M., Bryant, N.D., Carron, T.R., Carter, M., Caron, R., Charko, J., Charvez, D., Carron, T.R., Charler, M., Chardo, J., Charvez, D., Chen, G., Chen, G., Chowdhry, I., Christopoulos, C., Chen, G., Chen, G., Chowdhry, I., Ding, Y., David, R., Delandy, K.R., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delagdo, O., Denn, A.L., Ding, Y., Dinh, H.H., Barnhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Farlhart, C., Edgar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T. Perraguto, D., Flagg, N., Ford, J., Corter, P., Frantz, P., Falls, T. Perraguto, D., Flagg, N., Ford, J., Corter, P., Frantz, P., Harrandez, C., Harris, K., Harr, M., Halle, S., Hamilton, K., Harris, C., Harris, K., Harr, M., Halle, S., Hamilton, K., Harris, C., Harris, K., Harr, M., Halle, S., Hume, J., Jacobson, B., Jia, Y., Uhonson, R., Jolivet, S., Jouch, J., Kovar, C., Karlsson, E., Kally, S., Khan, U., King, L., Korah, J., Kovar, C., Lid, J., Liu, M., Loulseged, H., Maheshwari, M., Mapia, P., Martin, R., Martin, R., Marin, R., Marin, R., Marin, R., Marin, R., Marin, R., Martin, R., Ma
                                                                                                                                                                                                                                                                                                         Rattus norvegicus clone CH230-8B11, *** SEQUENCING IN PROGRESS ***, AC unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                     27 AsnProProAsnArgCysLeuLysAspThrAspCysProGlylleLysLysCysCysGlu 46
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Direct Submission

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Submitted (10-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.
On Jul 9, 2002 this sequence version replaced gi:18874114.

Center: Baylor Center Center Center Center and EDM Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 70 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * arbitrary. Gaps between the contigs are represented as tuns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: Plasmid,
Sequencing vector: Plasmid,
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 131293 bases at least 040
Consensus quality: 142936 bases at least 020
Consensus quality: 142936 bases at least 020
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1171: gap of unknown length
2607: contig of 1017 bp in length
3824: contig of 1017 bp in length
3824: gap of unknown length
4860: contig of 1017 bp in length
4860: contig of 1018 bp in length
6834: gap of unknown length
6834: gap of unknown length
8334: contig of 1774 bp in length
8434: gap of unknown length
8434: gap of unknown length
11608: gap of unknown length
11608: contig of 1329 bp in length
11608: gap of unknown length
11508: gap of unknown length
11515: contig of 1318 bp in length
11550: gap of unknown length
11550: contig of 1385 bp in length
11515: contig of 1385 bp in length
12511: contig of 1385 bp in length
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12513: contig of 1385 bp in length
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Center clone name: CH230-8B11
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194143 Conservative: Mismatches: Length: Matches: Indels: Gaps: 3.16e-06 156.00 54.72% 50.94% 47.71% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

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ROD 26-JAN-1999
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                    Mus musculus secretory leukoprotease inhibitor gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 2435)
Kikuchi, T., Abe, T., Hoshi, S., Matsubara, N., Tominaga, Y., Satoh, K. and Nukiwa, T.
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Kikuchi, T., Abe, T., Hoshi, S., Matsubara, N., Tominaga, Y., Satoh, K.
and Nukiwa, T.
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Submitted (06-MAY-1997) Department of Respiratory Oncology and
Molecular Medicine, Institute of Development, Aging and Cancer,
Tohoky University, 4-1 Seiryo-machi, Aoba-ku, Sendai, Miyagi-ken
                                                                  58638 CCCTATCTCTCACCAGTGAAGAAGAGCCTGGGAGGTGCCTCAAATTTCAAGGAAAATGT 58697
                                                                                                                                    58698 CTGATGCTTAACCCTCCCAATAAGTGCCAGAATGACGCCCAGTGTGATGGCAAATACAAA 58757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structure of the murine secretory leukoprotease inhibitor (Slpi) gene and chromosomal localization of the human and murine SLPI
                                   4 ProValLysGlyProValSerThrLysProGlySerCysProllelleLeulleArgCys 23
                                                                                                    24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlylleLysLys 43
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/strain="129SV"
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/chromosome="2"
09-833799-13B (1-57) x AC112730 (1-194143)
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/db_xref="taxon:10090"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL, Sw., SMISSPROT, TT., TREMBL, Wp., WORMPEP; Information on the WORMPEP database can be found at.
                                                                                                                                                                                                                                                                                                                                  linear ROD 17-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                  Mouse DNA sequence from clone RP23-462016 on chromosome 2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
umquaryasanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 20, 2001 this sequence version replaced gi:15020991.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-462016 is from the RPCI-23 Mouse PAC Library constructed by the group of Pierer de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
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be approximately 900bp by restriction digest data."
1 43425 c 42104 g 50027 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Single clone region. Sequence from reads from a short insert library derived from a clone PCR. Restriction digest data confirm the assembly."
1343 GGCCCTGTGAATCCTTTCTCAACAGTGTGGAAGCAAGCCTGGGAGGTGCGTCAAAACTCAG 1402
                                                                                                              1403 GCAAGATGTATGATGCTTAACCCTCCCAATGTCTGCCAGAGGGACGGGCCAGTGTGACGGC 1462
                                                       21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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                                                                                                                                                                                                                         1463 AAATACAÁGTGCTGTGAGGGTATATGTGGGAAAGTCTGCCTGCCCCCG 1510
                                                                                                                                                                        41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
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BASE COUNT ORIGIN

FEATURES

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/codon_start=1
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/product="secretory leukocyte protease inhibitor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4090)
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Direct Submission
Submitted (16-NOV-1999) Oral Infection and Immunity Branch,
National Institute of Dental & Craniofacial Research, 30 Convert
Dr., MSC4352, Bldg 30, Rm. B06, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97026 GGCCCTGTGAATCCTTTTCTCAACAGTGTGGAAGAAGCCTGGGAAGTGCGTCAAAAACTCAG 96967
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oin(1266. .1353,1923. .2080,2561. .2710)
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|gene="Slpi"
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PAT 30-NOV-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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twoor markers in ovarian canner
Patent: WO 0175177-A 311-027-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
      RECOMBINANT METHODS FOR PRODUCTION OF SERINE PROTEASE INHIBITORS
                                                                                                                                                                                                                                                                                                                145 GATCCGGTTGATACCCCGAACCCGACTCGTCGAAAACCGGGTAAATGCCCGGTAAACCTAT 204
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Matches:
Conservative:
Mismatches:
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Matches:
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                  AND DNA SEQUENCES USEFUL FOR SAME
Patent: WO 8603519-A 1 19-JUN-1986;
Location/Qualifiers
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Sequence 53 from Patent WO0175177.
AX302535
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/db_xref="taxon:9606"
a 100 c 111 g 97
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                                                                            /organism="unknown"
85 c 88 a
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Best Local Similarity:
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Best Local Similarity:
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                                                                                           BASE COUNT
                                                                                                                                                        No.:
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                                  JOURNAL
                                                                                                                                        Alignment
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Patent: US 5851983-A 5 22-DEC-1998;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 324)
Bandyopadhyay, P.K., Eisenberg, S.P., Stetler, G.L. and Thompson, R.C.
                                                                                                 2630 TGCCAGAGGGACGGCAGTGTGACGGCAAATACAAGTGCTGTGAGGGTATATGTGGGGAAA 2689
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                                                                      12 LysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsnArg 31
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Mismatches:
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Matches:
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AR067991
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   Indels:
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Sequence 1 from Patent WO 8603519.
108404
                 Gaps:
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42 c 53 g
                                          09-833799-13B (1-57) x AF205374 (1-4090)
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DEFINITION
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                                                                                ORGANISM
                           ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                          BASE COUNT
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AX069252
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AUTHORS
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                                                                                                                          AUTHORS
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                                                                                                            REFERENCE
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                                                                  SOURCE
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                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                    2 (bases 1 to 399)
Si-Tahar, M., Merlin, D., Sitaraman, S. and Madara, J.L.
Direct Submission
Submitted (Le-DEC-1998) Department of Pathology and Clinical
Medicine, Emory University, 1639 Pierce Drive, Atlanta, GA 30322,
                                                                               Homo sapiens secretory leukocyte proteinase inhibitor precursor, mRNA, complete cds.
AF114471. GI:4378758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GluproValLysGlyProValSerThr----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                      Si-Tahar,M., Merlin,D., Sitaraman,S. and Madara,J.L. constitutive and regulated secretion of secretory leukocyte protesinase inhibitor by human intestinal epithelial cells Gastroenterology 118 (6), 1061-1071 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="secretory leukocyte proteinase inhibitor
340 GACTTGAAGTGTTGCATGGGCATGTGGGGAAATCCTGCGTTTCCCCT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 GACTIGAAGIGITGCAIGGCAIGIGIGAAAICCTGCGIIICCCCI 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                   linear
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4 4 27
2 2 3
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Matches:
Conservative:
Mismatches:
Indels:
                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="intestine"
1. .399
                                                                                                                                                                                                                                                                                                                                                                                                      1. .399
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_line="Caco2-bbe"
/cell_type="epithelium"
                                                                     399 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:9606"
chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SLPI"
/codon_start=1
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143.00
55.36%
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                                                                                                                                                                   Homo sapiens
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                                                                     AF114471
                                                                                                                                                                                                                                                                              20295039
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                                                                                                                                                   human.
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DB:
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                                                                                DEFINITION
                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
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AUTHORS
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TITLE
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PUBMED
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KEYWORDS
SOURCE
                                         RESULT 53
                                                                                                                                                                                                          REFERENCE
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                                                    AF114471
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/codon_start=1
/protein_id=".0AC27294.1"
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/db_xxef=".01:12579134"
/translation="WKSSGIEPFIVULALGTLAPWAVBGSGKSFKAGVCPPKKSAQCLARNKRBCQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPRXKRBCQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPP
                                                                                                                                                                                                                                                   DNA sequences coding for proteins having the biological activity of HUSI-type I inhibitors, biotechnological methods for the preparation of said proteins and pharmaceutical compositions containing said proteins

Patent: US 4845076-A 2 04-JUL-1989;

Grunenthal GmbH;;
PAT 21-MAY-1993
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases 1 to 555)
Neilson, L. and Li, Z.
Treatment of endometriosis with antileukoprotease
Parent: WO 0101998-A 111-0AN-2001;
Reprogen, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 25-JAN-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GATCCTGTTGACACCCCAACAAAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 geccaargirrgargciriaaccccccaarrrcreigagargaargcargcaagcgr 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GluProValLysGlyProValSerThr----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                               1 (bases 1 to 498)
Heinzel,R., Appelhans,H., Gassen,H.G., Machleidt,W. and
Seemuller,U.
  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 GACTTGAAGTGTTGCATGGGCATGTGTGGGGAAATCCTGCGTTTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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Mismatches:
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101501
Sequence 2 from Patent US 4845076.
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/organism="Homo sapiens"
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59. .457
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
131 c 141 g
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                                                                     I01501.1 GI:270157
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55.36%
48.21%
43.73%
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r PRI 21-MAR-1995
protease
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/db_xref="G1:36491"
/db_xref="G1:36491"
/db_xref="SWISS-PROT:P03973"
/tanslation="MKSSGEPFLVLLALGTLAPWAVEGSGKSFKAGVCPPKKSAQCLRYKREPGSDWQCPRKRCEPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA"
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                                                                                                                                                                                                                                                               Isolation and sequence of a human gene encoding a potent inhibitor
                                                                                                                                                                                             Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 573)
Stetler,G., Brewer,M.T. and Thompson,R.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                              elastase inhibitor; protease inhibitor; secretory leucocyte protease inhibitor; trypsin inhibitor. Homo sapiens. Homo sapiens
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                                                   linear
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                                                 573 bp mRNA linear for secretory leucocyte
                                                                                                                                                                                                                                                                                                                                             Data kindly reviewed (15-SEP-1987) by Stetler G.
Location/Qualifiers
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227
23
23
                                                                                                                                                                                                                                                                                of leukocyte proteases
Nucleic Acids Res. 14 (20), 7883-7896 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="mature SLPI (AA 1-107)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/tissue_type="parotid gland"
1. .399
/note="SLPI-precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="put. polyA signal"
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                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Sequence 1 from Patent WO0190421.
AX328399
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145 c 152 g
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                                                                Human SLPI mRNA fragment inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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55.36%
48.21%
43.73%
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                                                                                                                                                                                                                                                                                                             87040761
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ACCESSION
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                                                               DEFINITION
                                                                                                                                                                                 ORGANISM
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PUBMED
                                                                                                 ACCESSION
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                  RESULT 57
                                                                                                              VERSION
KEYWORDS
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                                                                                                                                                                                                                                                 AUTHORS
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                              HSSLIPR
LOCUS
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                                                                                                                                                              SOURCE
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Patent: US 48450/6-A 3 04-JUL-1989;
Grunenthal GmbH;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT 21-MAY-1993
                                                                                                                                                                                                                                                                                                                         338 GGCCAATGITTGATGCTTAACCCCCCAATTTCTGTGAGGATGGATGGCCAGTGCAAGCGT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GluProvalLysGlyProvalSerThr----LysProGlySerCysProllelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 565)
Heinzel,R., Appelhans,H., Gassen,H.G., Machleidt,W. and
Seemuller,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                           398 GACTICAAGIGITGCAIGGGCAIGIGIGGGAAAICCIGCGIITGCCCT 445
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                                                                              565
27
23
23
                                                                                                             Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
NFCEMDGQCKRDLKCCMGMCGKSCVSPVKA"
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IO1502
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/organism="unknown"
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09-833799-13B (1-57) x AX334507 (1-594)
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Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature gene sets
Parent: WO 0194629-A 5016 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         Rastelli,L. and Smithson,G.
Method of detecting inflammatory lung disorders
Petent: WO 0190421-A 1 29-NOV-2001;
Curagen Corporation (US)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
. _156 c 155 g 153
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/db_xref="taxon:9606"
_156 c 155 g 151
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AX328399.1 GI:18098360
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
Patent: WO 0194629-A 5885 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 594)
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                                                                                                                    238 GATCCTGTTGACACCCCAAACCCAACAAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 297
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Matches:
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/db_xref="taxon:9606"
156 c 155 g 151
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/trānslation="MKSSGLFPFLVLLALGTLAPNAVEGSGKSFKAGVCPPKKSAQCLRYKKEGCGSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA"
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SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Heinzel, R., Appelhans, H., Gassen, G., Seemuller, U., Machleidt, W., Fritz, H. and Steffens, G. Molecular cloning and expression of cDNA for human antileukoprotease from cervix uterus Eur. J. Blochem. 160 (1), 61-67 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 GATCCTGTTGACACCCCAACAACAAGAAGAAGCCTGGGAAGTGCCCAGTGACTTAT 297
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Schmitt, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and
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                                                                                                                                            Data kindly reviewed (05-DEC-1986) by H. Appelhans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 GACTIGAAGTGTTGCATGGGCATGTGGGGAAATCCTGCGTTTCCCCT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="put. mature peptide (aa 1-107)"
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/proteIn_id="CAA28158.1"
/Daxref="GI:28639"
/db_xref="SWISS-PROT:P03973"
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/note="pot. polyA signal"
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/note="pot. polyA signal"
156 c 155 g 151
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Sequence 97 from Patent WO9953040.
AX014898
                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                       note="precursor ALP"
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Email: Cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 625)
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Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                            :::|||||||
233 GATCCTGTTGACACCCAAACCCAAGAGGAGGAAGCCTGGGAAAGTGCCCAGTGACTTAT 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 GACTIGAAGIGITGCAIGGGCAIGIGGGAAAICCIGCGITTCCCCT 400
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                                                                                                   150
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                    1. .599
/organism="Homo sapiens"
/db_xref="taxon:9606"
153 c 154 g 151
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/db_xref="LocusID:6590"
/db_xref="taxon:9606"
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BC020708.1 GI:18088404
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Best Local Similarity:
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http://www.sanger.ac.uk/HGP/Chr20
IMPORTANT: This sequence is not the entire insert of clone
RRP1-30012 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP1-172H20 is at 100 in this sequence.
The true right end of clone RP1-172H20 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all regions were either double-erranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP1-30012 is from the library RPC1-1 constructed by the group of Pieter de Jong. For the bear of the second o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Alusg/x repeat: matches 174. .298 of consensus"
7809. .8022
/note="Charlie2 repeat: matches 3505. .3724 of consensus"
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'note="MEK52C repeat: matches 894. .1278 of consensus"
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'note="LIM4c repeat: matches 1740. .1979 of consensus"
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/note="LIMAC repeat: matches 802. .1740 of consensus"
join(5925. .593,6243. .6400)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     035. .2766 'note="L1M4 repeat: matches 4215. .4986 of consensus"
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10328. .10905
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/note="L1 repeat: matches 2125. .3119 of consensus"
9340. .10314
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/note="AluSg repeat: matches 1. .293 of consensus"
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note="match: ESTs: Em:AI222267"
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complement(11008..11364)
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'note="L1M4 repeat: matches 5628.
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note="match: GSS: Em:AQ492607"
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/db_xref="taxon:9606"
/chromosome="20"
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251. .554
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/clone="RP1-30012"
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/note="L1M1 rep
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/note="76
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On Nov 29, 2000 this sequence version replaced gi:10198630.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                         /protein_id="AAH20708.1"
/db_xref="G1:18088405"
/tb_xref="G1:18088405"

Kranslation="MKSSGLFPFLVLLALGTLAPWAVEGSGKSFKAGVCPPKKSAQCL RYKVEECQSDWQCPEKKRCCPGTYGTKCLDPVDTPNPTRRKFGKCPVTYGQCLMLNPPNFCEMDGQCKRDLKCCMGMCGKSCVSPVKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human DNA sequence from clone RP1-30012 on chromosome 20g12-13.12 Contains ESTs, GSSs and STSs. Contains part of a novel gene and the SLPI gene for secretory leukocyte protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear PRI 07-APR-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GGCCAATGTTTGATGCTTAACCCCCCCCAATTTCTGTGAGATGGCCAGTGCAAGCGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GATCCTGTTGACACCCCAAACCCAACAAGGAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GluProValLysGlyProValSerThr-----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                         /codon_start=1
/product="secretory leukocyte protease inhibitor
(antileukoproteinase)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; antileukoproteinase; proteinase inhibitor; SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (antileukoproteinase), complete sequence.
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Mismatches:
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                                                                                                                            note="Vector: pDNR-LIB"
                     /tissue_type="Liver"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B"
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Best Local Similarity:
Query Match:
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δ d ò ò g

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/gene="SLPI"
complement (27226. 27231)
/gene="SLPI"
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143.00
52.83%
47.17%
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2 (bases 1 to 2657)
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Homo sapiens
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Best Local Similarity:
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Pred. No.:
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TITLE
JOURNAL
MEDLINE
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TITLE
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PUBMED
REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="LiM4 repeat: matches 67. .1979 of consensus"
21547. .21682
/note="magget4(Zombi) repeat: matches 1. .137 of consensus"
21690. .22537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EM:AF714471 EM:M31216
match: ESTS: Em:R71834 Em:AA683520 Em:AA316675 Em:A742512
match: ESTS: Em:R71834 Em:AA683520 Em:AA316675 Em:A742512
EM:AA57638119 Em:AA264545 Em:A1862145 Em:A1640954
EM:AA66425 Em:AA460433 Em:A1743345 Em:AW081599
EM:AN66622 Em:AA460433 Em:A1865550 Em:AW081599
EM:A1564663 Em:AA460433 Em:AA1865550 Em:AW38407
EM:AA93549 EM:A1377093 Em:AA166295 Em:AW190157
EM:AA557989 EM:AA16414 Em:H65171 Em:A7733 Em:AW103765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(27206. .27386,27969. .28118,28542. .28700,
29426. .29528))
                                                                                  /note="match: GSS: Em:AQ081155"
13218. 13397
/note="45 copies 4 mer gaaa 66% conserved"
13928. 14216
/note="matches 1. .310 of consensus"
14372. 14593
/note="LIME2 repeat: matches 5935. .6162 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                      // note="Always repeat: matches 2. 310 of consensus"
16501. 16608 repeat: matches 4027. .4145 of consensus"
// note="LIM4 repeat: matches 2. .179 of consensus"
// note="MER97b repeat: matches 2. .179 of consensus"
// note="LIM4 repeat: matches 3473. .4025 of consensus"
// note="LIM4 repeat: matches 3473. .4025 of consensus"
// note="LIM4 repeat: matches 4367. .6167 of consensus"
// note="LIM40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="dJ30012.2 (secretory leukocyte protease inhibitor (antileukoproteinase))" /note="match: cDNAs: Em:U88093 Em:X04470 Em:U73004 Em:X04503 Em:M57446 Em:U94341 Em:AF151982 Em:AF178426
                                                                                                                                                                                                                                                                                                                                         /note="match: GSS: Em:AQ017550"
16175. .16190
/note="L1M4 repeat: matches 4145. .4159 of consensus"
16191. .16500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22669. .22996
Note="L1M4 repeat: matches 3623. .3953 of consensus"
23636. .23896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1M2 repeat: matches 1943. .2572 of consensus"
23825. .26024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Tigger4(Zombi) repeat: matches 1872. .2730 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="match: GSS: Em:AQ470847"
26025. .26160
note="LTR13 repeat: matches 796. .936 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86161. .26235

note="L1 repeat: matches 5112. .5188 of consensus"

26204. .26681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1 repeat: matches 2121. .4337 of consensus"
                                                                                                                                                                                                                                   14895. .15168
/note="AluSx repeat: matches 5. .295 of consensus"
complement(14950. .15573)
/note="match: GSS: Em:AQ241185"
15703. .16159
                          .3052. .13153
"note="MIR repeat: matches 33. .137 of consensus"
.3131. .13392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="42 copies 4 mer tata 79% conserved"
9678. .21535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9499. .19670
.note="86 copies 2 mer at 79% conserved"
19502. .19669
/note="match: GSS: Em:AQ760198"
13052. .13153
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/note="match: STS: Em:G06121"
complement (27206. .29528)
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complement(join(27382. .27386,27969. .28118,28542. .28700,
29426. .29510))
/gene="SLPI"
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Em:AA460434 Em:R49913 Em:AA026192 Em:AW391622 Em:T28664
Em:AA026099 Em:AA026497 Em:AA488776 Em:AI247078
Em:AI27322 Em:AI37954 Em:AI826892"
/evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28074 TTGATGCTTAACCCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAAGCGTGACTTGAAG 28015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: proteins: Tr:044397 Sw:P03973 Tr:Q9WUQ4
Sw:P97430 Tr:Q9R0Z8 Tr:O95959 Sw:P09412 Sw:P22298
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                                                                                                                                                                                                                                             27229. .27315
/note="L2 repeat: matches 2627. .2710 of consensus"
complement(27230. .27235)
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Human SLPI gene for secretory leukocyte protease inhibitor.
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/product="dJ30012.2 (secretory leukocyte protease
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Nucleic Acids Res. 14 (20), 7883-7896 (1986)
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Matches:
Conservative:
Mismatches:
Indels:
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Stetler, G., Brewer, M.T. and Thompson, R.C.
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/db_xref="taxon:9606"
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41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
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26
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Matches:
Conservative:
Mismatches:
Indels:
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1. .321
                                                                                                                                                                                                              /organism="synthetic
                                                                                                                                                                                     Location/Qualifiers
1. .321
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                                                                                                                                                                                                                                                       /gene="ALP-242"
Synthetic ALP-gene 242.
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140.00
55.36%
46.43%
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                                                   synthetic construct.
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DEFINITION
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                                                                                                       AUTHORS
TITLE
              ACCESSION
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KEYWORDS
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                                                                                                                                            /protein_id="CAA28187.1"
/db_xref="G1:758101"
/db_xref="G1:758101"
/db_xref="SWISS-PROT: 103973."
/translation="WKSSGLEPFLULLALGTLAPWAVEGSGKSFKAGVCPPKKSAQCL
RYKKPECQSDWQCPGKKRCCPDTCGIKCLDPVDTPNPTRRKPGKCPVTYGQCLMLNPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT 28-JUL-1993
                                                                                                                                 /product="secretory leukocyte protease inhibitor (SLPI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1724 CCCCCCAATTTCTGTGAGATGGCAGTGCAAGCGTGACTTGAAGTGTTGCATGGCC 1783
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                                                                                        Join (291. .375,1092. .1250,1668. .1817,2397. .2401)
                                                                                                                                                                                                                           291. .365
hote="asignal peptide (AA -25 to -1)"
join(366. .375,1092. .1250,1668. .1817,2397. .2398)
gene="SLPI"
                                                                                                                                                                                                                                                                                           join(366. .375,1092. .1250,1668. .1817,2397. .2398)
gene="SLPI"
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                                                               /note="put. primary transcript of SLPI"
276. .375
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Conservative:
Mismatches:
                                                                                                                                                                                                                 NFCEMDGQCKRDLKCCMGMCGKSCVSPVKA"
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           note="put. CAAT-box" 42. .247
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                                     'note="put. TATA-box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="polyA signal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="polyA site"
649 c 704 g
                                                                                                                                                                                                                                                                                product="unnamed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="intron III" 397. .2574
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                                                                                                                                                                                                                                                                                                                                                                                                                              note="intron II"
667. .1817
                                                                                                                                                                                                                                                                                                                                               note="intron I"
.092. .1250
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1251. .1667
/gene="SLPI"
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                                                                                                                                                                                                                                                                                                                      76. .1091
gene="SLPI"
                                                                                                                                                                                                                                                                                                                                                                          gene="SLPI"
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Best Local Similarity:
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/gene="ALP-242"
/codon start=1
/transī_table=11
/proteim_id="CAAO0747.1"
/db xref="GI:41359"
/trānslation="SGKSFKAGVCPPKKSAQCLRYKKPECQSDWQCPGKKRCCPDTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKCLDPVDTPNPTRRKPGKCPVTYGQCLLLNPPNFCEMDGQCKRDLKCCMGMCGKSCV
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Synthetic construct artificial sequences.

I (bases 1 to 31)
Heinzel-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
Serine protease inhibitor proteins, medicaments containing them, DNA sequences coding for these proteins and methods for producing these proteins, medicaments and DNA sequences containing them, Serine Po37335-A 33 20-JUN-1990; Gruenenthal GmbH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 garcceeritgacaccccdedecccarectaaaccceeraaaccceeraagecceerraccrac 204
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synthetic construct
synthetic squences.
1 (bases 1 to 321)
Heinzel-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
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Matches:
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Mismatches:
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Mismatches:
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                                              5.51e-07
137.00
55.36%
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artificial sequences.
I (bases I to 31)
Heinzel-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
Serine protease inhibitor proteins, medicaments containing them,
DNA sequences coding for these proteins and methods for producing
these proteins, medicaments and DNA sequences
Patent: EP 0373335-A 29 20-JUN-1990;
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Mismatches:
Indels:
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/organism="synthetic construct"
/do.xref="taxon:32630"
1. .321
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Matches:
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                                               /gene="ALP-246"
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A08107
A08107.1 GI:413350
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55.36%
46.43%
42.20%
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SPVKA"
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1 (bases 1 to 321)

1 (bases 1 to 321)

Serine protease inhibitor proteins, medicaments containing them, DNA sequences coding for these proteins and methods for producing these proteins, medicaments and DNA sequences

Patent: EP 0373335-A 30 20-JUN-1990,
                                                                                                                                                                                                                                                 145 GATCCGGTTGACACCCCGACGCGTCGTAAACCCGGGAAGTGCCCGGTTACCTAC 204
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/db_xref="taxon:32630"
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A08109
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synthetic construct
artificial sequences.
                                                       artificial sequences.
1 (bases 1 to 74)
A31082.1 GI:1249296
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Heinzel-Wieland, R.,
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                                                                                                                                                                          PAT 28-JUL-1993
                                                                                                                                                                                                                                                                         artificial sequences.

1 (bases 1 to 321)

1 (bases 1 to 321)

Serine protease inhibitor proteins, medicaments containing them, DNA sequences coding for these proteins and methods for producing these proteins, medicaments and DNA sequences

Patent: EP 0373335-A 32 20-JUN-1990;
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 145 GATCCGGTTGACACCCCGAACCCGACGCGTCGTAAACCCCGGGAAGTGCCCCGGTTACCTAC 204
                                                         205 gercagiscarcergergaecescriaaerrerieceageregargeceagriceaaaga 264
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Mismatches:
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A08110
A08110.1 GI:413356
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synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 28-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease inhibitor proteins, medicaments containing them, DNA sequences coding for these proteins and methods for producing Patent: EP 037335-A 31 20-JUN-1990; Gruenenthal GmbH
Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D. Polypeptides and polypeptide analogues with inhibitory activity against human elastase Patent: EP 0402068-A 22 12-DEC-1990; IMPERIAL CHEMICAL INDUSTRIES PLC
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RVCGVKSCCADPR.</pre>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                         205 GGTCAGTGCCTGCTGCTGAACCCGCCTAACTTCTGCGAGGTCGATGGCCAGTGCAAACGA 264
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Furutani,Y., Kato,A., Yasue,H., Alexander,L.J., Beattie,C.W.
                                                                                                                                   3 GluProValLysGlyProValSerThr-----LysProGlySerCysProllelleLeu
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                                                                                                                                                                                                                                                                                            PAT 28-JUL-199
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synthetic construct
artificial sequences.

1 (bases 1 to 321)

1 (bases 1 to 221)

Serine protease inhibitor proteins, medicaments containing them, DNA sequences coding for these proteins and methods for producing Patent: EP 0373335-A 28 20-JUN-1990;
                                                                                                   489 GCTCAGTGCCCAGGGTTCCAGAAGTGCTGTAGA---GTCTGTGGTGTGAAAGTCCTGTGCG 545
                                                         372 GATCCAGTCAAAGCCCAACCTGCAGTCCCAAGGTGTATTCCCTTTCTCTAAGCTTGGCTTC 431
312 AGTCAAGATCCAGTTGAGGGTCAAGATCCAGTCCAAGCCCAACTTCCAGACAAAGTACAA 371
                                                                                   CysProllelleLeulleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAsp 35
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LHPVKGRNRVKGGTLMGRAVSVKGHGSLKSRMQVKGAGDLMGEEFLVQCNDPVI SHIWN
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ODLERAVSVKGVGTYKGPGSLKGRGSLKGHLQI KGQDLMGEEVSDKGLSPVKGHMQI KK
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VEEAGSAKGLSPIKGRSSLKGHGSLKGHTQLTGQLLIGEELLVQGQDPVVGRQHF
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GEAALVKGLAPEKGGTQVQGQDVLGDALSVKGLLPVKGDMGIKGQALIPEAVKGSSTM
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QIKGQDVMGKVVAAKGLGPVKSHTQLKEHNFQDAAVSVKTLGSIKRQGSSRSQSSLKG
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EHAAFKGQGMFKRRSFSKPGSCPDITGQCTQTSDSKCGSDVECPGTKKCCVGMCGGMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schalkwijk,J., Wiedow,O. and Hirose,S.
The trappin gene family: proteins defined by an N-terminal
transglutaminase substrate domain and a C-terminal four-disulphide
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furucani, Y., Hirose, S., Kato, A. and Kawai, R.
Direct Submission
Submitted (16-MR-2001) Yutaka Furutani, Tokyo Institute of
Technology, Dept. of Biological Science Hirose Lab.; Midori-ku
Nagatudachou 4259, Yokohama, Kanagawa 226-8801, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:81-45-924-5726,
                                       265 GATCTGAAATGCTGCATGGTATGTGCGGTAAAAGCTGCGTTAGCCCG 312
                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus male seminal vesicle cDNA to mRNA.
Cavia porcellus
41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                      Cavia porcellus mRNA for trappin, complete cds.
AB058645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Furutani,Y., Kawai,R., Kato,A. and Hirose,S.
Guinea pig trappin
Unpublished
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/codon_start=1
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/sex="male"
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AUTHORS
TITLE
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JOURNAL
                                                                                                                               RESULT 75
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FEATURES

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22 ArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIle 41
                                                                                                                                                          2 GlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeuIle 21
                                                                                                                                                                                                                                                                                4643 AAGAAGTGCTGTGGGCATGTGGGGTGGAATGGAGTGTTTGATCCCCCAG 4693
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                                 5109
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
Query Match:
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-0=/cgn2_1/USPTO spool/USO9833799/runat_12022003_120041_23624/app_query.fasta_1.199  
-0=-bar Geneeseq_101002 - QFMFT=fastap - SUPFIX=xng - MINMATCH=0.1_LCOOPCI==0  
-LOOPEXT=0 - UNITS=bits - START=1 - END=--1 - MATRIX=blosum62 - TRANS=human40.cdi  
-LIST=100 - DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=75  
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-WARN TIMBOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6 - FGAPEXT=7  
-YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                   Ovarian carcinoma
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/label= Elastase inhibitor
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90 ATTCGTTGCGTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 GCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 ileArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human head/neck tumour related protein partial coding sequence #5.
                                                                                                                      Gene product has inhibitory activity against human leukocyte elastase (HLE) and may be isolated from psoriatic scales. The sequence may be expressed from a plasmid transformed expression system and may be useful in the prevention of tissue damage associated with emphysema, adult respiratory distress syndrome, psoriasis and bullous dermatoses. Other treatable conditions include atherosclerosis, cystic fibrosis, bronchitis and acute non-lymphoblastic leukaemia.
                             Human leucocyte elastase inhibitor - is genetically engineered polypeptide for treatment of inflammatory, pulmonary and skin
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                                                                                              Disclosure; Fig 13; 45pp; English
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20-APR-2000; 2000US-0533870.
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The present invention relates to a number of nucleic acid sequences which encode proteins associated with head, neck and lung tumours. These tumours are often not diagnosed until they have spread, and, of those who survive, most must endure alterations in facial and neck appearance as well as changes in speech, sight, smell, chewing, swallowing and taste be used in the diagnosis, treatment and vaccination against cancer, particularly papillary and follicular carcinomas, papillary tumours, follicular adenoma, parathyroid hyperplasia, parotid cancer, lip cancer, equamques call cancer of the tongue, oral tongue cancers and larynx
such as head, neck and lung cancer
                                            Claim 3; Page 71; 77pp; English.
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Sequence 434 BP; 103 A; 103 C; 133 G; 94 T; 1 other;

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318 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 259
                                                                                                                                                                                        21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                       1 AlaGlnGluProVallysGlyProValSerThrLysProGlySerCysProllelleLeu
                                                                                                                                                                                                                               41 IleiysiysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                Conservative:
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Matches:
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tumour; vaccine; colon cancer; immunogenic;
                                             cDNA encoding colon tumour protein, SEQ ID No 1393.
           ABK45842 standard; cDNA; 480 BP
                                 05-JUN-2002 (first entry)
                                                             immunotherapy; gene; ss
                                                                                     WO200212328-A2.
                                                         colon
                                                                         Homo sapiens
                      ABK45842;
      ABK45842/c
RESULT
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New colon cancer polypeptides and polynucleotides, useful as vaccines, for diagnosing, preventing, and treating colon cancer, and as markers Secrist Χu J, GE, Meagher MJ, WPI; 2002-241739/29. King

03-AUG-2000; 2000US-223283P. 28-MAR-2001; 2001US-279763P. 29-JUN-2001; 2001US-302051P.

CORI-) CORIXA CORP.

31-JUL-2001; 2001WO-US24218

90EP-0306037.

04-JUN-1990;

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The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer. ABK4450-ARK4621 represent coding sequences of human colon tumour
                                                                                                                                                                                                                        proteins of the invention.

Note: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 GCGCAGAGCCAGTCAAAGGTCCAGINTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLE; Emphysemia; respiratory distress syndrome; atherosclerosis; arthritis; cystic fibrosis; leukaemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding human leukocyte elastase inhibiting peptide.
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/label= Upstream in-frame coding sequence
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                                                                                                                                                                                                                                                                                                          Sequence 480 BP; 113 A; 105 C; 139 G; 120 T; 3 other;
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Matches:
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/label= Elastase inhibitor
                            Claim 1; SEQ ID No 1393; 147pp; English.
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for the progression of cancer
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/*tag= c
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Best Local Similarity:
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158 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, colon cancer, cancer, tissue profiling, forensic, mapping, genetic analysis, diagnostic, antisense therapy, gene, ss.
                                                                                                                                                                                                                                                                                                       Gene product has inhibitory activity against human leukocyte elastase (HLE) and may be isolated from psoriatic scales. The sequence may be expressed from a plasmid transformed expression system and may be useful in the prevention of tissue damage associated with emphysema, adult respiratory distress syndrome, psoriasis and bullous dermatoses. Other treatable conditions include atherosclerosis, cystic fibrosis, bronchitis and acute non-lymphoblastic leukaemia.

Abs raised to the polypeptide may be used in detection.
                                                                                                                                                                                                            Human leucocyte elastase inhibitor - is genetically engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human colon cancer related nucleotide sequence SEQ ID NO:2513.
                                                                                                                                                                                                                  polypeptide for treatment of inflammatory, pulmonary and skin conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ileLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 504 BP; 110 A; 152 C; 120 G; 122 T; 0 other;
                                                                                                                            Wiedow O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
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                                                                                                                            Schroder JM, Pioli D,
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                                                                                                                                                                                                                                                                            Disclosure, Fig 16; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ58818 standard; cDNA; 571 BP.
                                                                                           (ICIL ) IMPERIAL CHEM INDS PLC.
            89GB-0024717.
89GB-0013346.
89GB-0013349.
                                                              89GB-0021613.
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                                                                                                                                                           WPI; 1990-370081/50.
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Best Local Similarity:
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                                                                                                                            Christophers E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200229086-A2
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                                                              25-SEP-1989;
             02-NOV-1989;
09-JUN-1989;
                                              09-JUN-1989
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ6078 to ABQ60787 uncleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of class from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate macroarrays on a soild surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
                                                                                                                                                                                                             New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 gegenagadecendrenanagerecentrecentrangeceregerecendecentrateria 269
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                                                                                                     Dwivedi P, Molino GA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psorisals; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA differentially expressed in granulocytic cells #390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; granulocytic cell; DNA chip; bacterial infection;
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                                                                                                     Carroll E,
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                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 796pp; English
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                  02-OCT-2000; 2000US-237271P.
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                                                                                                     Burgess C, Astle JH, Ca.
Thiaglingam A, Lewis ME;
                                                                                                                                                                       WPI; 2002-426115/45.
                                                             (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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The invention relates to detecting (MI) granulocyte (GC) activation CC (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chips analysis as given in the specification, and comparing the expression level to an expression of GS is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent capable of modulating GA by contacting GC with an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression of the gane is indicative of inflammation, the analysic response in a subject, exposure of a subject to a pathogen or sterile inflammation of especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject response in a subject, exposure of a subject to a pathogen or sterile inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for considering dA; M3 is useful for screening an agent capable of modulating GA; M3 is useful for screening an agent capable of modulating GA; M3 is useful for screening an agent capable of subject to a pathogen or sterile inflammation dispectally chronic) in a tissue, an allergic ersponse in a subject, exposure of a subject to a pathogen or sterile inflammation disease (e.g. psoriasis; rheumatory disease (e.g. psoriasis; rheumatory disease; also bacterial infection, viral infection, and infection, to prince or perfection, procozal infection, disease, ulcerating one of the above conditions. The present confidence represents a gene differentially expressed in granulocytes.

Of the printed specification, browned or the printed spe
                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
  Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                               Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
                       granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 390; 114pp; English.
                                                                                                                                                                                                                                                    03-OCT-2000; 2000US-237189P.
                                                                                                                                                                                                      03-OCT-2001; 2001WO-US30821
                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-435328/46.
                                                                                                              WO200228999-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug toxicity
                                                                   Homo sapiens.
                                                                                                                                                           11-APR-2002.
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Sequence 2309 BP; 595 A; 537 C; 603 G; 572 T; 2 other; ftp.wipo.int/pub/published\_pct\_sequences. Alignment Scores:

2309 57 0 0 0

Conservative: Mismatches: Matches: Length:

4.77e-28 327.00 100.00\$ 100.00\$ 24

Percent Similarity: Best Local Similarity:

Query Match: DB:

Indels:

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Human, cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                 1554 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 1613
                     20
                                                             40
                   1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu
                                                             21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                     Lung cancer related gene sequence SEQ ID NO:4153.
09-833799-13B (1-57) x ABK83819 (1-2309)
                                                                                                                                                                   ABL65816 standard; DNA; 2309 BP.
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2000US-234924P.
2000US-235077P.
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2000US-235711P.
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02-OCT-2000; 2000US-237316P.
03-OCT-2000; 2000US-237425P.
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2000US-236032P
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                                                                                                                                                                                                                                                                                                                             WO200194629-A2.
                                                                                                                                                                                                                                                                                                         Homo sapiens.
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28-SEP-2000;
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene given in ABLG1664 to ABLF0110), or is at least 95% identical to (S), where a change in comprises a sequence (S) selected from 847 sequences (given in ABLG1664 to ABLF0110), or is at least 95% identical to (S), where a change in activity and can be used in gene therapy. MI can be used for screening a nati-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the scrutture and/or properties of the agent. MI can be used in the structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, confiltrating and cancer  adamened cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1554 GCGCAAGAGCCAGTCAAAGGTCCACTAAAGCCTGGCTCCTGCCCCATTATCTTG 1613
                                                                                                                                                                                                                                                                                                                             Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                 Carter KC, Ebner R, Endress G, Horrigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AlaginGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1674 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 ileLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2309 BP; 595 A; 537 C; 603 G; 572 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2309
57
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 4153; 44pp; English
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03-OCT-2000; 2000US-237598P.
03-OCT-2000; 2000US-237604P.
03-OCT-2000; 2000US-237606P.
03-OCT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
01-NOV-2000; 2000US-245084P.
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                                                                                                                                                                                                                   Augustus M,
                                                                                                                                                                                                              Young PE, Augustus M
Soppet DR, Weaver Z;
                                                                                                                                                                  (AVAL-) AVALON PHARM.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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25-SEP-2000; 2000US-235082P.
25-SEP-2000; 2000US-235082P.
25-SEP-2000; 2000US-335280P.
26-SEP-2000; 2000US-33538P.
27-SEP-2000; 2000US-33538P.
27-SEP-2000; 2000US-33532P.
27-SEP-2000; 2000US-23503P.
28-SEP-2000; 2000US-23503P.
28-SEP-2000; 2000US-23503P.
28-SEP-2000; 2000US-23603P.
28-SEP-2000; 2000US-23603P.
28-SEP-2000; 2000US-23603P.
28-SEP-2000; 2000US-23603P.
28-SEP-2000; 2000US-236033P.
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20-SEP-2000; 2000US-234052P.
22-SEP-2000; 2000US-234569P.
22-SEP-2000; 2000US-234567P.
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2000US-234923P.
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29-SEP-2000; 2000US-236842P.
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20-SEP-2000; 2000US-234009P
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                                                                                 WO200194629-A2.
                                                         Homo sapiens.
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                           gene; ds.
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to ABL70110), or is at least 95% identical to (5), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the reatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
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1554 GCGCAAGAGCCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 1613
                                                                                                                                                                                                                                                                     1614 Arccegrececcarerrearcceccraaccecrecreaasaracrearesceccasea 1673
                                                                                                                                                                                      1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                             IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elafin, derivative, mutation, transformation, B. coli, yeast, Bacillus subtilis; elastase inhibitor; oxidation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant modified elafin with improved oxidation stability has pharmaceutical use as an elastase inhibitor
                                                                                                                                                                                                                                                                                                                         1674 Arcaagaagrecrergaagecrerrecegeargecererrecerer 1724
                                                                                                                                                                                                                                                                                                41 IleLysLysCysCluGlySerCysGlyMetAlaCysPheValProGln 57
                         Sequence 2309 BP; 595 A; 537 C; 603 G; 572 T; 2 other;
carcinoma, papillary carcinoma and Wilm's tumour.
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                                                                               Matches:
Conservative:
Mismatches:
Indels:
                                                                  Length:
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                                                                                                                                                                                                                                                                                                                                                                               AAQ56674 standard; DNA; 177 BP
                                                               4.77e-28
327.00
100.00%
100.00%
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                                                                                          Percent Similarity:
Best Local Similarity:
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                                                  Alignment Scores:
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DNA

The

The sequences given in AAQ56674-76 encode elafin derivatives.

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          vector and then used to transform E. coli, yeast, Bacillus subtilis or animal cells. The modified elafin is expressed when the transformed cells are cultured. The modified elafin are drugs with elastase inhibitor activity. They have improved oxidation stability over natural elafin and thus retain activity better under oxidative
                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                               1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu
                                                                                                                                                                                                                                                                                       1 GCACAGGAACCAGTTAAAGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCGATTATCCTG
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                                                                                                                                                                                                                                                                                                                 21 ileArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
encoding wild type elafin is mutated, inserted into a suitable
                                                                                                                                                                                                                                                                                                                                                                                    121 ATCAAAAAATGCTGCGAAGGTTCTTGCGGTATGGCATGCTTCGTTCCGCAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elafin, elafin 25L gene, Pichia pastoris, expression vector, alcohol oxidase 1; controlling region, promoter, ds.
                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPIC9/ELF25L cDNA construct containing the elafin 25L gene.
                                                                                                                                                                                                                                                                                                                                                                     41 IleLysLysCysGluGlySerCysGlyMetAlaCysPheValProGln
                                                                                                                                           177
56
1
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                                                                                                     Sequence 177 BP; 39 A; 49 C; 48 G; 41 T; 0 other;
                                                                                                                                                                       Conservative:
Mismatches:
                                                                                                                                             Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                      09-833799-13B (1-57) x AAQ56674 (1-177)
                                                                                                                                           4.55e-29
324.00
100.00$
98.25$
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949..1203
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1204..1374
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                                                                                                                                                                                  Best Local Similarity:
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                                                                                                                                                                    Percent Similarity:
                                                                                                                              Alignment Scores:
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                                                                            conditions.
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The present sequence represents a pPIC9/ELF25L cDNA construct containing the diafin 25L gene, used in an example of the present invention. The present invention describes: (1) an elafin (EL) expression vector comprising a gene encoding EL and a gene encoding alcohol oxidase 1 controlling region (AOCR) which controls the expression of EL encoding gene; (2) a microbial host transformed with the vector; (3) DNA fragment for recombinant transformation comprising: (a) a first region homologous to the genomic DNA of the host; (b) a promoter region of (AOCR) gene; (c) a gene encoding signal peptide; (d) a linker designed to secrete a matured elafin; (e) a gene encoding EL; (f) selection marker gene; (g) stop codon, and (h) a second region homologous to a part of the genomic DNA of the host, and (4) a microbial host can be used to prepare EL commercially. The production of EL by the microbial hosts can be carried
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1204 GCTCAAGAACCAGTTAAGGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCGATTATCCTG 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant modified elafin with improved oxidation stability -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elafin; derivative; mutation; transformation; E. coli; yeast; Bacillus subtilis; elastase inhibitor; oxidation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1324 ATCAAAAATGCTGCGAAGGTTCTTGCGGTATGGCATGCTTCGTTCCGCAG 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleLysLysCysCysGluGlySerCysGlyMethlaCysPheValProGln 57
                                                                                                                                                                                                                                                                                                Sequence 8598 BP; 2306 A; 2025 C; 1920 G; 2347 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okawa N, Yoshida M;
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                      Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ56675 standard; DNA; 177 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elafin derivative Val25 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93WO-JP01133,
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                                                                                                                                                                                                                                                                 on a large scale.
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The DNA
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                                                                                                                                                                                                                                                                                                                                                                                   1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysFroIleIleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                               21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                 GCACAGGAACCAGTTAAAGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCCGATTATCCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in AAQ56674-76 encode elafin derivatives. encoding wild type elafin is mutated, inserted into a suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elafin, derivative, mutation, transformation, E. coli, yeast, Bacillus subtilis, elastase inhibitor, oxidation, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant modified elafin with improved oxidation stability has pharmaceutical use as an elastase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATCAAAAATGCTGCGAAGGTTCTTGCGGTATGGCATGCTTCGTTCCGCAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ileLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                   09-833799-13B (1-57) x AAQ56675 (1-177)
              Claim 1; Page 24; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 25; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaji A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ56676 standard; DNA; 177 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elafin derivative Ile25 DNA.
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98.25%
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                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                            conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ56676;
                                                                                                                                                                                                                                                                                                      Query Match:
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This method

screened with total cDNA from normal and tumor cells.

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or animal cells. The modified elafin is expressed when the transformed cells are cultured. The modified elafin are drugs with elastase inhibitor activity. They have improved oxidation stability over natural elafin and thus retain activity better under oxidative
vector and then used to transform E. coli, yeast, Bacillus subtilis
                                                                                                                                                                                                                                                          conditions
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61 Arccecrececrarrergaacceeceaaccerrerergaagacacreacreeceeger 120
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                                                                                                                                                                              1 AlaGlnGluproValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                            1 GCACAGGAACCAGTTAAAGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCGATTATCCTG 60
                                                                                                                                                                                                                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosos and treatment of cancer - using candidate tumor suppressor genes or the corresp. antibodies.
                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                       41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln
                                              177
56
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Sequence 177 BP; 40 A; 49 C; 47 G; 41 T; 0 other;
                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial sequence of tumour suppressor gene U9
                                                                                                          Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DAND ) DANA FABER CANCER INST INC.
                                                                                                                                                  09-833799-13B (1-57) x AAQ56676 (1-177)
                                                                                                                                                                                                                                                                                                                                                                                              AAQ28757 standard; DNA; 321 BP
                                            5.94e-29
323.00
100.00%
98.25%
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                                                                                        Best Local Similarity:
                                                                         Percent Similarity:
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                            Alignment Scores:
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            produced some 20 additional cloned cDNAs. Also found by this method were several genes which, on the basis of the partial DNA sequences appear to be novel sequences not previously entered into GENBANK. The portion of the cDNAs so sequenced represents part of the coding region and/or part of the 3' untranslated region of each cDNA (see Q28749-58).
                                                                                                                                                                                                                                                                                        1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
                                                                                                                                                                                                                                                                                                           144 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCCCCGCTGCCCCATTATCTTG
                                                                                                                                                                                                                                                                                                                                                 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence (AAQ44862) encodes the SPAI peptide which is useful as a drug for treating cardiac and vascular diseases. The peptide is found as a pre-sequence (AAR50335) which is amplified using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp.
DNA - useful to treat cardiac and vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                       264 Archadadricridadadcircridciccaridectriricriricerrice 311
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                                                                                                                Sequence 321 BP; 81 A; 80 C; 84 G; 76 T; 0 other;
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                            09-833799-13B (1-57) x AAQ28757 (1-321)
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/product= SPAI
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                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPAI gene.
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Murine, serum amyloid, SAA3; riboprobe, LST-1; follistatin-like 1; FST1; SLPI; secretory leukocyte protease inhibitor; legumain; SOCS3; rheumatoid arthritis; CISH3; RAGE; AGER; LY117; hydroxymethyl glutarate; HMG-1; glucocorticoid leucine zipper; GILZ; PTPN-18; GADD-45A; GADD-45B; PRSC1; lipocalin 2; Lon2; glucose phosphate isomerase; GPI; SpiL; serine protease inhibitor; TSG-6; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (MI) for determining the difference between levels of expression of a number of genes characteristic of rheumatoid arthritis (RA) in cell and reference levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining difference between expression levels of genes characteristic of rheumatoid arthritis in cell and reference level, by comparing expression levels of the genes determined in a cell with
                                                                                                                                                                                                                                  439 CACTGCCCTAGGATTCTTTTTCGTTGCCCCCTGAGCAATCCCTCTAACAAGTGTTGGAGA 498
                                                                                                                                                                                                                                                                                                                                                        15 SerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsnArgCysLeuLys 34
                                                                                                                                                                                                                                                                                                                                      35 AspThrAspCysProGlyIleLysLysCysCluGlySerCysGlyMetAlaCysPhe 54
                                                                                                                                                                                                                -------ValSerThrLysProGly 14
                              Sequence 737 BP; 205 A; 192 C; 182 G; 158 T; 0 other;
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31
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17
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                                                                                                       Conservative:
Mismatches:
                                                                                          Matches:
                                                                        Length:
                                                                                                                                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 88; 296pp; English.
                                                                                                                                                                                                                2 GlnGluProValLysGlyPro-----
                                                                                                                                                                                 09-833799-13B (1-57) x AAQ44862 (1-737)
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                                                                        1.26e-11
179.50
61.90%
49.21%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                      54.89%
primers (AAQ44863-67)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-583494/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                 559 TATCCCAAG 567
                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                    55 ValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reference level
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-2002
                                                          Alignment Scores:
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                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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CC of expression of the genes, comprising: (a) providing RNA from a cell;

CC of RA including a number of genes (G) characteristic
CAGER), LST-1 (EV117), serum amyloid (SAA) 1-3, hydroxymethyl glutarate
(AGER), LST-1 (ST117), serum amyloid (SAA) 1-3, hydroxymethyl glutarate
(HMG)-1, S100 A8, A9, and A12, secretory leukocyte protease inhibitor
(GLPI), glucocorticoid leucine zipper (GLIZ), PTN-18, GADD-45A and B,
Legumain (PRSC1), follistatin-like 1 (FST1), lipocalin 2 (Lcn2), glucose
phosphate isomerase (GPI), serine protease inhibitor (SpiL), and TSG-6
(C) comparing the levels of expression of the genes in the cell to a
set of reference levels of expression of the genes, to determine the
(C) comparing the levels of expression of the genes, to determine the
difference between levels of expression of the genes, to determine the
cd difference between levels of expression of the genes, in the cell and reference levels of expression of
the genes. M1 is useful for determining whether a subject has or is
clikely to develop RA, or for determining whether a subject has or is
clikely to develop RA, or for determining whether a subject has or is
clikely to develop RA, or for determining the therapy. M1 is
also useful for determining the stage of RA in a subject, for
determining the efficacy of a therapy in a subject thing the likelihood of success of a particular therapy in subject
having RA. The present sequence represent invention. 

Sequence 396 BP; 94 A; 98 C; 118 G; 86 T; 0 other;

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396
22
0
0
              Conservative:
                       Mismatches:
        Matches:
Length:
                               Indels:
8.03e-10
       161.00
58.49%
52.83%
                              49.24%
                       Best Local Similarity:
                Percent Similarity:
                               Query Match:
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09-833799-13B (1-57) x ABQ73674 (1-396)

232 CCCATTCGCAAACCAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGT 291 4 ProValLysGlyProValSerThrLysProGlySerCysProIleIleLeuIleArgCys 23 В

292 ATGATGCTTAACCCTCCCAATGTCTGCCAGAGGGACGGGCAGTGTGACGGCAAATACAAG 351 24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly1leLysLys 43 ò

352 recrereadestararereseanastresecrecedes 390 44 CysCysGluGlySerCysGlyMetAlaCysPheValPro ò

ABQ73677 standard; DNA; 396 BP (first entry) 04-OCT-2002 ABQ73677; RESULT 16 

Murine SLPI antisense riboprobe SEQ ID NO:23.

Murine; serum amyloid; SAA3; riboprobe; LST-1; follistatin-like 1; FST1; SLPI; secretory leukocyte protease inhibitor; legumain; SOCS3; rheumatoid arthritis; CISH3; RAGE; AGBK; LY117; hydroxymethyl glutarate; HMG-1; glucocorticoid leucine zipper; GILZ; PTPN-18; GADD-458; GADD-458; PRSC1; lipocalin 2; Lon2; glucose phosphate isomerase; GPI; SpiL; serine protease inhibitor; TSG-6; ss.

WO200248310-A2.

20-JUN-2002

17-DEC-2001; 2001WO-US48968.

15-DEC-2000; 2000US-255861P.

```
Trepicchio WL;
   Shields KM,
(GENE-) GENETICS INST LLC
   Feldman JL,
   Pittman DD,
```

WPI; 2002-583494/62

Determining difference between expression levels of genes characteristic of rheumatoid arthritis in cell and reference level, by comparing expression levels of the genes determined in a cell with reference level

Example 3; Page 88; 296pp; English.

The present invention describes a method (M1) for determining the difference between levels of expression of a number of genes characteristic of rheumatoid arthritis (RA) in cell and reference levels of expression of the genes, computising: (a) providing RNA from a cell; of expression of the genes, computising: (a) providing RNA from a cell; of RA including a number of genes selected from SOCS3 (CISH3), RAGE (AGER), LST-1 (LY117), serum amyloid (SAA) 1-3, hydroxymethyl glutarate (HMG)-1, SIO AB, A9, and A12, secretory leukocyte protease inhibitor (SILPI), glucocorticoid leucine zipper (GIZI), PTPN-18, GADD-45A and B, Legumain (PRSC1), follistatin-like 1 (FST1), lipocalin 2 (Lon2), glucose phosphate isomerase (GFI), serine protease inhibitor (SpiL), and TSG-6 (c) comparing the levels of expression of the genes in the cell to a set of reference levels of expression of the genes, to determine the clifference between levels of expression of the genes, to determine the difference between levels of expression of the number of genes characteristic of RA in the cell and reference levels of expression of the number of genes in the cell in the cell and reference levels of expression of the sories of the genes. likely to develop RA, or for determining whether a therapy for RA is effective in a subject having RA who is receiving the therapy. MI is also useful for determining the stage of RA in a subject, for determining the efficacy of a therapy in a subject having RA, and for determining the likelihood of success of a particular therapy in subject having RA. The present sequence represents a murine SLPI antisense riboprobe, which is used in an example from the present invention.

Seguence 396 BP; 86 A; 118 C; 98 G; 94 T; 0 other;

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4 ProValLysGlyProValSerThrLysProGlySerCysProllelleLeulleArgCys 23
           9
8
0
0
0
0
0
0
0
                                 Conservative:
Mismatches:
           Length:
Matches:
                                                         Indels:
                                                                                       09-833799-13B (1-57) x ABQ73677 (1-396)
          8.03e-10
161.00
58.49%
                                          52.83$
                                             Best Local Similarity:
                                  Percent Similarity:
Alignment Scores:
                                                         Query Match:
                      Score:
                                                                                                              ò
                                                                                                                                   g
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106 43 165 CCCATTCGCAAACCAGTGTGGAAGACCTGGGAAGGTGCGTCAAAAACTCAGGCAAGATGT 24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLys ઠ

105 ATGATGCTTAACCCTCCCAATGTCTGCCAGAGGGACGGGCAGTGTGACGGCAAATACAAG 44 CysCysGluGlySerCysGlyMetAlaCysPheValPro 56 qq ò

45 recretedescrataristicscaaagrereceeeg g

RESULT 17 AAX18516

AAX18516 standard; cDNA to mRNA; 684 BP

(first entry) 05-MAY-1999

Mouse IMC carcinoma cell IMC-HA1 clone 28-1#3 cDNA #1. **EXEXEXEXEX** 

Mouse; carcinoma cell; IMC-HA1; cancer; metastasis; CMAP; inhibitor;

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Protein associated with cancer metastasis and gene encoding it useful for screening for potential inhibitors of cancer metastasis
cancer metastasis associated protein; ss.
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Ohta M;
                                                                                                                                                                                                                                                       98WO-JP01592
                                                                                                                                                                                                                                                                                               97JP-0105333
                                                                                                                                                                                                                                                                                                                                          (BANY ) BANYU PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-080732/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW98909
                                        Mus musculus
                                                                                                                                                                     WO9845431-A1
                                                                                                                                                                                                                                                       07-APR-1998;
                                                                                                                                                                                                                                                                                               08-APR-1997;
                                                                                                                                                                                                             15-0CT-1998
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The present invention provides gene sequences associated with cancer metastasis which are isolated from mouse IMC carcinoma cells by detection of their higher expression in IMC-HM cell lines than in IMC-LM cell lines using differential display of the mRNA in these cells. The gene sequences can be used for the screening of potential inhibitors of cancer metastasis by either: bringing into contact with the cancer metastasis associated protein (CMAP) and determining the degree of binding; or creating a transformant cell line which expresses CMAP and measuring the degree of expression of CMAP using an antibody recognising the protein, either in the presence or absence of the potential inhibitor. IMC-HM cells transformed with antisense CMAP DNA show a lowered ability to metastasise. The present sequence represents a specifically claimed gene sequence from the present invention. Claim 2; Page 46-47; 74pp; Japanese. the protein,

Sequence 684 BP; 175 A; 176 C; 179 G; 154 T; 0 other; 

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256 CCCATTCGCAAACCAGTGTGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGT 315
                                                                                                                                                                            23
                                                                                                                                                                                                                                                24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLys 43
                                                                                                                                                                            4 ProValLysGlyProValSerThrLysProGlySerCysProlleIleLeuIleArgCys
              Length:
Matches:
Conservative:
                                                                  Mismatches:
Indels:
                                                                                                                                          09-833799-13B (1-57) x AAX18516 (1-684)
                  1.57e-09
                               161.00
58.49%
52.83%
49.24%
                                                                  Best Local Similarity:
                                                     Percent Similarity:
Alignment Scores:
                                                                                      Query Match:
                                                                                                                                                                                                                                                                                   а
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316 ATGATGCTTAACCCTCCCAATGTCTGCCAGGGACGGGCAGTGTGACGGCAAATACAAG 375

26

CysCysGluGlySerCysGlyMetAlaCysPheValPro

44

376 recrereagegranareregeaaagrerecereceee 414 AAX18514 standard; cDNA to mRNA; 691 BP

05-MAY-1999 (first entry)

AAX18514;

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The present invention provides gene sequences associated with cancer metastasis which are isolated from mouse IMC carcinoma cells by defection of their higher expression in IMC-HM cell lines than in IMC-LM cell lines than in The gene sequences can be used for the screening of potential inhibitors of cancer metastasis by either: bringing into contact with the cancer binding; or creating a transformant cell line which expresses CMAP and measuring the degree of expression of CMAP using an antibody recognising the protein, either in the presence of a the potential thibitor. IMM-HM cells transformed with antisense CMAP by linhibitor. IMC-HM cells transformed with antisense CMAP pNA show a lowered ability to metastasise. The present sequence represents a specifically claimed gene sequence from the present invention.
                                                  Mouse; carcinoma cell; IMC-HAL; cancer; metastasis; CMAP; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 CCCATTCGCAAACCAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAAAACTCAGGCAAGATGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 ATGATGCTTAACCCTCCCAATGTCTGCCAGAGGACGGGCAGTGTGACGGCAAATACAAG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProValLysGlyProValSerThrLysProGlySerCysProllelleLeulleArgCys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlylleLysLys 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein associated with cancer metastasis and gene encoding it useful for screening for potential inhibitors of cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 691 BP; 160 A; 186 C; 183 G; 162 T; 0 other;
                   Mouse IMC carcinoma cell IMC-HA1 clone 28-1#3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              récréréadegrarardregaaagrerécerecede 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                        cancer metastasis associated protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 41-42; 74pp; Japanese.
                                                                                                                                          Location/Qualifiers
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ID 'AAX18515 standard; cDNA; 1114 BP.
                                                                                                                                                                                                                                                                                                                                                                                  Morita M, Ohta M;
                                                                                                                                                                                                                                                                                                                97JP-0105333.
                                                                                                                                                                                                                                                                              98WO-JP01592
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58.49%
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49.24%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW98908.
                                                                                                      Mus musculus
                                                                                                                                                                                                           WO9845431-A1.
                                                                                                                                                                                                                                                                              07-APR-1998;
                                                                                                                                                                                                                                                                                                                08-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                  Arakawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
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The present invention provides gene sequences associated with cancer metastasis which are isolated from mouse IMC carcinoma cells by detection of their higher expression in IMC-HM cell lines than in IMC-HM cell lines than in IMC-HM cell lines using differential display of the mRNA in these cells. The gene sequences can be used for the screening of potential inhibitors of cancer metastasis by either: bringing into contact with the cancer metastasis by either: bringing into contact with the cancer binding; or creating a transformant cell line which expresses CMAP and masuring the degree of expression of CMAP using an antibody recognising the protein, either in the presence or absence of the potential thinbiblox. IMC-HM cells transformed with antisense CMAP DNA show a lowered ability to metastasise. The present sequence represents a specifically claimed gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 CCCATTCGCAAACCAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 ATGALGCITAACCCICCCAAIGTCIGCCAGAGGGACGGCAGIGIGACGGCAAATACAAG 804
                                                                                                                          Mouse; carcinoma cell; IMC-HA1; cancer; metastasis; CMAP; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLys 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein associated with cancer metastasis and gene encoding it useful for screening for potential inhibitors of cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ProValLysGlyProValSerThrLysProGlySerCysProllelleLeulleArgCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1114 BP; 271 A; 299 C; 290 G; 254 T; 0 other;
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28
3
22
0
                                                                                     Mouse IMC carcinoma cell IMC-HA1 clone #8.323 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                           cancer metastasis associated protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 44-45; 74pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                               Ohta M;
                                                                                                                                                                                                                                                                                     98WO-JP01592.
                                                                                                                                                                                                                                                                                                                       97JP-0105333.
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                                                  05-MAY-1999 (first entry)
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58.49%
52.83%
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                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-080732/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                               Mus musculus.
                                                                                                                                                                                                                WO9845431-A1
                                                                                                                                                                                                                                                                                     07-APR-1998;
                                                                                                                                                                                                                                                                                                                       08-APR-1997;
                                                                                                                                                                                                                                                  15-0CT-1998.
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                                                                                                                                                                                                                                                                                                                                                                                              Arakawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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ID AAC9
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AAC97526 standard; DNA; 180 BP.

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protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                              Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis;
                   DNA encoding a serine protease inhibitory peptide.
                                                                                       91US-0712354.
          27-FEB-2001 (first entry)
                                              elastase; ds
                                                                                      07-JUN-1991;
                                                                  US6132990-A.
                                                                            17-OCT-2000
                                                       Synthetic.
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BOULDER INC (AMGE-) AMGEN

85US-0678822. 85US-0803471. 86US-0890526.

06-DEC-1984; 02-DEC-1985; 29-JUL-1986;

87US-0031846 87US-0082962

04-AUG-1987;

30-MAR-1987

89US-0293042

03-JAN-1989

Thompson RC; Stetler GL, Bandyopadhyay PK, Eisenberg SP, WPI; 2000-678667/66. New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors

Claim 22; Column 61-62; 47pp; English.

ABS3098 - AABS3122 represent the protease inhibitors. Peptide sequences AABS3098 - AABS3122 represent the protease inhibitor of the invention and various other peptides used in the isolation of the protease inhibitors. The protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating a protease—mediated condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis, pursular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97515 - AAC97573 and AAC95582 - AAC97613 are used in the proteins, especially by recombinant methods.

Sequence 180 BP; 42 A; 44 C; 50 G; 44 T; 0 other;

	180	27	4	23	7	н
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	1.65e-08			48.21%		21
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

09-833799-13B (1-57) x AAC97526 (1-180)

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3 GluProValLysGlyProValSerThr-----LysProGlySerCysProllelleLeu 20
                                      ****|||||||
4 GATCCTGTTGACACCCCAACAACAAGGAGGAGGAGGCCTGGGAAGTGCCCAGTGACTTAT 63
ઠે
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Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis; acute leukemia; ss.
              21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                     Secretory leukocyte protease inhibitor analogue encoding cDNA.
                                       124 GACTTGAAGTGTTGCATGGGCATGTGTGGGGAAATCCTGCGTTTCCCCT 171
                             41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                        Location/Qualifiers
                                                                        AAX16273 standard; cDNA; 183 BP
                                                                                                                                                                                                                                                                       84US-0678822.
86US-0890526.
86US-0903471.
90US-0563832.
                                                                                                                                                                                                                                                  94US-0279056
                                                                                                                                                                                                                                                                87US-0031846
                                                                                                      (first entry)
                                                                                                                                                                  Homo sapiens.
                                                                                                      19-APR-1999
                                                                                                                                                                                                                                                  22-JUL-1994;
                                                                                                                                                                                                                     US5871956-A
                                                                                                                                                                                                                                                                               29-JUL-1986
                                                                                                                                                                                                                                                                                     03-SEP-1986
                                                                                                                                                                                                                                                                30-MAR-1987
                                                                                                                                                                         Synthetic
                                                                                       AAX16273;
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Eisenberg SP, Stetler GL, Thompson RC; Bandyopadhyay PK,

(AMGE-) AMGEN INC.

94US-0279056

22-JUL-1994;

06-AUG-1990

WPI; 1999-166640/14. P-PSDB; AAW94481. New DNA sequence encoding mammalian serine protease inhibitor useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis, muscular dystrophy, and tumour invasion

Example 9; Column 43; 37pp; English.

The present invention describes a DNA sequence (A) encoding an analogue of a mammalian serine protease inhibitor (B). The DNA sequences and recombinant methods allow manufacture of a class of inhibitors of e.g. cathepsin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions caused by a disturbance in the native protease/protease inhibitor balance such as emphysema, arthritis, glomerulonephritis, peridontitis, muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A) caused by a compinantly produced in sufficient quantities and purities so as to provide economical pharmaceutical compositions. (B) is resistant to heat, acid, and a variety of proteolytic enzymes, is thermodynamically stable in extracellular conditions, and exhibits a high degree of self assembly forming an active tertiary structure in the absence of biochemical stimuli. The present sequence encodes a secretory conditions and exhibits a become of biochemical stimuli. The present sequence encodes a secretory conditions and secretory conditions.

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The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin
                                                                                                                                                                                                       3 GluProValLysGlyProValSerThr----LysProGlySerCysProllelleLeu 20
                                                                                                                                                            21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor protein; recombinant; leukocyte elastase;
                                                                                                                                                                                                                                                                                                                                                                                      Secretory leukocyte protease inhibitor (SLPI) analogue cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                           trypsin; secretory leukocyte protease inhibitor; SLPI; ss.
                                                                                                                                                                                                                                                        41 IleLysLysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_except= "(pos: 22..24, aa: Asn)"
                                  183
27
23
23
Sequence 183 BP; 43 A; 45 C; 51 G; 44 T; 0 other;
                                             Matches:
Conservative:
Mismatches:
                                                                                  Indels:
                                   Length:
                                                                                             Gaps:
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                                                                                                                     09-833799-13B (1-57) x AAX16273 (1-183)
                                                                                                                                                                                                                                                                                                                AAI67584 standard; cDNA; 183 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87US-0031846.
90US-0563832.
94US-0279056.
84US-0678222.
85US-0803471.
86US-0890526.
                                   68e-08
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                                            146.00
55.36%
48.21%
44.65%
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                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                     Alignment Scores:
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02-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1994;
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                                   No.
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Elastase inhibitor; human polymorphonuclear leukocyte elastase inhibiting
at least one operational element consisting of a promoter, an operator, a least sequence, a Shine-Dalgarno sequence, a riboscome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukcoyte elastase or trypsin. The present sequence represents the cDNA emncoding a secretory leukcoyte protease inhibitor (SLPI) analogue that has chymotrypsin and elastase inhibitory activity.
                                                                                                                                                                                                                                                                                                                       3 GluproValLysGlyProValSerThr----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                         4 GATCCTGTTGACACCCCAACACAACAAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT
                                                                                                                                                                                                                                                                                                  21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence encoding fragment of human polymorphonuclear leukocyte
                                                                                                                                                                                                                                                                                                                                                 41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                                                                                                                                                                                                        124 GACTTGAAGTGTTGCATGGCATGTGGGAAATCCTGCGTTTCCCCT
                                                                                                                                     183
27
23
23
                                                                                                 Sequence 183 BP; 43 A; 44 C; 51 G; 45 T; 0 other;
                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                           Mismatches:
                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                         09-833799-13B (1-57) x AAI67584 (1-183)
                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAN90354 standard; DNA; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elastase inhibiting protein.
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                                                                                                                                        1.68e-08
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                                                                                                                                               146.00
55.36%
48.21%
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7..12
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25..30
/*tag= c
56..61
/*tag= d
120..125
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185..189
/*tag= f
190..194
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                                                                                                                                                                           Best Local Similarity:
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                                                                                                                                                              Percent Similarity:
                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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The sequence encodes a fragment of human polymorphonuclear leukocyte elastase inhibiting protein (Asn 55-Ala 107). See AAP90126 for encoded peptide. Misc. features a-g are BamHI, SalI, MluI, NdeI, BglII, XhoI and PstI sites resp. See also AAP90384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secretory leukoprotease inhibitor; human, gene; ds; protease inhibitor; malaria; emphysema; asthma; chronic obstructive pulmonary disease; SLPI; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease; glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
                                                                                            Blastase-inhibiting peptide of low serine protease-inhibiting activity - contains C-terminal portion of human polymorphonuclear leukocyte elastase inhibiting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GGTCAGTGTCTGATGCTGAACCCGCCGAACTTCTGTGAAATGGACGGTCAGTGTAAACGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GluProValLysGlyProValSerThr----LysProGlySerCysProlleIleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding human secretory leukoprotease inhibitor (SLPI) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GATCCGGTCGACCCCCGAACCCGACGCGTCGTAAACCGGGGTAAATGTCCGGTTACATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GATCTGAAATGTTGTATGGGTATGTGTGTAAATCTTGTGTTTTCTCCG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
               Ohtsuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /partial
/note= "No start or stop codon shown"
                                                                                                                                                                                                                                                                                          other;
                                                                                                                                                                                                                                                                                                                                                                            Conservative:
               Okada M,
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                        Sequence 194 BP; 48 A; 42 C; 53 G; 51 T; 0
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               Masuda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-833799-13B (1-57) x AAN90354 (1-194)
                                                                                                                                                                 Disclosure, fig 2; 55pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK88016 standard; DNA; 321
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                                                                                                                                                                                                                                                                                                                                          4.01e-08
                                                                 P-PSDB; AAP90126, AAP90384.
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55.36%
48.21%
43.73%
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               Kamimura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                 WPI; 1989-220549/30
                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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               Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-OCT-2002
                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, officis exermal or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful cor treating dermatological diseases such as atopic dermaticis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating dermatological diseases such as atopic dermaticis, creaming connection, sepsis, rheumatoid arthritis, periodonial disease, tumour metascasis and tumour anglogenesis, gastric ulceration, chronic osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the human secretory leukoprotease inhibitor used to create the fusion protein
                                                                                                                                                                                                                     Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 GGTCAATGTTTGATGTTGAACCCACCAACTTCTGTGAAATGGACGGTCAATGTAAGAGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GluProValLysGlyProValSerThr----LysProGlySerCysProllelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic sequence capable of directing microbial synthesis of a serine protease inhibitor having similar properties to protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 GACTIGAAGIGITGIAIGGGIAIGIGGGAAGICCIGIGITICCCCA 312
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23
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
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                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 32; 134pp; English.
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                                                                                                                        Pemberton
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                 18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
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55.36%
48.21%
43.73%
                                                                                (ARRI-) ARRIVA PHARM INC.
                                                                                                                        Barr PJ, Gibson HL,
                                                                                                                                                                 2002-500631/53
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                                                                                                                                                                                     P-PSDB; AAU99874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                         The sequence directs synthesis of a single chain polypeptide serine protease-inhibitor, which believed to have at least 2 active sites, 1 exhibiting leukocyte-elastase-inhibiting properties and the other exhibiting activity against trypsin. See also AAN60464-69 and AAP60562-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 GATCCGGTTGATACCCCGACCCGACTCGAAAACCGGGTAAATGCCCGGTAACCTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 GGCCAGTGTCTGATGCTGAACCCGCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GluProValLysGlyProValSerThr-----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                     Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
                                                                                                                                                                                                                                                          New synthetic DNA sequences for directing microbial synthesis for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor; trypsin-; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic sequence capable of directing microbial synthesis of secretory leukocyte protease-inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 GATCTGAAATGCTGTATGGGGTATGTGCGGCAAATCTTGTGTTTCCCCCG 312
                                                                                                                                                                                                        Bandyopadh PK, Eisenberg SP, Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                   Disclosure; Page 14; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-833799-13B (1-57) x AAN60463 (1-324)
 isolated from parotid secretions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                         7.52e-08
143.00
55.36%
48.21%
                                                                                                                                                             85US-0803471,
                                                                                                                    85WO-US02385.
                                                                                                                                          85WO-US02385.
                                                                                                                                                   84US-0678822
                                                                                                                                                                                  (SYNE-) SYNERGEN BIOLOG INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1980 (first entry)
                               trypsin-; inhibitor; ss.
                                                                                                                                                                                                                            WPI; 1986-169458/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                                                                                                                                                                                                                                      P-PSDB; AAP60562.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                   04-DEC-1985;
                                                                                                                                       04-DEC-1985;
                                                                                                                                                             02-DEC-1985;
                                                                        WO8603519-A.
                                                                                               19-JUN-1986
                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                     Synthetic.
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145 GATCCGGTTGATACCCCGAACCCGACTCGAAAACCGGGTAAATGCCCGGTAACCTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence directs synthesis of a secretory leukocyte protease-
inhibitor. See also AAN60463, AAN60465-69 and AAP60562. AAP60564-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor, human, emphysema, arthritis, peridontitis, muscular dystrophy, tumour invasion; glomerulonephritis, sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 GGCCAGTGTCTGATGCTGAACCCGCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GluproValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                               New synthetic DNA sequences for directing microbial synthesis - for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor direct manufacturing DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                       Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                       Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-833799-13B (1-57) x AAN60464 (1-324)
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                                                                                                                                                                                                                                                                                                                  Bandyopadh PK, Eisenberg SP,
                                                                                                                                                                           85WO-US02385.
84US-0678822.
85US-0803471.
                                                                                                                                                                                                                                                                     (SYNE-) SYNERGEN BIOLOG INC.
                                                                                                                                  85WO-US02385.
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55.36%
48.21%
43.73%
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                                                                                                                                                                                                                                                                                                                                                             WPI; 1986-169458/26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAP60563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                             04-DEC-1985;
06-DEC-1984;
                                                                                                                                  04-DEC-1985;
                                                                                                                                                                                                                            02-DEC-1985;
                                          WO8603519-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                       19-JUN-1986
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Synthetic.
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DB:
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of a mammalian serine protease inhibitor (B). The DNA sequences and recombinant methods allow manufacture of a class of inhibitors of e.g. catheppin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions caused by a disturbance in the native protease/protease inhibitor balance such as emphysema, arthritis, glomerulonephritis, peridontitis, muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A) culties so as to provide economical pharmaceutical compositions. (B) is resistant to hear, acid, and a variety of proteolytic enzymes, is chermodynamically stable in extracellular conditions, and exhibits a high degree of self assembly forming an active tertiary structure in the absence of biochemical stimuli. The present sequence represents a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a DNA sequence (A) encoding an analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 GATCCGGTTGATACCCCGAACCCGACTCGTCGAAAACCGGGTAAATGCCCGGTAACCTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 geccagigicisariecisaacceeceaacinciesaangeaceecagisiaaacea 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GluProValLysGlyProValSerThr----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               absence of biochemical stimuli. The present sequence represents a I sequence which is used to direct manufacture of recombinant serine protease inhibitors.
                                                                                                                                                                                                                                                                                        New DNA sequence encoding mammalian serine protease inhibitor - useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis,
                                                                                                                                                                                                                   Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 GATCTGAAATGCTGTATGGGTATGTGCGGCAAATCTTGTGTTTCCCCG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
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27
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2
2
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                                                                                                                                                                                                                   Bandyopadhyay PK, Eisenberg SP, Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                  muscular dystrophy, and tumour invasion
                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Column 23; 37pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-833799-13B (1-57) x AAX16194 (1-324)
                                                87US-0031846.
84US-0678822.
86US-0890526.
86US-0903471.
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                                                                                                                           90US-0563832
               94US-0279056
                                                                                                                                            94US-0279056
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55.36%
48.21%
43.73%
                                                                                                                                                                                                                                                          4PI; 1999-166640/14
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                                                                                                                                                                                (AMGE-) AMGEN INC.
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                 22-JUL-1994;
                                                                     05-DEC-1984
29-JUL-1986
                                                                                                                           06-AUG-1990
                                                                                                                                              22-JUL-1994;
                                                                                                         03-SEP-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 28
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The present invention describes a DNA sequence (A) encoding an analogue of a mammalian serine protease inhibitor (B). The DNA sequences and recombinant methods allow manufacture of a class of inhibitors of e.g. cathepsin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions caused by a disturbance in the native protease/protease inhibitor balance such as emphysema, arthitis, glomerulonephritis, peridontitis, muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A) allows (B) to be recombinantly produced in sufficient quantities and purities so as to provide economical pharmaceutical compositions. (B) is resistant to heat, acid, and a variety of proteolytic enzymes, is thermodynamically tabble in extracellular conditions, and exhibits a thingh degree of self assembly forming an active tertiary structure in the absence of biochemical stimuli. The present sequence represents a DNA cabbeauch and surfacellular conditions.
                                 Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;
Serine protease inhibitor direct manufacturing DNA sequence (SLPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA sequence encoding mammalian serine protease inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                  Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324
27
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscular dystrophy, and tumour invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Column 29; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Bandyopadhyay PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                     84US-0678822.
86US-0890526.
86US-0903471.
90US-0563832.
94US-0279056.
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55.36%
48.21%
43.73%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-166640/14.
                                                                         acute leukemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
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Best Local Similari
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                                                                                                                                                                                                                                         22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                            06-AUG-1990;
22-JUL-1994;
                                                                                                                                                                  US5871956-A.
                                                                                                                                                                                                                                                                                           05-DEC-1984;
29-JUL-1986;
                                                                                                                                                                                                     16-FEB-1999
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                                                                                                                                                                                                                                                                        30-MAR-1987
                                                                                                                             Synthetic.
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                                                                                                              Homo
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205 GGCCAGTGTCTGATGCTGAACCCGCCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 264

21 IleargCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40

3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20

145 GAICCGGITGAIACCCCGAACCCGACTCGICGAAAACCGGGIAAAIGCCCGGIAACCTAI

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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97531, AAC97531 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonaclectide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95828 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB53098 - AAB53122 represent the protease inhibitors of the invention and represent so the resolution and anti-inflammatory activity. The serine protease inhibitors protein is useful for treating a protease inhibitor protein is useful for treating a destruction, e.g. emphysema, arthritis, glomerulonephritis, puscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the conteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a serine protease inhibitor peptide sequence.
                                                               265 GATCTGAAATGCTGTATGGCGCAAAATCTTGTGTTTCCCCG 312
41 IleLysLysCysCysGluGlySerCysGlyMetalaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandyopadhyay PK, Eisenberg SP, Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 34; Column 64-66; 47pp; English.
                                                                                                                                                                                                            AAC97527 standard; DNA; 324 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84US-0678822.
85US-0803471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elastase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                      AAC97527;
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Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 other;
                                                             Conservative:
Mismatches:
                                                   Matches:
                                       Length:
                                                                                    Indels:
                                     7.52e-08
                                                143.00
55.36%
48.21%
43.73%
                                                                      Similarity:
                                                           Percent Similarity:
                       Alignment Scores:
                                                                                 Query Match:
                                    No.:
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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB5302 represent the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitors protein is useful for treating a protease-mediated condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis,
                                                                           145 GATCCGGTTGATACCCCGAACCCGACTCGTCGAAAACCGGGTAAATGCCCGGTAACCTAT 204
                                                                                                                                                       205 GGCCAGTGTCTGATGCTGAACCCGCCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 264
                                      3 GluprovalLysGlyProvalSerThr-----LysProGlySerCysProllelleLeu 20
                                                                                                                  21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             emphysema or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New serine protease inhibitors and DNA sequences for treating protease-mediated condition or tissue destruction e.g. emphyse tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                              Secretory leukocyte protease inhibitor (SLPI) DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson RC;
                                                                                                                                                                                                                                  265 GATCTGAAATGCTGTATGGGGTATGTGCGGCAAATCTTGTGTTTTCCCCG 312
                                                                                                                                                                                                  41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandyopadhyay PK, Eisenberg SP, Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Column 5; 47pp; English.
09-833799-13B (1-57) x AAC97527 (1-324)
                                                                                                                                                                                                                                                                                                                  AAC97528 standard; DNA; 324 BP.
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87US-0031846.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elastase; ds.
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09-833799-13b.rng

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periodontitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                             145 GATCCGGTTGATACCCCGACTCGACTCGAAAACCGGGTAAATGCCCGGTAACCTAT 204
                                                                                                                                                                                                                                                                                                                                                             205 GGCCAGTGTCTGATGCTGAACCCCGCCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA
                                                                                                                                                                                                                                                               3 GluproValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                               21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                             265 GATCTGAAATGCTGTATGGGTATGTGCGGCAAATCTTGTGTTTTCCCCG 312
                                                                                                                                                                                                                                                                                                                                                                                               41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a serine protease inhibitory peptide.
                                                                    Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                               09-833799-13B (1-57) x AAC97528 (1-324)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC97579 standard; DNA; 324 BP
                                                                                                                7.52e-08
143.00
55.36%
48.21%
43.73%
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85US-0803471
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87US-0031846
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                                                                                                                                                                   Similarity:
                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bandyopadhyay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elastase; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1991;
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                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6132990-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                  Query Match:
                                                                                                                     Pred. No.:
                                                                                                                                                                   Best Local
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inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534,

AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences CAAB53089 - AAB53122 represent the protease inhibitor of the invention and various other peptides used in the isolation of the protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitors protease inhibitors protease inhibitors protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitors protein is useful for treating a destruction, e.g. emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful contains and andulating protease activity. The DNAs are useful for producing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GATCCGGTTGATACCCCGAACCCGACTCGAAAACCGGGTAAATGCCCGGTAACCTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 GGCCAGTGTCTGATGCTGAACCCGCCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GluprovalLysGlyProvalSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease inhibitor protein; recombinant; leukocyte elastase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 GATCTGAAATGCTGTATGGGTATGTGCGCAAATCTTGTGTTTCCCCG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleLysLysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "serine protease inhibitor"
                                                                                                                                                                                                                                                                                                                               Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant serine protease inhibitor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-833799-13B (1-57) x AAC97579 (1-324)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA167488 standard; DNA; 324 BP
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90US-0563832.
94US-0279056.
84US-0678222.
85US-0803471.
86US-0890526.
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143.00
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                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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02-DEC-1985;
29-JUL-1986;
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                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trypsin; ds
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No.:
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The invention relates to a DNA sequence encoding an analog of a mammalian escribe protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serihe protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents the coding strand of a DNA that directs the manufacture of a recombinant
                                                                                                              directing
leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::|||||||
145 GATCCGGTTGATACCCCGAACCCGACTCGTCGAAAACCGGGTAATGCCCGGTAACCTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant secretory leukocyte protease inhibitor (SLPI) DNA.
                                                                                                      sequences, useful in recombinant DNA techniques for
                                                                                                                       the production of a serine protease inhibitor protein, e.g. elastase or trypsin -
                                   Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 GATCTGAAATGCTGTATGGGTATGTGCGGCAAATCTTGTGTTTCCCCG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                    Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
Indels:
                                 Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                  Example 1; Column 4; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-833799-13B (1-57) x AAI67488 (1-324)
                                 Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI67489 standard; DNA; 324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                   7.52e-08
                                                                                                                                                                                                                                                                                                                                        serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                  143.00
55.36%
48.21%
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                                                           WPI; 2001-637974/73.
                              Bandyopadhyay PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                           P-PSDB; AAG65993
                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6291662-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
DB:
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87US-0031846. 90US-0563832. 94US-0279056. 84US-0678222.

06-AUG-1990; 22-JUL-1994; •05-DEC-1984;

98US-0158085

22-SEP-1998; 30-MAR-1987;

```
The invention relates to a DNA sequence encoding an analog of a mammalian exrine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents the coding strand of a DNA that directs the manufacture of a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovarian tumour marker gene; human; overexpression; upregulation; idepthelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; organical mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE; membrane localised; secreted; therapeutic target; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secretory leukocyte protease inhibitor ovarian tumour marker gene, #53.
                                                                                                                                                                                     New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 GATCCGGTTGATACCCCGAACCCGACTCGAAAACGGGGTAAATGCCCGGTAACCTAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 GGCCAGTGTCTGATGCTGAACCCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                        Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 GATCTGAAATGCTGTATGGGTATGTGCGCCAAATCTTGTGTTTCCCCG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                    Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secretory leukocyte protease inhibitor (SLPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                 Disclosure; Column 5; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-833799-13B (1-57) x AAI67489 (1-324)
                                                                                                    Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA83108 standard; DNA; 399 BP.
                      86US-0890526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.52e-08
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55.36%
48.21%
43.73%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; vaccine; ds.
                                                                                                                                         WPI; 2001-637974/73.
                                                                                                  Bandyopadhyay PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                              P-PSDB; AAG65996
                                                          (AMGE-) AMGEN
  02-DEC-1985;
                      29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match:
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WO200175177-A2
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11-OCT-2001

03-APR-2001; 2001WO-US10947

03-APR-2000; 2000US-194336P

USSH ) US DEPT HEALTH & HUMAN SERVICES

Sherman-Baust CA, Pizer ES, Hough CD; Morin PJ,

WPI; 2001-626450/72

P-PSDB; ABB50282

Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker dene

Claim 23; Page 98; 140pp; English.

The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA81081-ABA81182, ABA81180, ABA81181 and ABA81181). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma, borderline mucinous tumour, mucinous cystadenocarcinoma, endometriol carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, endometriol carcinoma, adenofibroma and Brenner cumour The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian folding, and many of these are membrane proliferation and in protein folding, and many of these are membrane potalised or secreted. In addition to their use as diagnostic and content of the diagnostic and content of their use as diagnostic and content of the diagnostic and content of their and content prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and orevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180, ABA83182 and ABA83184 represent the ovarian tumour marker genes of the invention 

G; 97 T; 0 other; Sequence 399 BP; 91 A; 100 C; 111

Conservative: Mismatches: Indels: Length: Matches: 9.7e-08 143.00 55.36% 48.21% 43.73% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Pred

399 27 23 23

09-833799-13B (1-57) x ABA83108 (1-399)

- 3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20 220 GATCCTGTTGACACCCCAACAAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 8 g
- 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly ઠે
- 41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56

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Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis; acute leukemia; ds.
340 GACTIGAAGIGITGCAIGGCAIGIGIGGGAAAICCIGCGITICCCCT 387
                                                               ONA sequence of ompA-tc-met-SLPI
                         BP.
                                                                                                                                                              87US-0031846.
84US-0678822.
86US-0890526.
86US-0903471.
90US-0563832.
                                                                                                                                                   94US-0279056
                        AAX16272 standard; DNA; 420
                                                                                                                                                                                               94US-0279056
                                                   (first entry)
                                                                                                      Homo sapiens
                                                                                                                                                  22-JUL-1994;
                                                   19-APR-1999
                                                                                                                         US5871956-A.
                                                                                                                                                                      05-DEC-1984;
                                                                                                                                                                                               22-JUL-1994
                                                                                                                                      16-FEB-1999
                                                                                                                                                                            29-JUL-1986
                                                                                                                                                                                   03-SEP-1986
                                                                                                                                                               30-MAR-1987
                                                                                                                                                                                         06-AUG-1990
                                                                                                             Synthetic.
                                      AAX16272;
             RESULT 35
                     AAX1627
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(AMGE-) AMGEN INC.

Thompson RC; Stetler GL, Bandyopadhyay PK, Eisenberg SP,

WPI; 1999-166640/14.

New DNA sequence encoding mammalian serine protease inhibitor - useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis, muscular dystrophy, and tumour invasion

Example 3; Column 37-40; 37pp; English.

(B) is thermodynamically stable in extracellular conditions, and exhibits a high degree of self assembly forming an active tertiary structure in the absence of biochemical stimuli. The present sequence represents the DNA The present invention describes a DNA sequence (A) encoding an analogue of a mammalian serine protease inhibitor (B). The DNA sequences and recombinant methods allow manufacture of a class of inhibitors of e.g. cathepsin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions caused by a disturbance in the mative protease/protease inhibitor balance such as emphysema, arthritis, glomerulonephritis, peridonitis, muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A) allows (B) to be recombinantly produced in sufficient quantities and purities so as to provide economical pharmaceutical compositions. (B) is resistant to heat, acid, and a variety of proceolytic enzymes, is thermodynamically stable in extracellular conditions, and exhibits a sequence of ompA-tc-met-SLPI.

Sequence 420 BP; 123 A; 98 C; 112 G; 87 T; 0 other;

	420	27	4	23	7	7
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
	1.03e-07	33	55.36%	48.21%	43.73%	20
Alignment Scores:	Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Ouery Match:	ĎB:

ò a 셤

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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 and AAC97581 and AAC97614 - AAC97631 are encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAS9358 - AAB33122 respressnt the protease inhibitors of the invention and construction of DNA encoding the protease inhibitors have cytostatic and anti-inflammatory activity. The protease inhibitors have cytostatic and anti-inflammatory activity. Construction, e.g. emphysema, arthritis, glomerulonephritis, protease inhibitor protein is useful for treating a condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis, puscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the
                                                                                                                                               245 GATCCGGTTGATACCCCGACTCGTCGAAAACCGGGTAAATGCCCGGTAACCTAT 304
                                                                                                                                                                                                                                                                                               305 GGCCAGTGTCTGATGCTGAACCCGCCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 364
                                                                         3 GluProValLysGlyProValSerThr----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                             21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                    365 GATCTGAAATGCTGTATGGGTATGTGCGGGCAAATCTTGTGTTTCCCCG 412
                                                                                                                                                                                                                                                                                                                                                                             41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Column 39-40; 47pp; English.
09-833799-13B (1-57) x AAX16272 (1-420)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC97624 standard; DNA; 436 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding ompA-tc-met-SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84US-0678822.
85US-0803471.
86US-0890526.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1984;
02-DEC-1985;
29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6132990-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC97624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC97624
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The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight expetaine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein,
                                                                                                                                                                                                                                                         245 GATCCGGTTGATACCCCGAACCCGACTCGTAAAACCGGGTAAATGCCCGGTAACCTAT 304
                                                                                                                                                                                                                                                                                                               305 GGCCAGTGTCTGATGCTGAACCCGCCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin
                                                                                                                                                                                                                            3 GluProValLysGlyProValSerThr----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                        365 GATCTGAAATGCTGTATGGCTATGTGCGCAAATCTTGTGTTTCCCCG 412
                                                                                                                                                                                                                                                                                                                                                           41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                 436
74 23
23
                              Sequence 436 BP; 128 A; 102 C; 116 G; 90 T; 0 other;
                                                                                                                Conservative:
Mismatches:
Indels:
proteins, especially by recombinant methods.
                                                                                 Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequence coding for ompA-tc-met-SLPI.
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                                                                                                                                                                                           09-833799-13B (1-57) x AAC97624 (1-436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI67583 standard; DNA; 436 BP
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90US-0563832.
94US-0279056.
84US-0678222.
85US-0803471.
                                                                                1.08e-07
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                                                                                            143.00
55.36%
48.21%
43.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-FEB-2002 (first entry)
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                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN INC.
                                                                                                              Percent Similarity:
                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6291662-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1985
                                                                                                                                               Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 37
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e.g. leukocyte elastase or trypsin. The present sequence represents the DNA sequence coding for ompA-tc-met-secretory leukocyte protease inhibitor (SLPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a DNA sequence (A) encoding an analogue of a mammalian serine protease inhibitor (B). The DNA sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;
                                                                                                                                                                                                                                                        245 GATCCGGTTGATACCCCGAACCCGACTCGTGGAAACCGGGTAAATGCCCGGTAACCTAT 304
                                                                                                                                                                                                                                                                                                                 305 GGCCAGTGTCTGATGCTGAACCGCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 364
                                                                                                                                                                                                                                3 GluProValLysGlyProValSerThr----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                     21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA sequence encoding mammalian serine protease inhibitor useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis,
                                                                                                                                                                                                                                                                                                                                                                          365 GATCTGAAATGCTGTATGCGCCCAAATCTTGTGTTTCCCCG 412
                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson
                                                                                                                                                                                                                                                                                                                                               41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                     436
27
4
                                                        Sequence 436 BP; 128 A; 102 C; 116 G; 90 T; 0 other;
                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscular dystrophy, and tumour invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Column 37-38; 37pp; English.
                                                                                                                                                                                                  09-833799-13B (1-57) x AAI67583 (1-436)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87US-0031846.
84US-0678822.
86US-0890526.
86US-0903471.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX16271 standard; DNA; 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0279056.
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94US-0279056
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55.36%
48.21%
43.73%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence of ompA-SLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-166640/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acute leukemia; ds
                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5871956-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX16271;
                                                                                                                                                           Query Match:
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                                                                                                    Pred.
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caused by a disturbance in the native protease/protease inhibitor
balance such as emphysema, arthritis, glomerulonephritis, peridontitis,
muscular dystrophy, tumour invasion, sepsis, and caute leukemia. (A)
allows (B) to be recombinantly produced in sufficient quantities and
purities so as to provide economical pharmaceutical compositions. (B) is
resistant to hear, acid, and a variety of proteolytic enzymes, is
thermodynamically stable in extracellular conditions, and exhibits a
high degree of self assembly forming an acive tertiary structure in the
absence of biochemical stimuli. The present sequence represents the DNA
recombinant methods allow manufacture of a class of inhibitors of e.g. cathegin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :::||||||| |||||| 269 GATCCGGTTGAAACCGGGTAAATGCCCGGTAACCTAT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 GGCCAGIGICIGAIGCIGAACCCGCCGAACITCIGCGAAAIGGACGGCCAGIGIAAACGA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GluProValLysGlyProValSerThr----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 GATCTGAAATGCTGTATGGGTATGTGCGCAAATCTTGTGTTTCCCCG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding OmpA secretory leukocyte protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                    460
27
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23
                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                         Conservative:
                                                                                                                                                                                                                                                            Sequence 460 BP; 123 A; 114 C; 125 G; 98 T; 0
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Indels:
                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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84US-0678822.
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87US-0031846
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                                                                                                                                                                                                                               sequence of ompA-SLPI.
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30-MAR-1987;
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No.:
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WPI; 2000-678667/66.

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New serine procease inhibitors and DNA sequences for treating a procease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors - tumor invasion and for recombinant production of inhibitors - tumor invasion and for recombinant production of inhibitors - procease inhibitors proteins which comprise at least 8 cysteine residues can on more than 107 amino acids. The procease inhibitors proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The procease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97534.

AC975781 and AAC97614 - AAC97614 - AAC97631 represent DNA encoding the procease inhibitors of the invention, and include oligomuclectical procease inhibitors of the procease inhibitors. Peptides are used in the isolation and characterisation of the proteins construction of DNA encoding the procease inhibitors of the procease inhibitors. Peptides used in the isolation of the procease inhibitors. Peptides used in the isolation of the procease inhibitors. Peptides used in the isolation of the procease inhibitors of the procease inhibitors procease inhibitors of the procease inhibitors procease mediated condition, which includes procease mediated condition, procease activity. The DNAs are useful for producing the conservation, e.g. emphysems, arthritis, glomerulonehritis, proteins, especially by recombinant methods.

Alignment Scores:

11.16e-07 Matches: 23

Alignment Scores:

11.16e-07 Matches: 23

Alignment Scores: 143.00 Matches: 23

Alignment Scores: 140.00 Matches: 23
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269 GATCCGGTTGATACCCCGAACCCGACTCGAAAACCGGGTAAATGCCCGGTAACCTAT 328
                                                                                                                                                                                                            329 GGCCAGTGTCTGATGCTGAACCCGCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 388
                                                                                                                    3 GluProValLysGlyProValSerThr----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI; ds.
                                                                                                                                                                                                                                                                          389 GATCTGAAATGCTGTATGGGGTATGTGCGGCAAATCTTGTGTTTTCCCCG 436
                                                                                                                                                                                                                                             41 IleLysLysCysCluGlySerCysGlyMetAlaCysPheValPro 56
                                             Indels:
                                                                                       09-833799-13B (1-57) x AAC97622 (1-460)
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence coding for ompA SLPI.
                                                                                                                                                                                                                                                                                                                                        AAI67582 standard; DNA; 460 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1998;
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The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight eysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents the production of a serine protease inhibitor protein, and sequence coding for ompA-secretory leukocyte protease inhibitor
                                                                                                                                                                                                         New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 GATCCGGTTGATACCCCCGACCCGACTCGTCGAAAACCGGGTAAATGCCCGGTAACCTAT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 GGCCAGTGTCTGATGCTGAACCCGCGAACTTCTGCGAAATGGACGGCCAGTGTAAACGA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GluProValLysGlyProValSerThr-----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding protein with the biological activity of HUSI (human seminal plasma inhibitor) type I inhibitors encoded on pRH31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bronchitis therapy; cervix inflammation; hyperfibrinolysis; ds.
                                                                                                                                          Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 GATCTGAAATGCTGTATGGGTATGTGCGCCAAATCTTGTGTTTCCCCCG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
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27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 460 BP; 123 A; 114 C; 125 G; 98 T; 0 other;
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Indels:
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Matches:
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                                                                                                                                      Bandyopadhyay PK, Eisenberg SP,
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                94US-0279056.
84US-0678222.
85US-0803471.
86US-0890526.
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                                                                                                     (AMGE-) AMGEN INC.
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Best Local Similarity:
                22-JUL-1994;
05-DEC-1984;
06-AUG-1990;
                                                02-DEC-1985;
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06-AUG-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence encoding protein with the biological activity of HUSI (human seminal plasma inhibitor) type I inhibitors encoded on pRH 34.
                                                                                                                                                                                                                                                                                                                                                                                                                 3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                     HUSI-type inhibitors are useful for treating chronic bronchitis, chronic cervical inflammation; inflammation associated with excessive mucus prodn.; post-operative bleeding caused by hyperfibrinolysis, or shock. They specifibrinolysis, or shock. They specifibrinolysis, or inhalation. The expression control sequence on the DNA fragment in AAN70928 is bound to the 5'-end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                          New protein with human seminal plasma inhibitor activity - and new DNA coding sequences, vectors and transformed organisms, useful e.g. for treating bronchitis or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bronchitis therapy; cervix inflammation; hyperfibrinolysis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GACTTGAAGTGTTGCATGGGCATGTGTGGGGAAATCCTGCGTTTCCCCT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 IlelyslysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                         Sequence 498 BP; 110 A; 131 C; 141 G; 116 T; 0 other;
                                                                                          Machleidt W;
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Matches:
Conservative:
Mismatches:
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                                                                                          Gassen HG,
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                                                                                                                                                                                                                                                                   HUSI cDNA in an expression vector.
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                              86DE-3600571
                                                 86DE-3600571
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                                                                                          Heinzel R, Appelhans H,
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                                                                     (CHEF ) GRUNENTHAL GMBH
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                                                                                                               WPI; 1987-222038/32
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Best Local Similarity:
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                                                 10-JAN-1986;
                                                                                                                                                                                                                                                                                                            Alignment Scores:
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         06-AUG-1987
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Human, cytostatic, gynecological, elastase, cathepsin G, gene therapy; endometriosis, antileukoprotease, ALP; secretory leukoprotease inhibitor; SLPI; alphal-proteinase inhibitor; alphal-PI; ss.
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278 GATCCTGTTGACACCCCAACCCCAACGAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                          HUSI-type I inhibitors are useful for treating chronic bronchitis, chronic cervical inflammation, inflammation associated with excessive mucus prodn.; post-operative bleeding caused by hyperfibrinolysis, and shock. They are esp. suitable for administration as spray or inhalation. The expression control sequence on the DNA fragment in AAN70928 is bound to the 5' end of
                                                                                                                                                        Seemuller U;
                                                                                                                                                                                                                                                                                   New protein with human seminal plasma inhibitor activity - a new DNA coding sequences, vectors and transformed organisms, useful e.g. for treating bronchitis or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 GACTTGAAGTGTTGCATGGCATGTGTGGGAAATCCTGCGTTTCCCCT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleLysLysCysGysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 565 BP; 106 A; 162 C; 171 G; 126 T; 0 other;
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27
4
23
23
                                                                                                                                                        Machleidt W,
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Matches:
Conservative:
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                                                                                                                                                        Gassen HG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-833799-13B (1-57) x AAN70930 (1-565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUSI cDNA in an expression vector.
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                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Fig 5; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF32043 standard; cDNA; 565
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143.00
55.36%
48.21%
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  86DE-3600571.
                                                   86DE-3600571
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                                                                                                                                                        Heinzel R, Appelhans H,
                                                                                                     (CHEF ) GRUNENTHAL GMBH
                                                                                                                                                                                                       WPI; 1987-222038/32.
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                                                                                                                                                                                                                                     P-PSDB; AAP70584
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10-JAN-1986;
                                                   10-JAN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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subject, comprising administering to the subject an amount of antileukoprotease (ALP) effective to inhibit the activity of elastase or estabepsin G, thereby inhibiting ectopic implantation of endometrial fragments. The present sequence is the coding sequence for human ALP. ALP is also known as secretory leukoprotease inhibitor (SLPI) and alphal-proteinase inhibitor (alphal-PI). ALP plays an important role in the defence of epithelial surfaces against proteolytic damage.
                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a method for treating endometriosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, cancer; colon, breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                  Treating and diagnosing endometriosis or promoting embryo implantation comprises determining or modulating antileukoprotease activity in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 GATCCTGTTGACACCCCAACAAGAAGAAGAAGCCTGGGAAGTGCCCAGTGACTTAT 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GluProValLysGlyProValSerThr-----LysProGlySerCysProllelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 565 BP; 106 A; 162 C; 171 G; 126 T; 0 other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 28pp; English.
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                         27-JUN-2000; 2000US-0605134.
  99US-0142157
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55.36%
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                                                                           (REPR-) REPROGEN INC
                                                                                                                                                                                         WPI; 2001-138062/14.
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                                                                                                                                 Li Z;
                                                                                                                                                                                                                     P-PSDB; AAB66864.
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01-JUL-1999;
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                                                                                                                                 Neilson L,
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used an used for producing a product which can anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical concertucture and/or properties of the agent. M1 can be used in the cospobageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, continuma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter KC, Ebner R, Endress G, Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                                                                20.5EP-2000; 2000US-234034P.
20.5EP-2000; 2000US-23455P.
22.5EP-2000; 2000US-234550P.
22.5EP-2000; 2000US-234557P.
25.5EP-2000; 2000US-234923P.
25.5EP-2000; 2000US-234924P.
                                                                                                                                                                                                                                                                          27-SEP-2000; 2000US-23571IP.
27-SEP-2000; 2000US-235720P.
27-SEP-2000; 2000US-235840P.
27-SEP-2000; 2000US-23863P.
28-SEP-2000; 2000US-236028P.
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28-SEP-2000; 2000US-236033P.
28-SEP-2000; 2000US-236034P.
28-SEP-2000; 2000US-236109P.
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29-SEP-2000; 2000US-236842P.
29-SEP-2000; 2000US-236891P.
 2000US-209531P
                                                  20-SEP-2000; 2000US-234009P
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25-SEP-2000; 2000US-235280P.
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03-OCT-2000; 2000US-237608P.
01-NOV-2000; 2000US-244867P.
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02-OCT-2000; 2000US-237316P
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26-SEP-2000; 2
27-SEP-2000; 2
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                      238 GATÓCTGTTGACACCCCAAACCCAACAAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 297
                                                                                                                                                                                                            298 GGCCAATGTTTGATGCTTTAACCCCCCCAATTTCTGTGAGATGGCTAGTGGCAAGCGT 357
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                                                                                                                                              3 GluprovalLysGlyProvalSerThr-----LysProGlySerCysProllelleLeu 20
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                                                                                                                                                                                                                                                                       358 GACTTGAAGTGTTGCATGGCCATGTGTGGGAAATCCTGCGTTTCCCCT 405
                                                                                                                                                                                                                                              41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 other;
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                                                         Conservative:
Mismatches:
Indels:
                                   Length:
Matches:
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                            1.58e-07
143.00
55.36%
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43.73%
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2000US-236033P.
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2000US-236109P.
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2000US-234034P.
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2000US-234509P.
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2000US-235082P.
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                                                         Percent Similarity:
Best Local Similarity:
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20-SEP-2000;
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25-SEP-2000;
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28-SEP-2000;
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                        Alignment Scores:
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                                                                                   Query Match:
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No.:
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RESULT 46

21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40

3 GluProValLysGlyProValSerThr----LysProGlySerCysProIlelleLeu 20

09-833799-13B (1-57) x ABL67548 (1-594)

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594 27 23 23

Conservative: Mismatches: Indels:

Length: Matches:

1.58e-07

Alignment Scores:

143.00 55.36% 48.21% 43.73%

> Percent Similarity: Best Local Similarity:

Query Match:

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PR 29-88P2-2000; 200008-23641P.
PR 29-88P2-2000; 200008-23643P.
PR 29-88P2-2000; 200008-23643P.
PR 20-67T-2000; 200008-237278P.
PR 20-67T-2000; 200008-237278P.
PR 20-67T-2000; 200008-237278P.
PR 20-67T-2000; 200008-23728P.
PR 20-67T-2000; 200008-23769P.
PR 20-67T-2000; 200008-23769P.
PR 20-67T-2000; 200008-23760P.
PR 20-67T-20009; 200008-23760P.
PR 20-67T-20009; 200008-23760P.
PR 20-67T-20009; 200008-23760P.
PR 20-67T-20009; 20008-23760P.
PR 20-67T-20009; 20008
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Human cDNA encoding an Antileukoprotease.
 AAS17499 standard; cDNA; 594 BP.
        (first entry)
       26-MAR-2002
    AAS17499;
AAS17499
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Human; ss; antileukoprotease; antiinflammatory; antiasthmatic; anti allergic; inflammatory lung disorder; cancer; thyroid tumour; emphysema; asthma, bronchitis; allergy; ovarian carcinoma; renal calcinoma;

Homo sapiens.

/product= "Antileukoprotease" Location/Qualifiers ಹ

WO200190421-A2.

29-NOV-2001.

25-MAY-2001; 2001WO-US17211.

25-MAY-2000; 2000US-207104P.

(CURA-) CURAGEN CORP.

Smithson G; Rastelli L,

WPI; 2002-106211/14. P-PSDB; AAU11763. Diagnosing inflammatory lung disorders by comparing expression of nucleic acid encoding antiliquor polypeptide in mammal-derived cell population to nucleic acid encoding the polypeptide in reference profile

Claim 8; Page 19; 36pp; English.

The invention relates to diagnosing an inflammatory lung disorder in a mammal, comprising comparing the expression of a nucleic acid encoding or an antileukoprotease polypeptide in mammal-derived cell population, and expression of a nucleic acid encoding the antileukoprotease in (sclosed are a method for identifying a compound that inhibits lung inflammation comprising providing a compound that inhibits lung inflammation comprising providing a cell expression at inthe cell with a test compound and measuring the expression of contacting the cell with a test compound inhibits lung inflammation.

Contacting the cell with a test compound inhibits lung inflammation. The cell where sees in expression of the test compound inhibits lung inflammation.

Also disclosed is assessing prognosis of a mammal with a cancer or a thyroid tumour, comprising measuring the expression of a nucleic acid encoding the antileukoprotease in a mammal-derived cell population of an uncleic acid encoding the antileukoprotease in a cancer reference profile; where a substantial similarity between the expression of the nucleic acid acid sequence in mammal-derived cell population and the cancer or profile; where a substantial similarity between the expression of the nucleic acid sequence in mammal-derived cell population and the cancer or profile; where a substantial similarity between the expression of the nucleic acid sequence in mammal-derived cell population and the cancer or profile; acid sequence in mammal-derived cell population and the cancer or profile; acid sequence in mammal-derived cell population and the cancer or emphysema, asthma, bronchitis, or allergy in a mammal. The compound is cuseful for treating or preventing an inflammatory lung disease in a mammal, an inflammatory disease in a mammal, and is an inflammatory disease in a mammal. antileukoprotease antibody, or antileukoprotease antisense nucleic acid. The methods are useful for assessing the prognosis of a mammal with thyroid carcinoma, ovarian carcinoma or renal cell carcinoma. The present sequence is a cDNA encoding a human antileukoprotease.

Sequence 594 BP; 132 A; 156 C; 155 G; 151 T; 0 other;

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594
7 2 3
2 3
                       Conservative:
Mismatches:
                Matches:
                                          Indels:
        Length:
        1.58e-07
              143.00
55.36%
48.21%
43.73%
                                Best Local Similarity:
                      Percent Similarity:
Alignment Scores:
                                         Query Match:
       No.:
                Score:
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09-833799-13B (1-57) x AAS17499 (1-594)

238 GATCCTGTTGACACCCCAACCCAACAAGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 297 3 GluProValLysGlyProValSerThr----LysProGlySerCysProllelleLeu 20 ò

298 GGCCAAIGITTGAIGCITAACCCCCCAAITTCTGTGAGATGGATGGCCAGTGCAAGCGT 357 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40 ò g

358 GACTIGAAGIGIIGCAIGGGCAIGIGIGGAAAICCIGCGIIICCCCT 405 29 41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPhevalPro g ò

AAZ77546

AAZ77546 standard; cDNA; 599 BP.

AAZ77546; 

(first entry) 10-APR-2000

Human ovarian tumor cDNA library derived EST fragment 97.

Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment; ss.

Homo sapiens.

DE19817557-A1.

21-OCT-1999.

98DE-1017557, 09-APR-1998;

98DE-1017557. 09-APR-1998;

(META-) METAGEN GES GENOMFORSCHUNG MBH.

Rosenthal A, Specht T, Hinzmann B, Schmitt A,

., Ш

Dahl

Pilarsky C,

WPI; 1999-591920/51.

New nucleic acid sequences expressed in ovarian, and some other, cancertissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents cancer

Claim 3; Page 221; 310pp; German.

This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gone therapy. (A) are used (i) for cancer tissue). The products of the invention can be used for gone therapy. (A) are used (i) for gones. (B) are used (i) to identify agents suitable for treatment of cancer (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of sequence tags) from a particular tissue type before comparison of sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the caper to be revealed, so should reduce the number of failures associated with the fact that BSTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAZ77450-Z77572 represent the human

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arian tumor cDNA library derived EST fragments described in the method the invention and encode the protein fragments represented in
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lung, liver, uterus, ovary, stomach, intestine, kidney, pancreas, ss,
metabolic disease, developmental disease, cytostatic, immunomodulatory,
neuroprotective, gene therapy, cancer, immunopathology, neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the
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                                                                                                                        Sequence 599 BP; 142 A; 153 C; 154 G; 150 T; 0 other;
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                                                          AAY76505-Y76638.
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      ovarian
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malaria, emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatod arthritis; periodontal disease; tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
                                                                                                                                                                                                                                                                                                                                275 GATCCTGTTGACACCCCAACACCCAACAGGAGGAAGCCTGGGAAGTGCCCAGTGACTTAT 334
                                                                                                                                                                                                                                                                                                                                                                                        differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a
                                                                                                                                                                                                                                                                                                                                                            3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                     name= "Ribosome binding site"
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                                                                                                                             Sequence 636 BP; 160 A; 159 C; 163 G; 154 T; 0 other;
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27
23
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                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence encoding SLAP1 fusion protein.
                                                                                                   cancer, immunopathology or neuropathology.
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'note= "linking codon"
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Best Local Similarity:
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Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention such as an inhibitor of protease activity. The fusion protein of the invention such as semphysema, asthma, chronic obstructive pulmonary disease. Cystic fibrosis, ottis media, ottis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating demanatological diseases such as actoric demanaticities. eczema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rhematoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 GGTCAATGITTGATGITGAACCCACCAAACTTCTGTGAAATGGACGGTCAATGTAAGAGA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GluProValLysGlyProValSerThr----LysProGlySerCysProllelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pphy. The present sequence represents the DNA encoding the fusion protein of the invention.
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                                                                                                                                                                                    Pemberton P;
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                                      18-DEC-2001; 2001WO-US49256.
                                                                               18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
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                                                                                                                                         (ARRI-) ARRIVA PHARM INC.
                                                                                                                                                                                Barr PJ, Gibson HL,
                                                                                                                                                                                                                           WPI; 2002-500631/53
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27-JUN-2002.
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malaria, emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis; otitis media, otitis external, HIV; psoriasis, eczema, human immunodeficiency virus, atopic dermatitis; muscular dystrophy; herpes, ulceration; sepsis; rheumatorid arthritis; periodontal disease; tumour metastasis, osteoporosis; Paget's disease; scleroderma; rSLAP1; gene; ds; Alzheimer's disease; tumour angiogenesis; 'standard\_name= "Ribosome binding site" /product= "rSLAP1 fusion protein" 12..1193 DNA sequence encoding rSLAP1 fusion protein. /\*tag≔ c /note= "AAT coding region" '\*tag= d 'note= "linking codon" Location/Qualifiers glomerulonephritis; hypertension. .1196 Д ø .1520 \*tag= /\*tag= Homo sapiens. misc\_feature misc\_feature Synthetic. Key CDS 

/\*tag= e /note= "SLPI coding region" 1197..1517 WO200250287-A2 27-JUN-2002.

misc\_feature

18-DEC-2001; 2001WO-US49256. 18-DEC-2000; 2000US-256699P. 20-NOV-2001; 2001US-331966P.

(ARRI-) ARRIVA PHARM INC. Barr PJ, Gibson HL,

Pemberton P;

WPI; 2002-500631/53. P-PSDB; AAU99884. Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor

Example 3; Page 89-90; 134pp; English.

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This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention inhibitor of protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermacological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating wounds, sepsis, rheumatorial article periodomical disease, normal measured and activity. tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the rSLAP1 fusion protein of the invention. Sequence 2274 BP; 459 A; 567 C; 602 G; 646 T; 0 other;

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1401 GGTCAATGTTTGATGTTGAACCCACCAAACTTCTGTGAAATGGACGGTCAATGTAAGAGA 1460
                                                                                                                                                                                                                                                                                                                21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                     3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIleIleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New synthetic DNA sequences for directing microbial synthesis for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic sequence capable of directing microbial synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                   1461 GACTTGAAGTGTTGTATGGGTATGTGTGTAAGTCCTGTGTTTCCCCA 1508
                                                                                                                                                                                                                                                                                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stetler GL, Thompson RC;
467 A; 287 C; 314 G; 457 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                       1525
27
4
23
23
                                                                                              Conservative:
Mismatches:
Indels:
                                                         Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                              x ABK88025 (1-1525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN60465 standard; DNA; 2274 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bandyopadh PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85WO-US02385.
84US-0678822.
85US-0803471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1986-169458/26.
P-PSDB; AAP60565, AAP60566.
                                                       02e-07
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1458..1607
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                                                                         143.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trypsin-; inhibitor; ss.
Sequence 1525 BP;
                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                              09-833799-13B (1-57)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-1985;
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                                      Alignment Scores:
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                                                                                                                                  Query Match:
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The sequence directs synthesis of a preferred secretory leukocyte protease-inhibitor. See also AAN60464, AAN60466-69 and AAP60562-

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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 - AAC97581 and AAC97614 - AAC97611 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide
                                                                                                                                                                               1454 ccagcaaggaggaagccroocaagroccaggrocratargccaargrrrgargcrraac 1513
                                                                                                                                                                                                                                           1514 ccccccaárrrcrergagargaargargaccagrecargcergacrreaagrerrecarged 1573
                                                                                                                                                                                                              47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                  8 ProValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsn
                                                                                                                                                                                                              28 ProProAsnArgCysLeuLysAspThrAspCysProGly1leLysLysCysCluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protease-mediated condition or tissue destruction e.g. emphysema tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New serine protease inhibitors and DNA sequences for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
            2274
24
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0
                           Matches:
Conservative:
Mismatches:
              Length:
                                                                         Indels:
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                                                                                         Gaps:
                                                                                                                                                                                                                                                                                              1574 ATGTGGGAAATCCTGCGTTTCCCCT 1600
                                                                                                                     09-833799-13B (1-57) x AAN60465 (1-2274)
                                                                                                                                                                                                                                                                            48 SerCysGlyMetAlaCysPheValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genomic DNA encoding SLPI.
                                                                                                                                                                                                                                                                                                                                                                      AAC97530 standard; DNA; 2274 BP
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84US-0678822.
85US-0803471.
86US-0890526.
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              39e-06
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                           141.00
55.10%
48.98%
43.12%
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                                                            Best Local Similarity:
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                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elastase; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1987;
Alignment Scores:
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29-JUL-1986;
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                               Score:
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Perimers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB53102 by Perimers and pacesses inhibitors. Peptide sequences various other peptides used in the isolation of the invention and Yne protease inhibitor of the invention and various other peptides used in the isolation of the protease inhibitors. The protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating a protease inhibitor protein is useful for treating a destruction, e.g. emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful consoluting and model and protease activity. The DNAs are useful for producing the
                                                                                                                                                                                                                                                                                                                                                                                                              |||
|1454 | CAAGCAAGGAAGCCTGGGAAGTGCCCAGTGACTTATGGCCAATGTTTGATGCTTAAC 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1514 ¢¢¢¢¢¢àrtrcrishaaangahrasarsiskanskarstraharrasarrasis 1573
                                                                                                                                                                                                                                                                                                                                                                                           8 ProValSerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsn 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 ProProAsnArgCysLeuLysAspThrAspCysProGlylleLysLysCysCysGluGly 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant secretory leukocyte protease inhibitor (SLPI) DNA
                                                                                                                                                                                                     Sequence 2274 BP; 459 A; 567 C; 602 G; 646 T; 0 other;
                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                           proteins, especially by recombinant methods.
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Matches:
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884..1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 SerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                             09-833799-13B (1-57) x AAC97530 (1-2274)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI67491 standard; DNA; 2274 BP.
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55.10%
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1460..1607
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                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                Best Local
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    8888888888888888
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The invention relates to a DNA sequence encoding an analog of a mammalian exerine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents the DNA that encodes a secretory leukocyte protease inhibitor (SLPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1514 CCCCCCAAITTCTGTGAGATGGCCAGTGCAAGCGTGACTTGAAGTGTTGCATGGGC 1573
                                                                                                                                                               New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGly 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ProValSerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine leucocyte protease inhibitor; SLPI; truncated SLPI; CLPI; retrovirus; retroviral infection; HIV; parotid inhibitor; enzyme; elastase; cathepsin G; trypsin; ss.
                                                                                           Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2274 BP; 459 A; 567 C; 602 G; 646 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2274
24 3
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/transl_except= pos:79..81, aa:Leu
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Matches:
Conservative:
Mismatches:
                                                                                         Stetler GL,
                                                                                                                                                                                                                       Disclosure; Columns 13-18; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                         Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerCysGlyMetAlaCysPheValPro
                 85US-0803471.
86US-0890526.
   84US-0678222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.39e-06
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55.10%
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43.12%
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                                                                                                                     2001-637974/73.
                                                                                                                                                                                              elastase or trypsin
                                                         (AMGE-) AMGEN INC.
                                                                                        Bandyopadhyay PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                   P-PSDB; AAG65996
05-DEC-1984;
                              29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ45442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GluprovalLysGlyProValSerThr-----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                            21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                           Retroviral infection is inhibited by admin. of an SLPI, or its analogue or deriv. A useful SLPI deriv. is CLPI, a truncated SLPI mol. having only the last 60 amino acids of the native parotid inhibitor. SLPI acts by blocking a host cell enzyme essential for retroviral infection; it is a powerful inhibitor of human leucocyte elastase, cathepain G and human trypsin. The inhibitor provides an effective and relatively safe method for treating HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secretory leukocyte protease inhibitor; retroviral; infection, HIV; AIDS; SLPI; CLPI; parotid inhibitor; antiviral; anti-HIV; ss.
                                                                                                                                                 Inhibiting retroviral infection with serine leucocyte protease inhibitor - esp. for treating or preventing HIV infection, also new protease inhibitors and nucleic acids encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Truncated SLPI encoding nucleotide sequence CLPI SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                           Sequence 180 BP; 42 A; 45 C; 50 G; 43 T; 0 other;
                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                    (SYND ) SYNERGEN INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                 Wahl SM
                                                                                                                                                                                                                                                                                                                                                                                             09-833799-13B (1-57) x AAQ45442 (1-180)
                                                                                                                                                                                          Claim 29; Page 17; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ88483 standard; DNA; 180 BP
                                                                                                                                                                                                                                                                                                                        1.06e-07
139.00
53.57%
46.43%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0483503
                                                 92US-0943369
                               93WO-US08486
                                                                                                 Eisenberg S, Thompson RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-2000 (first entry)
                                                                                                                      WPI; 1994-118153/14.
                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                              P-PSDB; AAR51172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                               09-SEP-1993;
                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6017880-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2000
           31-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ88483;
                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 55
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The present invention describes a method for inhibiting, in vitro, retrovirus infection of CD4+ cells comprising contacting the cells with a secretory leukocyte protease inhibitor (SLPI) having the amino acid sequence of a naturally occurring SLPI or a substitution analogue having 107 amino acid residues. SLPI inhibitos enzymes whose function are necessary for retroviral infection of the cell. SLPI is a potent inhibitor of elastase, trypsin, cathepsin G and chymotrypsin. The method is useful for treating retrovirus infection in a patient and associated diseases such as acquired immunodeficiancy syndrome (AIDS). The present sequence encodes a truncated version of SLPI designated CLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; peptidase; cell proliferative disorder; arteriosclerosis; psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease; inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis; Grave's disease; multiple sclerosis; scleroderma; infection; diabetes; metabolic disorder; Addison's disease; cystic fibrosis; diagnosis; glycogen storage disease; obesity; therapy; HPEP-9; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 GluprovalLysGlyProvalSerThr ----- LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                              Inhibiting retrovirus infection using secretory leukocyte protease inhibitors for treating diseases such as acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValDro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 180 BP; 42 A; 45 C; 50 G; 43 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                            Thompson RC, Wahl SM, Eisenberg S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human peptidase, HPEP-9 coding sequence.
                                                                                                                                                  DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Column 3-5; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-833799-13B (1-57) x AAZ88483 (1-180)
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92US-0943369.
93WO-US08486.
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                                                            94US-0209040
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53.57%
46.43%
42.51%
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                                                                                                                                                                                                                                                                           2000-170378/15.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                           P-PSDB; AAY79951
                                                                                                                     (AMGE-) AMGEN
(USSH ) US DEI
09-SEP-1992;
09-SEP-1993;
09-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                    syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
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Homo sapiens

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This sequence encodes the human peptidase, designated HPEP-9. The respectively. The peptidases can be used for treating a disease or foundition associated with decreased expression or over expression of prevented and treated include cell proliferative disorders (such as arteriosalerosis, psoriass, myelofibrosis, and cancers), crohn's disease, asthma, atherosclerosis, allergies, crohn's disease, asthma, atherosclerosis, Grave's disease, multiple Addison's disease, diabetes, cystic fibrosis, and metabolic disorders (such as Addison's disease, diabetes, cystic fibrosis, glycogen storage diseases
                                                                                                                                                                                                                                                                                                    An isolated polypeptide for diagnosis, prevention and treatment of cell proliferative, autoimmune/ inflammatory and metabolic disorders comprises a sequence encoding a human peptidase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 GTCTCTGTGAAGCTGGGCAGCTGCCCAGAGACCAACTGCGCTGC-----CTCAGCCCC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 ATGAACCACTGTGTTACAAGGACTCAGACTGCTCGGGCAAAAAGGGTGCTGCCACGC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 valSerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnPro 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 ProAsnArg----ÇysLeuLysAspThrAspCysProGlylleLysLysCysCysGluGly 47
                                                                                                                                                                                                                                          Lal P;
                                                                                                                                                                                                                                  Azimzai Y, Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1010 BP; 223 A; 308 C; 243 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
        Location/Qualifiers
                                                                                                                                                                                                                                Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 GCCTGCGGGGGGATTGCCGGGATCCT 449
                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 118; 131pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-833799-13B (1-57) x AAA37665 (1-1010)
                                 /*tag= a
/product= HPEP-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 SerCysGlyMetAlaCysPheValpro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD38698 standard; cDNA; 1013 BP.
                                                                                                                                                99US-0172247.
99US-0132253.
99US-0136653.
                                                                                                                    11-JAN-2000; 2000WO-US00641.
                                                                                                                                                                                               (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.4e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123.50
61.22%
51.02%
37.77%
                    90..461
                                                                                                                                                                                                                              Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                  WPI; 2000-482832/42.
P-PSDB; AAY90292.
                                                                                                                                                                                                             Bandman O, Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity:
                                                                 WO200042201-A2
                                                                                                                                              11-JAN-1999;
                                                                                                                                                              03-MAY-1999;
                                                                                                                                                                         27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                            20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
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diabetic retinopathy; severe combined immunodeficiency; pancreatitis; rheumatoid arthritis; colorectal adenoma; haemolytic anaemia; cancer; reperfusion injury; arteriosclerosis; wound healing; transgenic animal; gene therapy; neoplasm; transgenic; psoriasis; ischaemia; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                       Novel proteins and polynucleotides of secreted proteins useful for treating various diseases e.g. rheumatoid arthritis, cancer, psoriasis, diabetic retinopathy, arteriosclerosis, ischemia or reperfusion injury.
                              secreted protein; atherosclerosis; Alzheimer's disease; LP229;
                                                                                                                                                                                                   /product= "Mature human LP229 secreted protein"
                                                                                                                                           /*tag= a
/product= "Human LP229 secreted protein"
         Human LP229 secreted protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 138-139; 145pp; English.
                                                                                                                        Location/Qualifiers
                                                                            chromosome 20q12-13.2; gene; ss.
                                                                                                                                                                                                                                                                                 28-SEP-2000; 2000US-236088P.
                                                                                                                                                                                                                                                            14-SEP-2001; 2001WO-US26026.
                                                                                                                                                                        /*tag= b
144..458
                                                                                                                                                             90..143
                                                                                                                                   90..461
                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                  (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                          WPI; 2002-471259/50.
                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAE23983
                                                                                                                                                                                                                                                                                                                        Wang H;
                                                                                                                                                                                                                     WO200226801-A2
                                                                                                 Homo sapiens
                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                          04-APR-2002
                                                                                                                                                                                mat peptide
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The invention relates to human secreted polypeptides designated LP095, 2C LP191, LP217, LP220, LP229, LP237 or LP238 and nucleic acid molecules encoding such polypeptides. Novel secreted proteins of Alzheimer's disease, diabetic retinopathy, psoriasis, pancreatitis, arteriosclerosis, rheumatoid arthritis, colorectal adenomas, severe reperfusion injury, neoplasms and cancer especially liver cancer. They be used to generate transgenic animals or knock out animals, which in the development and screening of the invention can current sequence for useful reagents for use in the treatment of diseases associated with The polypeptide associated activity. They are also used in gene therapy. CC The present sequence is human LP229 secreted protein encoding cDNA.

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Sequence 1013 BP; 226 A; 308 C; 243 G; 236 T; 0 other;
                                      1013
25
5
16
3,
                                              Matches:
Conservative:
Mismatches:
                                     Length:
                                                                             Indels:
                                5.42e-05
123.50
61.22%
51.02%
37.77%
                                                              Similarity:
                                                  Percent Similarity:
Best Local Similarit
                    Alignment Scores:
                                                                      Query Match:
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09-833799-13B (1-57) x AAD38698 (1-1013)

9 ValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPro 28 ò

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This invention relates to new purified and isolated mammalian serine procease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534 AAC97534 and AAC97614 - AAC97641 represent DNA encoding the sequences inhibitors of the invention, and include oligonuclectide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC9582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB53028 - AAC97613 are used in the various other peptides used in the isolation of the protease inhibitors. The protease inhibitors and various other peptides used in the isolation of the protease inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 destruction, e.g. emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods.
309 GTCTCTGTGAAGCTGGCCAGCTGCCCAACTGCGCTGC-----CTCAGCCCC 362
                                                                                            363 Argaaccaccrerérracaaddacreadacrecresceanaaadceardcrecree 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The serine protease inhibitor protein is useful for treating a protease-mediated condition, which includes protease mediated tissue
                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                           47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or
                                                           29 ProAsnArg --- CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema tumor invasion and for recombinant production of inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 321 BP; 60 A; 54 C; 60 G; 44 T; 103 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                DNA encoding a protease inhibitory peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 12-13; 47pp; English
                                                                                                                                                                       423 GCCTGCGGGGGTTGCCGGGATCCT 449
                                                                                                                                 SerCysGlyMetAlaCysPheValPro 56
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84US-0678822.
85US-0803471.
86US-0890526.
87US-0031846.
87US-0082962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0712354.
                                                                                                                                                                                                                                                 AAC97529 standard; DNA; 321
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                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              elastase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1991;
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02-DEC-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                       AAC97529;
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                                                                                                                                                                                                            RESULT 58
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chromosome 20412-13; cytostatic; gene therapy; tumour cell; inducer; diagnosis; therapeutic; proliferative disease; cell cycle arrest; cancer; treatment; apoptosis; knockout animal; cancer susceptibility; ALP; antileukoproteinase; secretory leukocyte proteinase inhibitor; SLPI; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                   PRG5; p53 target; human; modulate; cell proliferation; immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
product= "Mature human PRG5 protein"
/note= "High cysteine content (16 out of 107 residues)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New p53-inducible isolated nucleic acid molecule including open reading
                                                                                                                                            :::|||||||
145 GAYCCNGTNGAYACNCCNAAYCCNACNCGNCGNAARCCNGGNAARTGNCCNGTNACNTAY 204
                                                                                                                                                                                                      205 GGNCARIGYCINAIGCINAAYCCNCCNAAYTTYTGNGARAIGGAYGGNCARIGYAARCGN 264
                                                                                                                           3 GluProValLysGlyProValSerThr-----LysProGlySerCysProIlelleLeu 20
                                                                                                                                                                              21 IleargCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product= "Human PRG5 protein"
function= "Proteinase inhibitor activity"
                                                                                                                                                                                                                                                265 GAYCTNAARTGYTGYATGGGNAINTGYGGNAARTCNTGYGTNTCNCCN 312
                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                 41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
         321
25
4
25
2
1
                                   Conservative:
Mismatches:
Indels:
            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                          Human p53 target molecule, PRG5 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                 x AAC97529 (1-321)
                                                                                                                                                                                                                                                                                                                AAZ51673 standard; cDNA; 1411 BP
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                       122.00
51.79%
44.64%
37.31%
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113..433
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                                     Percent Similarity:
Best Local Similarity:
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                                                                                                    09-833799-13B (1-57)
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                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2000
Alignment Scores:
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5'UTR
            No.:
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are upregulated in response to induction of p53 activity in human colon cancer EB1 cells. It has a high content of cysteine residues and shares a cysteine motif with antileukoproteinase (ALP) or secretory leukocyte proteinase inhibitor (SLPI). RedS has proteinase inhibitor activity and is involved in p53-mediated growth suppression pathways. They are potential targets of p53 regulatory activity and are useful for modulation of cellular proliferation. PRG5 gene is localised to human chromosome 20q12-13. The PRG target molecules have cytostatic and immonomidatory activity. PRG polynucleotides, proteins and antibodies are useful as diagnostic and therapeutic agents for detection and treatment of cancer and therapeutic agents for detection and treatment of cancer and therapeutic agents for detection and treatment of cancer and therapeutic agents for detection and treatment of cancer and therapeutic agents for detection and treatment of cancer and therapeutic and function downstream of p53, that cannot be activated in the p53-deficient tumour cell. Antibodies can be used as inducers of cell cycle arrest and/or apoptosis. The DNA sequences can be used to generate 'knockout' animals as a model of
                                                                                                                                                              The present sequence is the complete cDNA of PRG5 gene, whose RNA levels
frame encoding human homolog of Drosophila melanogaster peroxidasin, useful e.g. in detection and treatment of cancer -
                                                                                                   Disclosure; Fig 8; 83pp; English
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Sequence 1411 BP; 338 A; 397 C; 321 G; 355 T; 0 other;

cancer susceptibility.

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284 GTCTCTGTGAAGCTGGCAGCTGCCCAGAGGACCAACTGCGCTGC-----CTCAGCCCC 337
                                                                                                                                                                                                                         338 ATGAACCACCTGTGTCACAAGAACTGCTCAGAGGAAAAAAGGATGCTGCCACAGC 397
                                                                                                                                             9 ValSerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnPro 28
                                                                                                                                                                                                      29 ProAsnArg---CysLeuLysAspThrAspCysProGlyIleLysLysCysGluGly 47
                  1411
255
5
16
3
                                             Conservative:
Mismatches:
Indels:
                               Matches:
                 Length:
                                                                                                                                                                                                                                                                                             398 GCCrGcGGGGGATTGCCGGGATCCT 424
                                                                                                                 09-833799-13B (1-57) x AAZ51673 (1-1411)
                                                                                                                                                                                                                                                                 SerCysGlyMetAlaCysPheValPro 56
                 0.000139
                             121.50
61.22%
51.02%
                                                                        37.16%
                                                         Best Local Similarity:
                                           Percent Similarity:
Alignment Scores:
                                                                        Query Match:
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RESULT 60

AAH78211 standard; DNA; 558 BP

AAH78211;

(first entry) 26-NOV-2001

Nucleotide sequence of a human secreted polypeptide.

Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; overy disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; lymph node disease; macular system disease, colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.

Homo sapiens.

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Location/Qualifiers
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/product= "secreted polypeptide"
                                                             CORP.
                                         13-MAR-2000; 2000US-0188916.
03-OCT-2000; 2000US-0236874.
                                                   03-OCT-2000; 2000US-0237846.
                            05-MAR-2001; 2001WO-US07143.
                                     06-MAR-2000; 2000US-0187107
                                                            (SMIK ) SMITHKLINE BEECHAM (SMIK ) SMITHKLINE BEECHAM
         WO200166690-A2.
                  13-SEP-2001.
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Smith RF, Xiang Z; Rizvi SK, Agarwal P, Murdoch PR,

WPI; 2001-570768/64. P-PSDB; AAG67519. Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immune disorders, microbial diseases, inflammation and transplant rejection -

Claim 2; Page 47; 102pp; English.

The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and netastasis, for treating gastrointeetinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, small intestine, heart, trachea, thymus, lymph node, remainstant system and colon, for treating lipase deficiency in cystic fibrosis and pancreatitis, for treating undesirable clot formation such as myocardial infarction, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating increasing on disorders and microbial diseases, for treating inflammation and transplant treating indisorders and microbial diseases, for treating the loss of essential ferroxidases, for suppressing appotosis, and for regulating vascular smooth cell proliferation. They may also be used as vaccines.

Sequence 558 BP; 119 A; 148 C; 169 G; 122 T; 0 other;

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558
6 4
116
2
                Matches:
Conservative:
Mismatches:
                                         Indels:
         9.86e-05
                118.50
61.22%
48.98%
36.24%
                        Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                         Query Match:
                 Score:
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09-833799-13B (1-57) x AAH78211 (1-558)

ò	σ	ValSerThrIvsDroGlvSerCvsDroTleIleIleI.iI]
,	1	The state of the
qq	247	247 GTTGCAGTGAAGCTGGGCAGCTGCCCAGAGGACCAACTGCGCTGCCTCAGCCCC 300
٥y	29	29 ProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGly 47
qq	301	301 ATGAACCACCTGTGTCACAAGGACTCAGACTCCTCGGGCAAAAAGCGATGCTGCCACAGC 360
ò	48	48 SerCysGlyMetAlaCysPheValPro 56
qq	361	361 GCCTGCGGGGATTGCCGGGATCCT 387

RESULT 61 AAH78210 ID AAH7 XX AC AAH7

AAH78210 standard; DNA; 732 BP.

AAH78210;

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secreted polypeptides and polymorleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, small intestine, heart, trachea, thymus, lymph node, remal gland, system and colon, for treating lipase deficiency in cystic fibrosis and panoreatisis, for treating undesirable clot formation such as myocardial infarction, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating inver diseases, coagulation disorders and microbial diseases, for treating immune disorders, for treating inflammation and transplant rejection, for enhancing bone thickness and increasing bone density, for reducing the loss of essential ferroxidases, for suppressing appoptosis, and for requiring vascular smooth cell proliferation. They
                                                                                                                                                                          Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; wall intestine disease; thymus disease; lymph node disease; muscular system disease; colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; myocardial infarction; angioplasty; liver disease, coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.
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                                                                                       Nucleotide sequence of a human secreted polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "secreted polypeptide"
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13-MAR-2000; 2000US-0188916.
03-OCT-2000; 2000US-0236874.
03-OCT-2000; 2000US-0237846.
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26-NOV-2001 (first entry)
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Human; reproductive system related antigen; reproductive system disorder;
                                                                                584 ATGAACCACCTGTGTCACAAGGACTCAGACTGCTCGGGCAAAAAGCGATGCTGCCACAGC 643
                                                            29 ProAsnArg---CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGly 47
                    9 ValSerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnPro 28
                                Human reproductive system related antigen DNA SEQ ID NO: 9939.
                                                                                                                          644 GCCTGCGGGCGGGATTGCCGGGATCCT 670
                                                                                                     SerCysGlyMetAlaCysPheValPro 56
09-833799-13B (1-57) x AAH78210 (1-732)
                                                                                                                                                                 AAL07251 standard; DNA; 5690
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2000US-0224519.
2000US-0225213.
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2000US-0189874
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2000US-0209467
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2000US-0225267
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                                                                                                                                                                                                                                                              cancer; gene therapy; ds
                                                                                                                                                                                                                                                                                                     WO200155320-A2
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30-JUN-2000;
07-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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11-JUL-2000;
11-JUL-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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16-MAR-2000;
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18-APR-2000;
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07-JUN-2000;
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22-AUG-2000;
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30-AUG-2000; 2000US-0228924

732 24 6 16 3

Conservative: Mismatches: Indels: Matches: Length:

0.000138

Alignment Scores:

118.50 61.22% 48.98% 36.24%

Percent Similarity: Best Local Similarity:

Score:

Query Match:

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2000US-0234998.
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2000US-0246610.
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2000US-0230437.
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2000US-0249211
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17-NOV-2000;
17-NOV-2000;
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29-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
20-CT-2000;
20-CT-2000;
13-CT-2000;
13-CT-2000;
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08-NOV-2000;
08-NOV-2000;
            01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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14-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition
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Matches:
Conservative:
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                                                                                                     20000S-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249297.
2000US-0249299.
                                                  2000US-0249216.
2000US-0249217.
2000US-0249218.
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2000US-0251868.
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            2000US-0249213.
2000US-0249214.
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2000US-0251030.
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2000US-0251479.
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Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
                            Human testicular antigen encoding DNA fragment SEQ ID NO: 3451
                                                                                                                                         04-FEB-2000; 200005-0186628.
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16-MAR-2000; 200005-0198750.
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30-JUN-2000; 200005-0214886.
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11-JUL-2000; 200005-0214887.
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2000US-0229343
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              21-JUN-2002 (first entry)
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ABL98799;
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PR 14-SEP-2000; 2000US-0232499.
PR 14-SEP-2000; 2000US-0233401.
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PR 20-CCT-2000; 2000US-0249211

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                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||::: ||| |||||||||||||| GTTGCAGAGGACCAAGAGGCTAGCCTAGCCCC 4659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    28
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                                                                                                                                                                         Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ValSerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
trypsin-inhibitor; ompA-tc-met-SLPI; ds.
                                                                                                                                                                                                                                                                                                                    Sequence 5690 BP; 1336 A; 1453 C; 1505 G; 1396 T; 0 other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                               Rosen CA, Barash SC, Ruben SM;
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      06-DEC-2000; 2000US-0251479.

08-DEC-2000; 2000US-0251856.

08-DEC-2000; 2000US-0251869.

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08-DEC-2000; 2000US-0251989.

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05-DEC-2000;
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DB:
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485 GATCCGGTTGATACCCCCGAAACCCGACTCGTCGAAAACCGGGTAAATGCCCGGTAACGGAC 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   545 CTAGGCCCAACTATGGGGCTTGGGCTGAGCAGCTTTTGGCCCCATTTACGGGCCATTGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GlyIleLys------
                                                                                                                                                                                                                                                                                      New synthetic DNA sequences for directing microbial synthesis -
for prodn. of single poly:peptide chain serine protease inhibitor
having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
trypsin-inhibitor; ompA-SLPI; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence directs synthesis of a secretory leukocyte protease-
inhibitor. See also AAN60463-68, and AAP60562-66.
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                                                                                                                                                                                            Thompson RC;
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Mismatches:
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                                               85WO-US02385.
84US-0678822.
85US-0803471.
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85WO-US02385.
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Best Local Similarity:
    04-DEC-1985;
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Pred. No.:
                                                 04-DEC-1985;
                                                                        06-DEC-1984;
                                                                                              02-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO8603519-A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN60468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
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serine protease; Mus musculus secretory leucocyte protease inhibitor; extracellular matrix degradation; multiple sclerosis; cancer; arthritis; inflammation; immune system disorder; neurodegenerative disorder; serpin; Kallmann's syndrome; Down's syndrome; Alzheimer's; fusion protein; galactorrhea; hypogonadism; somatostatin; protein purification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA clone HKABR62; secreted protein; serine protease inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 GCAGCAAAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCGGCCG 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 656 AACTITITIGGCCCATITACGGCCATIGGATACCGGTCACAGACTACGACTIGGGCGGC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716 TTGAACTGCGAAATGGACGCCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGC 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 SerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProPro
                                                                                                                                                                                                                                                                                                                                                          New synthetic DNA sequences for directing microbial synthesis for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ---ArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence directs synthesis of a secretory leukocyte protease-
inhibitor. See also AAN60463-67, AAN60469, and AAP60562-66.
                                                                                                                                                                                                                                                Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "Serine protease inhibitor"
19..75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               920
22
20
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 221 A; 239 C; 238 G; 221 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                Stetler GL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 46; 59pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-833799-13B (1-57) x AAN60468 (1-920)
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                                                                                                                                                                                                                                          Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 GlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX80909 standard; cDNA; 478
                                                                                          84US-0678822.
85US-0803471.
   85WO-US02385.
                                                           85WO-US02385
                                                                                                                                                                           (SYNE-) SYNERGEN BIOLOG INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.000354
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40.30%
32.84%
35.47%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19..249
                                                                                                                                                                                                                                                                                                     WPI; 1986-169458/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                          Bandyopadh PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                       06-DEC-1984;
02-DEC-1985;
   04-DEC-1985;
                                                           34-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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inflammation or neurodegenerative disorders e.g. Kallmann's and Down's syndromes, Alzheimer's and Huntington's diseases. It may also be used to reduce excess levels of prolactin in the treatment of galactorrhea and hypogonadism, and decrease the amount of free circulating somatostatin to prevent somatostatin's inhibitory effect on the release of growth hormone. The fusion of this protein to His-tag, HA-tag, IgG domains, etc. facilitates protein purification and fusion to IgG-1, IgG-3 and albumin increases the half life time in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a human cDNA clone HKABR62 which encodes serine protease inhibitor (serpin) and is obtained from human keratinocyte tissue cDNA library. The protein obtained from this clone shows a high degree of sequence similarity to Mus musculus secretory leucocyte protease inhibitor. The cDNA and the serpin are used in the diagnosis and treatment of disorders related to abnormal level of the protein or mutation in the nucleotide sequence. The serpin can be used for treating disorders characterised by degradation of extracellular matrix, e.g. cancer, arthritis, multiple sclerosis and immune system disorders, for treating wasting associated with excessive protease production during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                         New isolated human serine protease and serpin polypeptides, used to develop products for treating e.g. immune disorders, cancers, inflammation, transplant rejection or infections, or as food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 GCTGTGGAAGGAGTTAAAGAGGGTATAGAG---AAAGCAGGGGTTTGCCCCAGCTGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                 /*tag= c
/label= Mature_serine_protease_inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 478 BP; 115 A; 121 C; 135 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 GAAAGGAAGTGTTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               478
6478
24
22
23
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 88; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA99904 standard; cDNA; 762 BP
                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                       98US-0073961.
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53.57%
42.86%
34.25%
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76..246
                                                                                                                                                                                                                                                                                                                  WPI; 1999-508502/42.
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                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY28645.
                                                                                                                                                                                                                                                                               Ni J, Ruben SM;
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                                                                                                                                                                  04-FEB-1999;
                                                                                                                                                                                                       06-FEB-1998;
                                                                                         WO9940183-A1
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                 mat peptide
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g
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Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J, Baker KP, Ferrara N, Gerber H, Gerritsen ME;
Gurney AL, Hillan KJ, Marsters SA, Paoni NF, Pitti RM;
, Williams PM, Wood WI;
                                                                                               Cardiovascular; endothelial; angiogenic disorder; PRO179;
PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333;
PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 762 BP; 197 A; 194 C; 194 G; 177 T; 0 other;
                                                                                                                                                                                                     Location/Qualifiers
                                                                     cDNA encoding human protein PRO844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 60; Fig 7; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         99US-0144758.
99US-0145698.
99WO-US20111.
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99WO-US28409.
99WO-US28565.
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                                                                                                                                                                                                                                                                                                                      24-FEB-2000; 2000WO-US05004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-2000; 2000WO-US04342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2000; 2000WO-US04414
                                         26-JAN-2001 (first entry)
                                                                                                                                                                                                                                 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-611444/58.
                                                                                                                                             gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAB27652
                                                                                                                                                                                                                                                              WO200053757-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard A, G
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1999;
01-SEP-1999;
15-SEP-1999;
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                               12-MAR-1999;
02-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-NOV-1999
                                                                                                                                                                                                                                                                                         14-SEP-2000
             AAA99904;
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Conservative: Mismatches: Indels: Gaps:

09-833799-13B (1-57) x AAA99904 (1-762)

Length: Matches:

0.000813 112.00 53.57% 42.86% 34.25%

Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

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Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping; ss.
             119 gracecrecratecanterecenterice -- cagrereacada en de constructedes 175
                                  21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
                                                                               41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                             Membrane-bound protein PRO844 encoding cDNA.
                                                                                                                         AAZ65078 standard; cDNA; 762 BP.
                                                                                                                                                                                                                                                                                                                                                                         98US-0088033.
98US-0088136.
98US-0088167.
98US-0088212.
98US-0088212.
98US-008855.
98US-008865.
98US-0088739.
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98US-0088740.
98US-0088741.
98US-0088142.
98US-0088810.
98US-0088811.
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98US-0089090.
98US-0089105.
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98US-0088028.
98US-0088029.
98US-0088030.
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98US-0088826.
98US-0088858.
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98US-0088863.
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors. TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be remployed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                       Gurney AL, Smith V, Watanabe CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Membrane-bound proteins and related nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 239; 822pp; English.
                                                                                                                                                                                                                                                                                                                                                      Goddard A,
          98US-0096895.
98US-0096897.
98US-0096949.
98US-0096950.
98US-0096959.
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98US - 0097141
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Yuan J;
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62 GCTGTGGAAGGAGTTAAAGAGGGTATAGAG---AAAGCAGGGGTTTGCCCAGCTGACAAC 118 40 1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly Sequence 762 BP; 197 A; 194 C; 194 G; 177 T; 0 other; Length:
Matches:
Conservative:
Mismatches: 09-833799-13B (1-57) x AAZ65078 (1-762) 0.000813 112.00 53.57% 42.86% 34.25% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: .. 0 0 ò g ò

by recombinant techniques.

41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56

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proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski PJ;
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Wood WI;
                                                                                                                                                                                   death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes human secreted and transmembrane PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eaton DL;
                                                                                                                                                                      Human; secreted and transmembrane protein; PRO; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ong S, Gerber H, Gerritsen ME, Goddard A, Gurney AL, Kljavin IJ, Napier MA, Pan J, art TA, Tumas D, Watanabe CK, Williams PM,
Human PRO844 (UNQ544) nucleotide sequence SEQ ID NO:344.
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                                                                 AAF44224 standard; cDNA; 762 BP
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24-FEB-2000; 2000WO-US04914.
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                                                                                                                    02-APR-2001 (first entry)
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                                                                                                                                                                                                  diagnostic assay; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-032160/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB65255.
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Grimaldi CJ,
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11-FEB-2000;
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                                                                                           AAF44224;
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Zhang Z;
                                         RESULT 69
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The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH.
and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO uncleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                  62 GCTGTGGAAGGAGTTAAAGAGGTATAGAG---AAAGCAGGCTTTGCCCAGCTGACAAC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 gracecrecricaagiccearcerece---caerereacacacacacacireredes 175
                                                                                                                                                                                                                                                                                                                                                                                               1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 lleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro
                                                                                                                                                                         Sequence 762 BP; 197 A; 194 C; 194 G; 177 T; 0 other;
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                              09-833799-13B (1-57) x AAF44224 (1-762)
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42.86%
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Alignment Scores:
Pred. No.:
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The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue. (I) comprises the comparise of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles. (I) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH. The methods are useful to present information identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stomach, lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 CCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAAGCGTGACTTGAAGTGTTGCATGGG 222
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Matches:
Conservative:
Mismatches:
Indels:
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 5% identical to (S), where a change in cativity and can be used for anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening a nati-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the structure and/or properties of the agent. M1 can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, ossophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                                                         2000US-234924P.
2000US-235077P.
2000US-235082P.
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2000US-235637P.
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Sequence 411 BP; 98 A; 97 C; 94 G; 94 T; 28 other;

Length: Matches:

0.00144 107.00

Score:

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Human, cancer; colon, breast; ovary, oesophagus, kidney, thyroid,
stomach, lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                              8 ProValSerThrLysProGlySerCysPro-IlelleLeulleArgCysAlaMetLeuAs
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Conservative:
Mismatches:
Indels:
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                                                       09-833799-13B (1-57) x ABL66677 (1-411)
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Percent Similarity:
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20-SEP-2000;
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                     Query Match:
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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 comprises a sequence (S) selected from 847 sequences (given in ABL61664 comprises a sequence (S) activity, where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used an be used for producing a product which an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the structure and/or properties of the agent. M1 can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, sequences.
                                                                                                                                                                                                                                                                                    Carter KC, Ebner R, Endress G, Horrigan S;
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Mismatches:
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Matches:
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              02-OCT-2000; 2000US-237294P.

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03-OCT-2000; 2000US-237598P.

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stomach, lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                               Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
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                        Ovary cancer related gene sequence SEQ ID NO:6148.
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15-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young PE, Augustus M, Soppet DR, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AVAL-) AVALON PHARM.
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02-0CT-2000;
03-0CT-2000;
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18-SEP-2000;

18-SEP-2000;

20-SEP-2000;

20-SEP-2000;

20-SEP-2000;

22-SEP-2000;

22-SEP-2000;

25-SEP-2000;

25-SEP-2000;

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27-SEP-2000;

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28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                                                                            Homo sapiens.
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02-OCT-2000;
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                                                                                   gene; ds.
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anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) comprises a sequence (S) selected from 847 sequences (given in AB161664 to AB170110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a structure and/or properties of the agent. MI can be used in the tructure and/or properties of the agent. MI can be used in the transmit of cancer such as colon, breast, stomach, lung, thyroid, cosophageal, ovarian, kidney, prostate or pancreatic cancer, each or carcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine carcinoma and Milm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, ovarian carcinoma, ovarian cancer, therapy, diagnosis, tumour antigen, identification, cytostatic, gene therapy; vaccine, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 CCAACAAGGNGNAACCCTTGGNAAGTNCCNAGTGANTINTGGCCAATGTTNGATGCTNAA 282
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present invention describes a method (M1) for screening for an
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Mismatches:
Indels:
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99US-0338933.
99US-0404879.
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WPI; 2000-431589/37.

Claim 1; SEQ ID 6148; 44pp; English

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Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of
                                                  acid encoding it, useful for the dis
cancer, preferably ovarian cancer -
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Claim 18; Page 192; 299pp; English.

The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.

Sequence 292 BP; 63 A; 71 C; 75 G; 83 T; 0 other;

292 118 2 15 0 Conservative: Mismatches: Indels: Length: Matches: Gaps: 0.00161 105.00 57.14% 51.43% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local Score:

09-833799-13B (1-57) x AAA70066 (1-292)

22 ArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIle 41 1 CAATGITTGAIGCITAACCCCCCCAATTTCTGIGAGATGGATGGCCAGTGCAAGCGTGAC 60 ò g

61 TTGAAGTGTTGCATGGGCATGTGGGGAAATCCTGCGTTTCCCT 42 LysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro

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Search completed: February 15, 2003, 20:26:35 Job time: 232 secs

61 TTGAAGTGTTGCATGGGCATGTGGGAAATCCTGCGTTTCCCCT 105 42 LysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56 셤

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RESULT 75

ABN72960 standard; DNA; 292 BP ABN72960 HANDER STANDER 
ABN72960;

(first entry) 02-JUL-2002

Ovarian carcinoma antigen polynucleotide #65.

Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.

Homo sapiens.

WO200206317-A2

24-JAN-2002

17-JUL-2001; 2001WO-US22635.

10-AUG-2000; 2000US-0636801. 20-SEP-2000; 2000US-0667857. 04-APR-2001; 2001US-0827271. 17-JUL-2000; 2000US-0617747.

18-JUN-2001; 2001US-0884441

(CORI-) CORIXA CORP.

Fling SP, Retter MW, Fanger GR; Hill P, Albone E; Algate PA, Carter D, Mitcham JL, King GE, Reed SG, Vedvick TS,

WPI; 2002-164781/21.

Polypeptides comprising an immunogenic portion of an ovarian carcinoma protein or its variants, useful for stimulating an immune response in a patient and treating ovarian cancer

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portion of an ovarian carcinoma protein which acts as an immunostimulant and is cycostatic. The polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells that express the polypeptides are useful for stimulating an immune response in a patient and treating ovarian cancer. This sequence represents DNA related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          22 ArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly1le 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAATGITIGAIGCITAACCCCCCCAATITCIGIGAGAIGGAGGCCAGIGCAAGCGIGAC 60
                                                      This invention relates to polypeptides comprising an immunogenic
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                  Example 2; Page 310; 408pp; English.
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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-Q=/Cgn2\_1/USPTO\_spool/USO9831799/runat\_12022003\_120042\_23664/app\_query.fasta\_1.199
-DB-EST -QPMT=fastap -SUFFTX=rst -MINMATGH=0.1 -LOOPEXT=0
-LOOPEXT=0
-DOCALIGN=200 -THR SCORE=pct -THR MAX=looum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=75 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USO9833799\_GCGN 1 1 2874 @runat 12022003 120042 23664 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries Command line parameters:

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A.1858070 BE715619 BF836201 BF836201 BF836201 BF836201 BF73673 BM748969 BM748969 BM768573 BM768573 AA586983 AA586983 AA586983 AA586983 BF73673 BF73673 BF837730 BF8376294 BF8376294	BF094327 BE711090 BE711090 BE71164 BE183902 BE183902 BF836725 BF836725 BF83650 AW860590 AI 830232 AI 831365 AA583567 AA583567 AA583567 AA583567 BE118433 BE184433 BE184433 BE184433 BE184433 BE184433	ALIGNMENT: 219 bp 88 Rodata, Crairimates, Cat. Correa, R., V. W. Jr., Zago. io, A. F., Matsi	Shotgun sequencing of the human tran sequence tags sequence tags broc. Natl. Acad. Sci. U.S.A. 97 (7) 20202663 Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Ray Prof. Antonio Prudente 109, 4 and Brazil Tel: +55-11-2704922 Fax: +55-11-2704922 Fax: +55-11-270401 Email: asimpson@ludwig.org.br This sequence was derived from the F. This sequence was derived from the F. (http://www.ludwig.org.br/scripts/99
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 289)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Sliva,W. Jr., Zago,M.A., Bordin,S., Coste,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunscein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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mail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-HT0633-240
300-304-212&ta=2000-03-24&ta=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 289.
Location/Qualifiers
1. 289
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Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/organism="Homo sapiens"
/db xref="taxon:966"
/clonelib="HT0641"
/dev stage="Adult"
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/dev stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from Organisms PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Email: asimpson@ludwig.org.br
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Brazil

Fax: +55-11-2707001

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Email: asimpsonGludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0653-180
400-146-all&t3=2000-04-18&t4=1)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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High quality sequence start: 21
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                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3.HTI190-
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Seq primer: puc 18 forward
High quality sequence start: 6
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0652-150

400-143-a07&t3=2000-04-15&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 39

High quality sequence stop: 359.
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CM4-HT0744-160600-201-a06 HT0744 Homo sapiens cDNA, mRNA sequence.
BE715602
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 364)

                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 231
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                                                                                                                                          Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-HT0634-270 300-308-foots=22000-03-27&t4=1)
Seq primer: puc 18 forward: 6
High quality sequence start: 6
High quality sequence store: 344.
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//dev stage="Adult"
//note="Organ: head neck; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products
Site 2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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(Lases I to 359)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                          Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 600-201-aloka5=2000-06-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stop: 370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Mead neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under lustringency conditions:
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Bukaryota, Detazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 370)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Ur., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
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                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Shotgun sequencing of the human transcriptome with ORF expressed
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                                                             Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="HT0744"
/dev_stage="Adult"
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//dev stage="Organ: head_neck; Vector: puc18; Site_1: Smal;
//note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 370)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bodini,S., Coste,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsteain,A., deOliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                    Email: asimpsonedludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 600-201-ao6&t3=2000-06-16&t4=1)
Seq primer: puc 18 forward
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High quality sequence start: 20
High quality sequence stops: 364.
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                                                                                            Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                       Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
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/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
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Seq primer: puc 18 forward
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                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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/clone_lib="FT0104"
/dav stage="Adult"
/dav stage="Adult"
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Site_2: Sma1; A mini-library was made by cloning products
derived from ORBSISE PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
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IL5-HT0990-251100-263-g08 HT0990 Homo sapiens CDNA, mRNA sequence.
BF838555
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goddman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence start: 8
High quality sequence stop: 370.
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/dev_erage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions:"
1 (bases 1 to 371)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivaira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Phttp://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL5&t2=LL5-HT0990-
251100-263-g0&k13=2000-11-25&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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GE69f06.X1 NCI CGAP Eso2 Homo sapiens cDNA linear EST 23-NOV-1998 similar to qb:S58717 rnal ELAFIN PRECURSOR (HUMAN); contains element THR repetitive element; mRNA sequence.
A1285400. GI:3923633
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This advance was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230 600-215-d05&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
High quality sequence state: 8
High quality sequence stop: 371.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 371)
Dias Neto. B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/clone_lib="FT0104"
/dev_stage="Adult"
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                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Nan Hu, W.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: esophagus; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo Average insert size 1.1 kb. Life Technologies catalog #: 11502-010"
                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 375)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seq primer: -40UP from Gibco
High quality sequence stop: 356.
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/lab_host="DH10B"
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
Seq primer: puc 18 forward
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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09-833799-13b.rst

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev stage="Adulto".
/dev stage="Adulto".
/note="Organ: prostate tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A min1-library was made by cloning products Site_2: Smal; A min1-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                        Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230 600-215-b05&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward High quality sequence start: 10 High quality sequence stop: 365.
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    Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Golman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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BE772171.1 GI:10225829
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Fax: +55-11-2707001
                                                                                                              Simpson, A.J.
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    AUTHORS
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/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: prostate tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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CM4-HT0652-150400-143-g08 HT0652 Homo sapiens cDNA, mRNA sequence.
BE182879
BE182879.1 GI:8662055
EST.
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Bmail: asimpsonaludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
600-215-907&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
1 (bases 1 to 380)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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Site 2: Smal; A mini-library was made by cloning products
Site 2: Smal; A mini-library was made by cloning products
Site 2: Letters Parent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4.HT0652-150
400-143-g0&&t3=2000-04-15&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 61.
                                                      1 (bases 1 to 386)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                          \mbox{Simpson}, \mbox{A.J.} Shotgun sequencing of the human transcriptome with ORF expressed
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230 600-215-f02&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 45
High quality sequence start: 45
High quality sequence stop: 386.
                                                                Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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    Euteleostomi;
                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/clone_lib="FT0104"
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                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert Buck, M.D., Ph.D.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnh.gov/bbrp/image/image.html
Insert Length: 480 Std Error: 0.00
Seq primer: -40ml3 fwd. Effrom Amersham.
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Dases 1 to 388)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="INAGE:1088712"
/clone_lib="NCI_CGAP_Lar1"
/tissue_type="larynx"
/lab_hogt="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
600-215-c06&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 388.
Location/Qualifiers
1. 388
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/note="Organ: prostate tumor; Vector: puc18; Site 1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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CM4-FT0104-230600-215-d07 FT0104 Homo sapiens CDNA, mRNA sequence.
BE772168
                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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TITLE

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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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      AI393896.1 GI:4223443
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Unpublished (1997)
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A1989737
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//dev.stage="Adult"
//dev.stage="Adult"
//note="Organ: prostate_tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
600-215-d07&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 32
High quality sequence stop: 389.
Location/Qualifiers
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 389)
1 (bases I to 380)
1 (bases) To 380, M.R., Briones, M.R., Bordin, S., Briones, M.R., Rogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Matches:
Conservative:
Mismatches:
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FEATURES

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Contact: Kober Strade, Strade, M.D., Mike Grever, Chract. Kober Strade, John Byrd, M.D., Mike Grever, Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 802 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 381.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/lab_host="DH10B"
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Simpson, A.J.
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(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT713 vector. Library
went through one round of normalization. Tissue samples
provided by Dr. Brian Dieckgraefe (Washington University,
dieckaim.wustl.edu), colonic mucosa represents a range of
disease; nowlyement from moderate to severe Crohn's
disease; samples include both perforating (fistulas) and
non-perforating samples. Library constructed by Bento
86 c 126 g 84 t
                                                                                                                                                                                                                                                                                                                                                                                                                                            BE715611 390 bp mRNA linear EST 12-SEP-2000 CM4-HT0744-160600-201-C07 HT0744 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:0606"
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/tissue type="colonic mucosa from 3 patients with Crohn's
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 390)
                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40UP from Gibco.
Location/Qualifiers
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 GI:5836618
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/note="Organ: head neck; Vector: Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160

600-201-c07&t3=2000-06-16&t4=1)

Seq primer: puc 18 forward
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 390)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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BE715615
BE715615.1 GI:10103880
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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High quality sequence stop: 390.
Location/Qualifiers
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priofiles into the pUC18 vector. Reverse transcription of pissue mRNA and CDNA amplification were performed under
low stringency_conditions."
                                                                                                                                                                    Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230 S600-215-al2&t32454=1) Seq primer: puc 18 forward High quality sequence start: 4 High quality sequence story: 397. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 397)
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Site_2: Smal; A minl-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
600-201-d10&t3=2000-06-16&t4=1)
                                                                                                              Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 395)

                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 395.
Location/Qualifiers
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                       Homo sapiens
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                                                                                          REFERENCE
                                                                                                                   AUTHORS
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FEATURES

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Score:

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BE715609.1 GI:10103874
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp//image/image.html
Insert Length: 523 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham.
Location/Qualifiers
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nn69d08.sl NCI CGAP Larl Homo sapiens cDNA clone IMAGE:1089135 3' similar to gb:558717 rnal ELAFIN PRECURSOR (HUMAN);contains element THR repetitive element;, mRNA sequence.
                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 399)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
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Mismatches:
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Matches:
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Unpublished (1997)
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Best Local Similarity:
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BE715592
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VERSION
KEYWORDS
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VERSION
KEYWORDS
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AUTHORS
TITLE
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/organism="Homo sapiens"
/db xref="taxon:966"
/clone_lib="HT0744"
/dev stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORENTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwing Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 400)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 &0.0201-blokt3=2000-06-16&t4=1)

Seq primer: puc 18 forward:
High quality sequence start: 7

High quality sequence stop: 400.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 gegenadadeceagrenanagerecagrerecentrangeeregeerecetecearraterig 182
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09-833799-13b.rst

Page 17

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similar to gb:S58717_rnal ELAFIN PRECURSOR (HUMAN);, mRNA sequence.
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Conservative:
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                                                                                                         Homo sapiens
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Best Local Similarity:
                                                                                       human.
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/db xref="taxon:9606"
/clonellb="HT0744"
/dev stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Pattent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                         Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., M.J., Soares, F., Brentani, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI874186 405 bp mRNA linear EST 07-MAR-2000 wm50a02.xl NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2439338 3'
                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Eua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Conservative:
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High quality sequence stop: 403.
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                                       Homo sapiens
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 644 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 405)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:2439338"
/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2
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UI-H-BII-acs-b-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2715238 3', mRNA sequence.
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// Indo host="DH10B (Life Technologides)
// Indoce="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site_2: Eco RI; The
NCI CGAP Sub3 library; as subtracted library derived from El.
NCI CGAP Sub3 library; which is a subtracted library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI CGAP Pi28, NCI CGAP Ed31,
NCI CGAP P22, NCI CGAP P728, NCI CGAP Kid12,
NCI CGAP P22, NCI CGAP F728, NCI CGAP Kid12,
NCI CGAP P22, NCI CGAP F728, NCI CGAP Ed31,
NCI CGAP End3, NCI CGAP Ed3, NCI CGAP L11, NCI CGAP L24,
NCI CGAP End3, NCI CGAP G4, NCI CGAP L124,
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                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
The sequence contained an Oilgo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LINIA qt:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                         Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 406)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Clone lib="NCI CGAP Sub3"
/lab_host="DH10B (Life Technologies)"
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Mismatches:
Indels:
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Seg primer: M13 Forward
POLYA-Yes.
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                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:9606"
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Unpublished (1997)
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                                                                 REFERENCE
                                                                                                 AUTHORS
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                                                                                                                      TITLE
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                                                                                                                                                                                                              COMMENT
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09-833799-13B (1-57) x AW137392 (1-406)

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/db xere="caron:0606"
/clone_lib="HT0744"
/dev_gege="Adult"
/dev_gege="Adult"
/note="Corgan: head neck; Vector: puc18; Site_l: Smal;
/note="Corgan: head neck; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Mo. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This enty can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM4-HT0744-160
                                                                                                                                                                                                                                                                                                                                                      BE715604 406 bp mRNA linear EST 12-SEP-2000
CM4-HT0744-160600-201-a08 HT0744 Homo sapiens cDNA, mRNA sequence.
BE715604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 406)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones; M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.P., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                        306 Arccedececearerreaarcccccraaccecrecricaaaearacreacceceaea 247
                                                366 ecechagaeccagronahaderccagrorccacraaccraeccreeccescarrarcrie 307
20
                                                                                                     21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
1 AlaClnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
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                                                                                                                                                                                                                                                246 AICAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 196
                                                                                                                                                                                                              41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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High quality sequence start: 21
High quality sequence stop: 406.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE715604.1 GI:10103869
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09-833799-13B (1-57) x AI392753 (1-418)
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 609 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 bp mRNA linear EST 30-MAR-1999 tg23g03.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109652 3' similar to gb:$58717_rnal ELAFIN PRECURSOR (HUMAN);contains element AI392753
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 418)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                           133 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 192
                                                                                                                       193 Arccegrececcarerreaarceceraaceerecraaaaaaraceereereaaa 252
                                                                                          21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                               1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu
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/organism="Homo sapiens"
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09-833799-13B (1-57) x BE715604 (1-406)
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ORGANISM
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AUTHORS
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KEYWORDS
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nn69a01.s1 NCI CGAP Larl Homo sapiens cDNA clone IMAGE:1089096 3' similar to gb:S58717 znal ELAFIN PRECURSOR (HUMAN);contains element AA586943
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNAS Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 515 Std Error: 0.00
Seq primer: -40ml3 fwd. ETf from Amersham
High quality sequence stop: 335.
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ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Larynx. 5' adaptor sequence: 5' GAATTCGGCACGAG
3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
Average insert size: 0.9 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 419)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unmor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                   349 GCGCAAGAGCCAGTCAAAGGTCCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 290
                                                                                                                                                                                289 ArccdGrGcGcCArGrrGAArcccCCTAACCGCrGCrrGAAGATACTGACTGCCCAGGA 230
                                                                                                                   21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
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                                                                                                                                                                                                                                                                                                          229 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 179
                                                                                                                                                                                                                                                 41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMACE:1089096"
/clone_lib="NCI_CAPP_Larl"
/tissue_type="larynx"
/lab_host="SOLR (kanamycin resistant)"
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Mismatches:
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Matches:
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xb60d08.x1 NCI CGAP Eso2 Homo sapiens cDNA clone IMAGE:2580687 3'
similar to gb:\(\overline{5}\)58717\(\overline{7}\) rnal ELAFIN PRECURSOR (HUMAN); contains element
MER28 MER28 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov

Lisaue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael B. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Generation Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 422) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Eso2"
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/dev stage="Adult"
/note="Organ: prostate tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Fuman Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
600-215-b04&t3=2000_06-23&t4=1)
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                                                                                                                                                                                                                                       BE772154 11near EST 20-SEP-2000 CM4-FT0104-230600-215-b04 FT0104 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence start: 13
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/clone lib="FT0104"
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Confact: Robert Strausberg, Ph.D.

Email: gapbs-r@mail.nih.gov
Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michel R. Bamert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/inage/image.html
Insert Length: 626 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 128.
                                                                                                                                                                 qt66al0.x1 NCI CGAP Eso2 Homo sapiens cDNA clone IMAGE:1960218 3' similar to gb:558717 rnal ELAFIN PRECURSOR (HUMAN);contains element AI283910
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/tissue_type="squamous_cell_carcinoma"
/lab_host="DH10B"
/note="Organ: esophagus; Vector: pCMV-SPORT6; Site 1: Sall
; Site 2: NotI; Cloned unidirectionally. Primer: Oligo
#: 11902-010"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:1960218"
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                              human.
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AUTHORS
TITLE
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KEYWORDS
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BF836224 437 bp mRNA linear EST 13-JAN-2001
QV3-HT1016-171100-474-h01 HT1016 Homo sapiens CDNA, mRNA sequence.
BF836224
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Galdman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016-171100-474-h01&t3=2000-11-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence start: 13
High quality sequence stope: 437.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCCATTATCTTG 257
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
230 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCCAG 180
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/db xref="taxon:0566"
/clone lib="HT0744"
/dev_stage="Adult"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
a 102 c 132 g 100 t
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This end be seen in the following URL
Project. This can be seen in the following URL
http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
600-201-a04&t3=200-06-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 437.
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                                       BE715601 A18 bp mRNA linear EST 12-SEP-2000 CM4-HT0744-160600-201-a04 HT0744 Homo sapiens CDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Liaboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                             BE715601.1 GI:10103866
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  RESULT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                       EST 09-MAR-2000
                                                                                                                                                                                    AW001880

WRNA linear EST 09-MAR-2000
WRS1066.x1 Soares thymus MHFTH Homo sapiens CDNA clone
IMAGE:2513867 3' similar to gb. 558717 rnal ELAFIN PRECURSOR (HUMAN
); contains element MER28 repetitive element; mRNA sequence.
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rgfthaccharctghagftgggaggggggggaggttrftfffffffffff 3'],
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 438)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 552 and Error: 0.00 Seq primer: -40UP from Gibco.
Location/Qualifiers
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318 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 368
                                              41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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/db_xref="taxon:9606"
/clone="INAGE:2513867"
/clone_lib="Soares_thymus_NHFTh"
/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
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VERSION
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TITLE
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21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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96
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                                                                                                                                 RESULT 43
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// Organism="Homo sapiens"
// Ob zref="taxon:966"
// Ob zref="taxon:966"
// Orde="taxon:966"
// Ord
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ibases 1 to 41.

I (bases 1 to 41.

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Grunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                             BF836743 441 bp mRNA linear EST 13-JAN-2001 CM2-HT0969-181100-509-b06 HT0969 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-HT0969-181100-509-bo6&t3=2000-11-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 441.
Location/Qualifiers
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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207 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 157
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                                                                                                                                                                                                                       BF836743.1 GI:12188790
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                                                              RESULT 42
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KEYWORDS
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 598 Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                                                                         tq66g09.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2213824 3' similar to gb:558717_rnal ELAFIN PRECURSOR (HUMAN);contains element THR repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone="IMAGE:2213824"
/clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 GCGCAAGAGCCAGTCAAAAGGTCCAGTTACCACTAAGCCTGGCTCCTGCCCCATTATCTTG 305
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/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized nimedified polylinker; Plasmid DNA from the normalized made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 141920-1417991 and 1220904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                         tkiic09.xi NCI CGAP Lu24 Homo Sapiens cDNA clone IMAGE:2150704 3' similar to gb:858717 rnal ELAFIN PRECURSOR (HUMAN); contains element THR repetitive element; ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                          EST 14-APR-1999
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ogapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
366 GCGCAAGAGCCAGTCAAAAGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
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                                                                                                        244 Arcaadaadridergridaadgererrideddegarideererriregrideeria 194
                                                              41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 554 Std Error: 0.00
Seg primer: -40UP from Gibco.
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone="INAGE:2150704"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_hogt="DH108"
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Unpublished (1997)
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DB:
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                                                                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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/clone lib="HN0039"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Corgan: head normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 465)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa, F.F.,

Brunstein,A., deOliveira,P.S., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis, D.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HN0039-101100-500-bo&&t5=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 465.
                                                                                                                                                                                                                                  BF824934 11100-500-b06 HN0039 Homo sapiens CDNA, mRNA sequence.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
183 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 242
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                                                                                                                  246 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 196
                                                          41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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Matches:
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                                                                                                                                                                                                                                                                                                                         BF824934.1 GI:12167001
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DEFINITION

LOCUS

RESULT 46

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BF824930

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

MEDLINE COMMENT

JOURNAL

TITLE

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/organism="Homo sapiens"
/db xref="taxon:966"
/clon=lib="HN0039"
/dev stage="Adult"
/note="Organ: head normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HN0039-
101100-500-c03&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 466.
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1 (bases 1 to 446)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                         184 GCGCAAGACCCAGTCAAGGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 243
21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                       304 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGGAIGGCCTGTTTCGTTCCCCCAG 354
                                                                                                                                                                                  41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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Conservative:
Mismatches:
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Best Local Similarity:
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BF824935
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IID-HN0039-101100-500-a05 HN0039 Homo sapiens cDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL0&t2=ILO-HN0039-
Seq primer: puc. 18 forward
High quality sequence stop: 466.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 466)

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                            303 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGGATGGCCTGTTTCGTTCCCCAG 353
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                                                                                                                   41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln
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source

FEATURES

Query Match:

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Pred. No.:

COUNT

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/dev_efage="Addit"
/note="Organ: head_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                               BF824920
LLO-HN0039-101100-500-c05 HN0039 Homo sapiens cDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&t2=IL0-HN0039-
101100-500-c05&t3=2000-11-10&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                            21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                         304 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 354
                                                                                          41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln
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Location/Qualifiers
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/clone_lib="HN0039"
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09-833799-13B (1-57) x BF825207 (1-467)
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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu 20

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467 00 00 00 00

Conservative: Mismatches: Matches: Length:

3.51e-29 327.00 100.00% 100.00% 100.00%

Similarity:

Query Match:

Best Local

Percent Similarity:

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Pred. No.:

Score:

BASE COUNT

ORIGIN

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derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
lissue mRNA and conditions."
a 115 c 137 g 99 t

organism="Homo sapiens"

source

FEATURES

High quality sequence stop: 467. Location/Qualifiers

Seq primer: puc 18 forward

Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HN0039-131100\_501-d07&t3=2000-11\_13&t4=1)

Tel: +55-11-2704922 Fax: +55-11-2707001

Brazil

Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shorgun sequencing of the human transcriptome with ORF expressed

Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

sequence tags

20202663

JOURNAL

COMMENT

TITLE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 467)

JEB25207 467 bp mRNA linear EST 13-JAN-2001 100039-131100-501-d07 HN0039 Homo sapiens CDNA, mRNA sequence.

BF825207.1 GI:12167451

BF825207

BF825207

DEFINITION

ACCESSION

KEYWORDS VERSION

BF825207/c RESULT 49

Homo sapiens

ORGANISM

REFERENCE AUTHORS

human.

244 Arccesificacionarionaricoccompacceorionamentacionacamentacional 303

21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly

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184 GCGCAAGAGCCGGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 243

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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
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QV3-HT1016-221100-480-g03 HT1016 Homo sapiens cDNA, mRNA sequence.
BF837734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001

Email: asimpsonoludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016-Seq Primer: puo 18 forward

High quality sequence stop: 468.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
283 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 224
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                                                                                                                                               41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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Matches:
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HN0039-
101100-500-al2&t3=2000-ll-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 476.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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299 GCGCAAGACCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 240
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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09-833799-13B (1-57) x BF824932 (1-477)

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 647 Std Error: 0.00
Seq primer: -40m13 fwd. ETF from Amersham
High quality sequence stop: 430.
                                                                                                                                                                                                                                                                        AA582866 HOLI CGAP Larl Homo sapiens cDNA clone IMAGE:1089400 3/ similar to gb:558717_rnal ELAFIN PRECURSOR (HUMAN); contains element HGR repetitive element; , mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGGTCCTGCCCATTATCTTG 304
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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
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                                                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                              304 Archadaagrecrereaagecrerrecegearecererreceration
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/db xref="taxon.9606"
/clone="IMAGE:1089400"
/clone_lib="NCI_CGAP_Larl"
/tissue_type="larynx"
/lab_hogt="SOLR (kanamycin resistant)"
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Unpublished (1997)
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AUTHORS
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KEYWORDS
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/dev stage="Adult"
/note="Organ: head normal; Vector: pucl8; Site 1: Smal;
/note="Organ: head normal; Vector: pucl8; Site 1: Smal;
/ste 2: Smal, A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
a 146 c 120 g 121 t
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL0&t2=LLO-HN0039-
131100-501-a07&t3=2000-11-3&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence stort: 11
High quality sequence story: 487.
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1 (Bases I to 487)

1 (Bases I to 487)

1 (Bases I to 487)

Nagai,M.A., da Silva,W. Jr., Zaqo,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Bruntein,A., deolivetare,P.S., ubcher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                   BF825204
ILO-HN0039-131100-501-a07 HN0039 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
                                  21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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                                                                                                                                                 243 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 193
                                                                                                 41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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/clone_lib="HN0039"
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                                                                                                                                                                                                              RESULT 53
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KEYWORDS
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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20

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DEFINITION
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Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (base 1 to 490)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
205 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 264
                                                                                      21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                          325 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGATGGCCTGTTTCGTTCCCCAG 375
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/db xref="taxon:9606"
/clone="IMAGE:3314575"
/clone=lib="NCI CGAP_Co16"
/tissue_type="colon tumor, RER+"
/lab_host="DH108"
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Mismatches:
Indels:
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Seg primer: -40UP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
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Unpublished (1997)
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Best Local Similarity:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                 ACCESSION
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SOURCE
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Shotgun sequencing of the human transcriptome with ORF expressed

Simpson, A.J.

sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 498)

EST 13-JAN-2001

BF837735 QV3-HT1016-221100-480-g08 HT1016 Homo sapiens CDNA, mRNA sequence.

BF837735.1 GI:12189957

BF837735

Homo sapiens

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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu 20
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                      Matches:
Conservative:
Mismatches:
                                                       Indels:
            Length:
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Query Match:
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Alignment Scores:
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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProlleleLeu 20

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Site\_2: Smal; A mini-library was made by cloning products
Site\_2: Smal; A mini-library was made by cloning products
derived from ORB/STS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cubAR amplification were performed under
low stringency conditions."

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: ssimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016221100-480-908&t2=22000-11-22&t4=1)

Seq primer: puc 18 forward.

High quality sequence stop: 498.

1. .498

Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

09-833799-13b.rst

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human.
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                                                                                                           RESULT 57
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                                                                                                                                                                                                                                               EST 21-AUG-2002
                                                                                                                                                                                                                                                 BQ941085 522 bp mRNA linear EST 21-AUG-2000
AGENCOURT_8794612 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6374832
                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM254 row: h column: 01
High quality sequence stop: 521.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                         203 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 262
                                                     21 IleargCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
323 Arcaadaadrdcrdrdaaddcrcrrdcdddardccrdrrrcdrrcccad 373
                                                                                                                               41 11eLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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Best Local Similarity:
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BG490472 SET 27-MAR-2001
602519610F1 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:4637906 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 565)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. d column: 03
plate: LLCM1399 row: d column: 03
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                    276 arcaagaagrecrereaaggererreceggaregeererrecreed 326
                                            41 IleLysLysCysCluGlySerCysClyMetAlaCysPheValProGln
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Mismatches:
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Matches:
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Tissue Procurement: DCTD/DTP/Gazdar
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Location/Qualifiers
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86 a 85 c 105 g 85 t
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
600-215-c09&ts=2000-06-23&t4=1)
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High quality sequence start: 25
High quality sequence stop: 360.
Location/Qualifiers
                                                                                                                                                                                                                                    1 (bases 1 to 361)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                          BE772161 361 bp mRNA linear EST 20-SEP-2000 CM4-FT0104-230600-215-C09 FT0104 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                        Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 GCGCAAGATCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 197
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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                                                                                                         BE772161.1 GI:10225819
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Best Local Similarity:
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RESULT 58
BE772161/c
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                                                            DEFINITION
ACCESSION
                                                                                                                                                                      ORGANISM
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/organism="Homo sapiens"
/db xref="taxon:9606"
/dloxe=lib="uroll6"
/dev stage="Adult"
/dev stage="Adult"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
94 a 116 c 113 g 98 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was derived from the FAPBSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0116-020201-464-F04&t3=2001-02-02&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                      31061069 421 bp mRNA linear EST 15-JUN-2001
IL3-UT0116-020201-464-F04 UT0116 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                   86
136 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG
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Mismatches:
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                                                                BI061069.1 GI:14468596
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Fax: +55-11-2707001
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Best Local Similarity:
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AUTHORS
TITLE
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KEYWORDS
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0649-270
700-012-f03&t3=2000-07-27&t4=1)
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Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector: Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                           BE711100 263 bp mRNA linear EST 12-SEP-2000 RC3-HT0649-270700-012-f03 HT0649 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Homo.
1 (bases 1 to 263)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTGAGCCTGGCTCCTGCCCGTTATCTTG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                             305 ATCAGGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 355
41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence start: 50
High quality sequence stop: 263.
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BE711100.1 GI:10099365
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                                                                                                                                                              DEFINITION
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VERSION
                                                                                          RESULT 60
                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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420 bp mRNA linear EST 08-MAR-2000 wn64c08.X1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2450222 3' similar to gb:\(\overline{\text{Sign17}}\)_rnal ELAFIN PRECURSOR (HUMAN); contains element PTRS repetitive element '; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbpp/image/image.html
Insert Length: 511 Std Error: 0.00
Seq primer: -40UP_from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stagge="adult"

//dev_stagge="adult"
// Tab_host="PHIOB (phage-resistant)"
// Tab_host="Durg" (phage-resistant)"
// Tab_host="Organ: lung; Vector: pT7730-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a not I pooled lung tumor tissue, and was then primed with a not I pooled lung tumor. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /_clone_lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 299
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                                                                                                             177 Archaghacrecrerenandecrerrecesearesecrerrecena 227
                                                         41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:2450222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/organism="Homo sapiens"

/db xref="taxon:9606"

/clonelib="HT1016"

/dev stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: Smal;

Site_2: Smal; A mini-library was made by cloning products

Site_2: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

low stringency conditions.

10 10 t
                                                                                                                                                                                              QV3-HT1016-151100-463-c10 HT1016 Homo sapiens cDNA, mRNA sequence. BR835679 BP835679.1 GI:12186947
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 447)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Buschkuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome rorject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016-151100-463-c10&t3=2000-11-15&t4=1)
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
  40
21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                        sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                   238 ATCAAGAAGTGCTGTAAAAGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 188
                                                                                           57
                                                                                         41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 447.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .447
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ACCESSION
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KEYWORDS
SOURCE
                                                                                                                                                                                    RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.B., da Silva, W. Jr., Zago, M.R., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=ILO-CT0008-140 599-007&t2=1999-06-14&t4=1)
Seq primer: puc 18 forward High quality sequence start: 39
High quality sequence stop: 454.
                                                                                                                                                                                                                        AW845140 453 bp mRNA linear EST 19-MAY-2000 LLO-CT0008-140599-007 CT0008 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                      189 GCGCGAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCCTCTGCCCCATTATCTTG 248
                                     21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
                                                                                                                              309 ATCAAGAAGTGTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCCAG 359
                                                                                                           41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                             AW845140.1 GI:7940657
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COMMENT
                                                                                                                                                                                     RESULT 63
                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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//dev stage="Adult"
//note="Organ: colon; Vector: puc18; Site_1: Smal; Site_2:
//note="Organ: colon; Vector: puc18; Site_1: Smal; Site_2:
//note_mini-library was made by cloning products derived
from ORESTES POR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the DVC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=ILO-CT0008-140
599-001&t3=1999-05-14&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotzi, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (Bases I to 453)
1 (Bases I to 453)
1 (Bases I to 453)
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                EST 19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                        21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                  AW845142 455 bp mRNA linear EST 19-MAN
ILO-CT0008-140599-001 CT0008 Homo sapiens cDNA, mRNA sequence
1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="CT0008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: puc 18 forward
High quality sequence stop: 455.
Location/Qualifiers
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VERSION
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-C&PR clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llhi.gov/bbry/hange/image.html

Insert Length: 551 Std Error: 0.00

Seq primer: -40UP from Gibco.

Location/Qualifiers
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/lab_host="adult"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (vector: pT7T3D-pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco R adaptors (Pharmacia), digested with Not I and Cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                               A1858070 444 bp mRNA linear EST 21-DEC-1999 wj70a03.x1 NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2408140 3' similar to gb:558717_rnal ELAFIN PRECURSOR (HUMAN); contains element THR repetitive element; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="squamous cell carcinoma, poorly differentiated (4 pooled tumors, including primary and
                               282 GCGCAAGAGCCAGTCAAAGGTCCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 223
                                                                                                                                                               222 Arccegrececcarerrearrecectraacecrecreaasearacrecreceaga 163
1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
                                                                                                           21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                       162 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCGG 112
                                                                                                                                                                                                                      41 ilelysLysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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/clone lib="NCI_CGAP_Lu19"
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/organism="Homo sapiens"

/db xref="taxon:966"

/clone_lib="HT1016"

/dev stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

Site_2: SmaI; A mini-library us made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."
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QV3-HT1016-171100-474-c05 HT1016 Homo sapiens cDNA, mRNA sequence.
BF836201
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Diasser to 374)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Rogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3.HT1016-171100-474-c05&t3=2000-11-17&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                       234 GCGCAAGAGCCAGTCAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 175
                                                                                                                                       1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                    41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln
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High quality sequence start: 11
High quality sequence stop: 374
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/db xref="texon.9606"
/clone_lib="HT0744"
/dev_grage="Adult"
/dev_grage="Adult"
/dev_grage="Adult"
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Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 342)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Magai,M.A., da Carvahho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE715619
342 bp mRNA linear EST 12-SEP-2000
6MS+HT0744-160600-201-f0l HT0744 Homo sapiens cDNA, mRNA sequence.
BE715619.1 GI:10103884
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 600-201-f01&t3=2000-06-16&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                       300 Arccegrececcarerreaarcceccraaccecrreaaaaaaracreacaacaa 241
                                                                                                                                                                                   21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                            20
                                                                      1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                           240 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 190
                                                                                                                                                                                                                                                                                             41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
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High quality sequence start: 15
High quality sequence stop: 342.
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              09-833799-13B (1-57) x AI858070 (1-444)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 501)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., ac Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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This sequence was derived from the FAPESP/IICR Human Cancer Genome roject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&tc2=ILO-HN0039-131100-501-dlo&t3=2000-11-13&t4=1)
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ILO-HN0039-131100-501-d10 HN0039 Homo sapiens cDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCCAG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                   Mismatches:
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Location/Qualifiers
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Fax: +55-11-2707001
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98.17%
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                           Best Local Similarity:
Query Match:
DB:
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Length:

Pred. Mo.:

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/organism="Homo sapiens"
/db xref="taxon:9666"
/clone_lib="HT0649"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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1 (Bases I to 316)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Sodai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvahho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Fax: +55-11-2700902
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0649-270
700-012-[60&kc3=2000_07-27&kc4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE711083 316 bp mRNA linear EST 12-SEP-200
RC3-HT0649-270700-012-f06 HT0649 Homo sapiens cDNA, mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                              Conservative:
Mismatches:
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Matches:
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High quality sequence start: 22
High quality sequence stop: 316.
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                                                             Best Local Similarity:
Query Match:
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                                     Percent Similarity:
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Query Match
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BM768573
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JOURNAL
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/db xref="taxon:966"

/clonelib="CT0006"

/dev stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

89 c 88 g 85 t
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR0-CT0006-280
599-008&t3=1999-05-28&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence start: 7
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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MRO-CT0006-280599-008 CT0006 Homo sapiens cDNA, mRNA sequence.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                     Length:
Matches:
Conservative:
Mismatches:
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                                                                                        96.49%
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                                                               Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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DB:
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AUTHORS
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VERSION
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LOCUS
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BASE COUNT

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/note="Organ: Stomach; Vector: pT218RP1; Site_1: EcoRI; Site_2: Not!; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR is site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 6nnt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli TOD10F' by electroporation method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM768573 14K402 Homo sapiens cDNA clone S14K402-6-G01 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 428)
                                                                                                                                                                                                                                                                                                                                                       174 GCGCAGGAGCCAGTCAAAGGTCCAGTAAAGCCTGGCTCCTGCCCCATTATCTTG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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                          Length:
Matches:
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Indels:
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/db xref="taxon:966"
/db colone=1844402-6-601"
/clone=1b==1844402"
/cell_line="K402"
/lab_host="Topl0F"
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Plate: 6 row: G column: 01
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High quality sequence stop: 428.
Location/Qualifiers
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Contact: Kim YS
Genome Research Center
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Best Local Similarity:
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Alignment Scores:
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/dev_stage="Adult"
/note="Organ: marrow; Vector: puc18; Site_1: Smal; Site_2:
/note="Organ: marrow; Vector: puc18; Site_1: Smal; Amin-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
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1 (bases 1 to 394)

Dias Neco,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Sogai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This unry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0316-
170101-673-e02&t3=2001-01-17&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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The cDNA libraries constructed by this method are full-length enriched cDNA library."
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="MT0316"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmail: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/fimage.hmil
Insert Length: 642 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nn69el0.sl NCI CGAP Larl Homo sapiens cDNA clone IMAGE:1089162 3' similar to gb:S58717 rnal ELAFIN PRECURSOR (HUMAN); contains element THR repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 386)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                            229 GCGCAAGAGGCAGTCAAAGGTCCAGTCTCACTAAGCCTGGCTCCTGCCCCATTATCTTG 170
                                                                                                                                                                                                                                                                                                                                                                                                                        21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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Mismatches:
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                                                            108 g
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/organism="Homo sapiens"
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/dev_stage="Adult"
/dev_stage="Adult"
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Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF736734 11near EST 10-JAN-2001 PM1-KT0004-241100-001-c04 KT0004 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D. H., M. J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Slorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +55-11-270701

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PMI&t2=PM1-KT0004-
241100-001-c04&t3=2000-11-24&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                384 GAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTGATCCGG 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 AAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 220
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Conservative:
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                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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MEDLINE
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AUTHORS
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Email: cgapDs-remail.nif.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 534 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1830872 423 bp mRNA linear EST 21-DEC-1999 wj61c08.xl NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2407310 3' similar to gb:$58717_rna1 ELAFIN PRECURSOR (HUMAN); contains element
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTACCTTG 226
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/db_xref="taxon:9606"
/db_colone="InAgE:240710"
/clone="InDe"NCI CGAP Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary
                                                                                                                                                                                                                                                                                                                                                                                            1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleLeu
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/lab_host="DH10B (phage-resistant)"
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91
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Best Local Similarity:
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Search completed: February 15, 2003, 21:12:55 Job time : 1467 secs

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Sequence 2288, Ap
Sequence 661, App
Sequence 1, Appli
Sequence 18387, A
Sequence 1898, App
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Sequence 225, App
Sequence 154, App
Sequence 7863, Ap
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Sequence 344, App
Sequence 495, App
Sequence 1987, Ap
Sequence 377, App
Sequence 377, App
Sequence 214, App
Sequence 169, App
Sequence 169, App
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Sequence 29, Appl
Sequence 57, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 57, Appl
Sequence 51, Appl
Sequence 519, Appl
Sequence 1130, Appl
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Sequence 702, App
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Sequence 243, App
Sequence 255, App
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Sequence 249, App
Sequence 750, App
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Sequence 747, App
Sequence 1, Appli
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Sequence 34, Arro
Sequence 34,
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Seguence 344,
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US-09-852-659A-121
US-09-813-311-747
US-09-819-136-1
US-09-894-882-240
US-09-894-882-249
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US-09-864-761-198
US-09-864-761-12659
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US-09-864-761-12659
US-09-862-812-154
US-09-962-812-154
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US-09-894-882-243
US-09-894-882-255
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US-09-852-659A-34
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-MODEL=frame+ p2n.model-DEV=xlp
-Q=CQGN2 1120044 23813/app_query.fasta_1.199
-Q=CQGN2 1/USFO_SPOO1/USO9833799/runat_12022003_120044 23813/app_query.fasta_1.199
-Q=CQGN2 1/USFO_SPOO1/USO9833799/runat_12022003_120044 23813/app_query.fasta_1.199
-Q=D=Published Applications NA -QFMT=fastap -SUFFIx=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 -ENDL-1 -MATRIX=blosum62
-TRAMS=human40.cdi -LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-TRAMS=human40.cdi -LIST=100 -DOCALIGN=200 -UNFMT=ptc -NORM=ext -HEAPSTZE=500 -MINLEN=0
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-NAXIEN=200000000 -USRE=US09833799 @CGN 1 1 80 @runat_12022003 120044_23813
-DEV TIMBOUT=120 -WARN TIMBOUT=30 -THROSPEND=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 1393, A
Sequence 1126, A
Sequence 1798, A
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                                                                                                                           February 15, 2003, 20:49:11; Search time 108 Seconds (without alignments) 268.810 Million cell updates/sec
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| cgn2_6/ptodata/1/Pubpna/USO7_PUBCOMB.seq:*
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| cgn2_6/ptodata/1/Pubpna/PCT_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/Pubpna/USO7_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/Pubpna/USO6_PUBCOMB.seq:*
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                                    GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-033-528-1393
US-09-954-456-1126
US-09-954-456-1798
                                                                                               nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 100 summaries
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

09-833799-13B 327

Perfect score:

Sequence:

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protein

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Run on:

Scoring table:

Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0, **BLOSUM62** 

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100.0 100.0 100.0

327 327 327 327

1264

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Query Match Length DB

Score

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Result

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Sequence 1, Appliseduence 124, Appliseduence 324, Appliseduence 156, Appleduence 15, Appliseduence 1, Appliseduence 1, Appliseduence 1, Appliseduence 161, Appliseduence 161, Appliseduence 121, Appliseduence 122, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 13, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Appliseduence 224, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1

US-09-920-300A-1393/C

Sequence 1393, Application US/09920300A

Sequence 1393, Application US/09920300A

Sequence 1393, Application US/09920300A

Sequence 1393, Application US/09920300A

Sequence 1394, Application Second E

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Meagher, Madeleine Joy

APPLICANT: Nu. Jiangher, Madeleine Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER

TITLE OF INVENTION: 2010.12.547

CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT APPLICATION NUMBER: US/09/920,300A

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH 480

LENGTH 480
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                                                                                               10 US-09-967-768A-324
9 US-10-108-605-158
9 US-10-108-605-158
9 US-10-108-605-18
9 US-10-007-271-3
9 US-10-007-271-3
9 US-09-989-442-163
10 US-09-989-442-164
10 US-09-989-442-164
10 US-09-989-42-164
10 US-09-764-883-922
10 US-09-764-883-922
10 US-09-764-898-50
10 US-09-764-898-50
10 US-09-164-898-123
10 US-09-167-186-7
10 US-09-113-7
10 US-09-919-113-7
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US-09-815-242-9218
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Matches:
Conservative:
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LOCATION: 27, $6, 343
OTHER INFORMATION: n = A,T,C or G
         243
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1644
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity:
Query Match:
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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca
TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 GCGCAACAGCCAGTCAAAGGTCCAGTNTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 310
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                                                                                                      GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: W. Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION NUMBER: US/10/033,528
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 480
249 ATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAG 199
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Matches:
Conservative:
Mismatches:
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FILE REFERENCE: 69920-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR PLING DATE: 2000-09-20
PRIOR PELING DATE: 2000-09-20
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR PILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
                                 RESULT 2
US-10-033-528-1393/c
; Sequence 1393, Application US/10033528
; Patent No. US20020131971A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1126, Application US/09954456
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: 27, 56, 343
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-UY-964-824A-582
Sequence 582, Application US/09964824A
Sequence 582, Application US/09964824A
Sequence 582, Application US/09964824A
Sequence 582, Application Setent No. US20020102531A1
GENERAL INFORMATION:
SETENTIAGO FOR INVENTION: Setent TITLE OF INVENTION: Setent NUMBER: US/09/964,824A
CURRENT PELING DATE: 2001-09-27
CURRENT FILING DATE: 2000-09-28
PRIOR PILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR PILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR PILING DATE: 2000-09-28
PRIOR PILING DATE: 2000-09-28
PRIOR PILING DATE: 2000-09-28
SPRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: PALENTING DATE: 2000-09-38
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Mismatches:
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55.36%
48.21%
                                                                                                                              NAME/KEY: misc feature

NAME/KEY: misc feature

CHER INFORMATION: n=a,t,g or

US-09-954-456-1798
SOFTWARE: Patentin version 3.0 SEQ ID NO 1798 LENGTH: 2309
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Best Local Similarity:
                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-954-456-1798

Sequence 1799, Application US/09954456

Sequence 1799, Application US/09954456

Sequence 1799, Process for Identifying Anti-Cancer Therapeutic Agents Using Cand Application's Process for Identifying Anti-Cancer Therapeutic Agents Using Cand TITLE OF INVENTION: Bets FILE OF INVENTION: Bets FILE OF INVENTION WINGER: US/60/233,617

PRIOR PELICATION NUMBER: US/60/233,617

PRIOR FILING DATE: 2000-09-18

PRIOR PAPLICATION NUMBER: US/60/234,923

PRIOR PAPLICATION NUMBER: US/60/235,134

PRIOR PELING DATE: 2000-09-26

PRIOR PELING DATE: 2000-09-26

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PRIOR APPLICATION NUMBER: US/60/235,710

PRIOR PELING DATE: 2000-09-27

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Matches:
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PRIOR FILING DATE: 2000-09-27
PRIOR PTLING DATE: 2000-09-27
PRIOR PTLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR PILING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PATENTIN VEYSION 3.0
SSEQ ID NO 1126
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, OTHER INFORMATION: n=a,t,g or
US-09-954-456-1126
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ORGANISM: Homo sapiens
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238 GATCCTGTTGACACCCCAAACCCCAACAAGGAGGAAGGCTGGGAAGTGCCCAGTGACTTAT 297
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                                                                  APPLICANT: Smithson, Glennda
TITLE OF INVEXTION: Method of Detecting inflammatory Lung Disorders
FILE REFERENCE: 21402-018 US
CURRENT APPLICATION NUMBER: US/09/865,812
PRIOR APPLICATION NUMBER: 05/207,104
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic FILE REFERENCE: P2730P1C20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 GACTIGAAGIGIIGCAIGGGCAIGIGGGAAAICCIGCGITICCCCI 405
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 344, Application US/09992598; Patent No. US20020160384A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 594
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Botstein, David
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Best Local Similarity:
Query Match:
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                                                                                                                            Sequence 1989, Application US/0954456
Sequence 1989, Application US/0954456
Sequence 1989, Application US/0954456
SERVERAL INPORMATION: Process for Identifying Anti-Cancer Therapeutic Agents US/09164456
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents US/09/054,456
FILE REPERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR PELICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR PELICATION NUMBER: US/60/235,134
PRIOR PELICATION NUMBER: US/60/235,134
PRIOR PELICATION NUMBER: US/60/235,134
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PRIOR PELICATION NUMBER: US/60/235,840
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PRIOR PELICATION NUMBER: US/60/235,840
PRIOR PELICATION NUMBER: US/60/235,863
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238 GATCCTGTTGACACCCCAACAAGGAGGAAGCCTGGGAAGTGCCCAGGAAGTGACTTAT 297
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                                                         358 GACTTGAAGTGTTGCATGGGCATGTGTGGGAAATCCTGCGTTTCCCCT 405
                                   41 11eLysiysCysCysGluGiySerCysGlyMetAlaCysPheValpro 56
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Patent No. US20020115626A1
GENERAL INFORMATION:
APPLICANT: Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
LENGTH: 594
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ORGANISM: Homo sapiens
                                                                                                                 US-09-954-456-1989
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR APPLICATION NUMBER: 60/08855
PRIOR APPLICATION NUMBER: 60/088655
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-06
PRIOR FILING DATE: 1998-06-06
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10 DICATION NUMBER: 60/088858 RIOR FILING DATE: 1998-06-11 RIOR PPLICATION NUMBER: 60/088861 RIOR APPLICATION TILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 PRIOR APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088738 PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088028
PRIOR APPLICATION NUMBER: 60/088028
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PRIOR APPLICATION NUMBER: 60/088028 DR FILING DATE: 1998-06-02
DR PILING DATE: 1998-06-02
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DR PILING DATE: 1998-06-04
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DR PILING DATE: 1998-06-04 RIOR FILING DATE: 1998-06-04 PRIOR FILING DATE: 60/088033 PRIOR APPLICATION NUMBER: 60/088029 PRIOR FILING DATE: 1998-06-04 PRIOR FILING LATION NUMBER: 60/088030 PRIOR APPLICATION NUMBER: 197-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065710
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11

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FILING DATE: 1998-06-1

PRIOR APPLICATION NUMBER: 60/090676
PRIOR PEDIGCATION NUMBER: 60/090676
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR PRIOR PLING DATE: 1998-06-25 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090862 PRIOR FILING DATE: 1998-06-26 PRIOR FILING DATE: 1938-06 (0)090431
PRIOR PEPLICATION NUMBER: 60/090435
PRIOR APPLICATION NUMBER: 60/090435
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1938-06-24
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PRIOR FILING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
PRIOR FILING DATE: 1938-06-24
PRIOR PILING DATE: 1938-06-24 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 PRIOR PILING DATE: 1238 60/090696
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION 1998-06-25 PRIOR APPLICATION NUMBER: 60/089514
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17
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TITLE OF INVENTION;
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
                                                                                                                                                                                                                                                                                                                                                                                                                                            THE REFERENCE: P. 1309111.

CURRENT APPLICATION NUMBER: US/09/990,444

CURRENT FILING DATE: 2001-11.14

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PRIOR PILING DATE: 1997-10-17

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                                                                                            Paoni, Nicholas F.
Roy, Margaret Ann
Kljavin, Ivar J.
                                  Napier, Mary A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GCTGTGGAAGGAGTTAAAGAGGGTATAGAG---AAAGCAGGGTTTGCCCAGCTGACAAC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 IleargCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
Conservative:
Mismatches:
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             R APPLICATION NUMBER: 60/090690
R APPLICATION NUMBER: 60/090690
R APLILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090694
R FILING DATE: 1998-06-25
R FILING DATE: 1998-06-25
R FILING DATE: 1998-06-25
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090696
R FILING DATE: 1998-06-25
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R APPLICATION NUMBER: 60/091544

R FILING DATE: 1998-07-01

R PELLING DATE: 1998-07-01

R FILING DATE: 1998-07-02

R APPLICATION NUMBER: 60/091519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/091633
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Grimaldi, J.Christopher
Gurney, Austin L.
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Fong, Sherman
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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R APPLICATION NUMBER: 60/088876
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R APPLICATION NUMBER: 60/089440
R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089532
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APPLICATION NUMBER: 60/090246
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090445
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FILING DATE: 1998-06-10
APPLICATION UNDRER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/089952
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090429
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FILING DATE: 1998-06-24
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                                                                                                      FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089653
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/08861
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Mismatches:
Indels:
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PRIOR FILING DATE: 1988-06-26
PRIOR FILING DATE: 1988-06-26
PRIOR FILING DATE: 1988-06-26
PRIOR PELLING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PELLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091636
PRIOR PELING DATE: 1998-07-02
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PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/09182
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PRIOR APPLICATION NUMBER: 60/09182
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PRIOR APPLICATION NUMBER: 60/09182
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090557
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090676
R APPLICATION NUMBER: 60/090678
R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090678
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                                                                                                                                                                                                                            FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
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Ferrara, Napoleone
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity:
Query Match:
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Fong, Sherman

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC69
                                                                                                                                                                                                                                FILE REFERENCE: E.O. SURLOS
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PELING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
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R FILING DATE: 1998-06-05
R PPLICATION NUMBER: 60/088202
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R APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
                                  Godowski, Paul<sup>°</sup>J.
Grimaldi, J.Christopher
                                                                                                                                                    Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                       Paoni, Nicholas F.
Gerber, Hanspeter
Gerritsen, Mary E.
                                                          Gurney, Austin L.
                                                                      Kljavin, Ivar J.
                                                                                Napier, Mary A.
                        Soddard, Audrey
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08810
R FILING DATE: 1998-06-10
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RR FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
RR FILING DATE: 1998-06-18
RAPLICATION NUMBER: 60/089908
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APPLICATION NIMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NIMBER: 60/090349
FILING DATE: 1998-06-23
             APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089440
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
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FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/078910
PRIOR PILLING DATE: 1998-03-20
PRIOR PELLING DATE: 1998-03-20
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PRIOR FILLING DATE: 1998-05-28
PRIOR PILLING DATE: 1998-05-08
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
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Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                            Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey Wood, William I.
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                                                                              Ferrara, Napoleone
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Gerritsen, Mary E.
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Napier, Mary A.
Baker, Kevin P.
Botstein, David
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                                                             Eaton, Dan L.
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R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090542
R FILING DATE: 1998-06-24
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R FLING DATE: 1998-06-24
R APPLICATION NUMBER: 60/09057
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R APPLICATION NUMBER: 60/090678
R FILING DATE: 1998-06-25
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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090696
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R APPLICATION NUMBER: 60/090862
R FILING DATE: 1998-06-26
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Publication No. US20020198148A1
BENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-09
                     FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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Query Match:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C14
                                                                                                           CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
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APPLICATION NUMBER: 60/088326
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PRIOR APPLICATION NUMBER: 60/088167

FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 LING DATE: 1998-06-12 PLICATION NUMBER: 60/089440 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 LING DATE: 1998-06-11 PLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18 FILING DATE: 1998-06-19
APPLICATION UNDBER: 60/690246
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090252 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: 60/088824 ICATION NUMBER: 60/088858 APPLICATION NUMBER: 60/088861 LICATION NUMBER: 60/089532 ING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 009680/09 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/090429 LING DATE: 1998-06-10 1998-06-10 1998-06-16 1998-06-16 FILING DATE: 1998-06-17 1998-06-17 FILING DATE: 1998-06-19 FILING DATE: 1998-06-23 FILING DATE: 1998-06-23 1998-06-1 FILING DATE: 1998-06 APPLICATION NUMBER: LING DATE: LING DATE: LING DATE: ING DATE: PRIOR
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PRIOR APPLICATION NUMBER: 60/090435
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PRIOR PLILING DATE: 1998-06-24
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PRIOR PRILING DATE: 1998-07-07
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PRIOR PRILING DATE: 1998-07-07
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Alignment Scores:
1.9e-05 Length: 76
Score: 112.00 Matches: 24
Percent Similarity: 53.57% Conservative: 6
Best Local Similarity: 42.86% Mismatches: 24
Ouery Match: 9 Gaps: 2

09-833799-13B (1-57) x US-09-990-436-344 (1-762)

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CURRENT FILING DATE: 2001-11-16
PRIOR PAPLICATION NUMBER: 00/049787
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-13
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                                                                                                          ; Sequence 344, Application US/09991181; Publication No. US20020197615A1; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/088029
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APPLICATION NUMBER: 60/088030
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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RESULT 14
US-09-991-181-344
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08824
PRIOR PILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08826
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PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/08861
PRIOR APPLICATION NUMBER: 60/08861
PRIOR APPLICATION NUMBER: 60/08861
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-11
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
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R APPLICATION NUMBER: 60/089532

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089598
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R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08810
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/089907
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119 GTACGCTGCTTCAAGTCCGATCCTCCC --- CAGTGTCACACAGACCAGGACTGTCTGGGG 175

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Alignment Scores:

Pred. No.:

Pred. No.:

112.00

Matches:

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Soore:

Percent Similarity:

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Conservative:

Best Local Similarity:

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Mismatches:

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Query Match:

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Gaps:

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09-833799-13B (1-57) x US-09-991-181-344 (1-762)

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Publication No. US20020198149A1
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Williams, P. Mickey
Wood, William I.
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Pan, James
Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                           Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                         Fong, Sherman
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762 24 6 24 22 22 Length: PRIOR APPLICATION NUMBER: 60/090254
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Matches: Conservative: Mismatches: Indels: 1.9e-05 112.00 53.57% 42.86% 34.25% Percent Similarity:
Best Local Similarity:
Query Match:
DB:

09-833799-13B (1-57) x US-09-993-687-344 (1-762)

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ITILE OF INVENTION: Secreted and Transmembrar
ITILE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2730P1664
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CURRENT FILING DATE: 2001-11-19
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US-09-989-734-344
; Sequence 344, Application US/09989734
; Publication No. US20030003531A1
; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/087827
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Botstein, David
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PRIOR APPLICATION NUMBER: 60/08861
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APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-03
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Length: Matches: Conservative:

1.9e-05 112.00 53.57%

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TITLE OF INVENTION. Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C38
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                                                                                                        1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
                                                                                                                                                                                          21 IleargCysalaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
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CURRENT APPLICATION NUMBER: 00/049787
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PELING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-03-07
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Grimaldi, J.Christopher
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Gurney, Austin L.
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Williams, P. Mickey
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Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerritsen, Mary E.
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PRIOR FILING DATE: 1998-07-09
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                                                                                                        Pred. No.: 1.9e-05
Score: 112.00
Percent Similarity: 53.57%
Best Local Similarity: 42.86%
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Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Godowski, Paul
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PRIOR FILING DATE: 1998-66-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR PLING DATE: 1998-66-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR APPLICATION NUMBER: 60/088810
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR APPLICATION NUMBER: 60/087106

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PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/088826
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PRIOR PLING DATE: 1998-06-24
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PRIOR PRILING DATE: 1998-06-25
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Publication No. US20030027754A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Paoni, Nicholas F.
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Gerber, Hanspeter
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Napier, Mary A.
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Botstein, David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/990,562
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-06-16
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Publication No. US20030027985A1
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Gurney, Austin L.
Kljavin,Ivar J.
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Watanabe, Colin K.
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Wood, William I.
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Roy, Margaret Ann
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Gerber, Hanspeter
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/088326
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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               PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-03
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Publication No. US20030027162A1
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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Grimaldi, J. Christopher
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Botstein, David
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FILE REPERENCE: P2730PLC44

CURRENT PAPLICATION NUMBER: US/09/97/428

PRIOR FILING DATE: J001-11-12

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PRIOR APPLICATION NUMBER: 60/08916
PRIOR PLILING DATE: 1998-06-11
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DR APPLICATION NUMBER: 60/090696

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DR PELING DATE: 1998-06-26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 66/091982
PRIOR PILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/091978
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Grimaldi, J. Christopher
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Stewart, Timothy A.
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Gerritsen, Mary E.
Goddard, Audrey
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Pan, James
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Botstein, David
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Eaton, Dan L.
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Tumas, Daniel
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Best Local Similarity:
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APPLICANT: Watenabe, COLIN K.
APPLICANT: Wood, Williams P. Mickey
APPLICANT: Wood, Williams P. Mickey
APPLICANT: Wood, Williams P. Mickey
APPLICANT: Zahni, Zahni, Zahni
TITLE OF INVENTION: SECRET Zahni
TITLE OF INVENTION: SECRET ZAHNI
TITLE OF INVENTION: DARGE ENCOLUSE THE SAME
TITLE OF THE PROPERTY OF MICKEY STATES THE SAME
TELLING DATE: 1997-06-16
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Patent No. US20020072067A1
GENERAL INFORMATION:
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Ferrara, Napoleone
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Goddard, Audrey
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Gurney, Austin L. Kljavin, Ivar J.

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                         Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watranabe, Colin K.
Williams, P. Mickey
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Napier, Mary A.
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Mismatches:
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R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090557

R FILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090676

R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090678

R FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/091982
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FILING DATE: 1998-07-09
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Patent No. US20020072092A1
GENERAL INFORMATION:
                                                                                                            APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090694
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FILING DATE: 1998-06-26
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APPLICATION UNDBER: 60/091478
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APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/091633
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Eaton, Dan L.
Fertrara, Mapoleone
Fong, Sherman
Gerber, Hanspeter
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLCS
CURRENT FILING DATE: 12071-11-19
RIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/062310
PRIOR PELLING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/063311
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R APPLICATION NUMBER: 60/088021

R FILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088025

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R APPLICATION NUMBER: 60/088026
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 66/088030
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088326
                                                                 Godowski, Paul J.
Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Pan, James
Paoni, Nicholas F.
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Kljavin, Ivar J.
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Gerritsen, Mary E
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PRIOR APPLICATION NUMBER: 60/08855
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PRIOR FILING DATE: 1998-06-10
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PRIOR PILING DATE: 1998-06-24
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GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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APPLICATION NUMBER: 60/090542
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APPLICATION NIMBER: 60/088326
FILING DATE: 1998-06-04
APPLICATION NIMBER: 60/088167
FILING DATE: 1998-06-05
                                                                                                                                                                                                                                               Godowski, Paul J.
Grimaldi, J. Christopher
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                              errara, Napoleone
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Kljavin, Ivar J.
Botstein, David
Desnoyers, Luc
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                                                                    Saton, Dan L.
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R FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088810
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R APPLICATION NUMBER: 60/088824
R PILING DATE: 1998-06-10
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R FILING DATE: 1998-06-19

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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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| PRIOR PILING DATE: 1998-07
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Matches:

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Percent Similarity:
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Matches:
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FILING DATE: 1998-06-04

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RESULT 26

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C65
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CURRENT FILING DATE: 2001-11-19
PRIOR PRIORATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/06216
PRIOR FILING DATE: 1997-11-12
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PRIOR PLILNG DATE: 1997-11-24
PRIOR PLILNG DATE: 1998-02-25
PRIOR PLILNG DATE: 1998-02-25
                Sequence 344, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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APPLICATION OF 06-04
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                                                                                                                                                                                                                                                                                                                                             Grimaldi, J. Christopher
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Paoni, Nicholas F.
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Kljavin, Ivar J.
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US-09-989-727-344
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PRIOR FILING DATE: 1998-06-23
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Length:

Alignment Scores:

Pred. No.:

Score:

09-833799-13B (1-57) x US-09-989-727-344 (1-762)

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  - :::||||||| 119 GTACGCTICAAGTCCGATCCTCCC---CAGTGTCACACAGACCAGACTGTCTGGGG 175 21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40 QQ

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                                  176 GAAAGGAAGTGTTGCCTGCACTGTGGCTTCAAGTGTGTGATTCCT 223
41 IleLyslysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: P2730P1C70
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CURRENT FILING DATE: 2001-11-20
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                                                                                                                                                               Sequence 344, Application US/09989731 Patent No. US20020103125A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
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PRIOR FILING DATE: 1998-06-19
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62 GCTGTGGAAGGAGTTAAAGAGGGTATAGAG---AAAGCAGGGGTTTGCCCAGCTGACAAC 118

21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40

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41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValpro 56

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R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090254

R FILING DATE: 1998-06-22

R APPLICATION NUMBER: 60/090349

R FILING DATE: 1998-06-23

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APPLICAWT: Wood, Mills and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TILE REFERENCE: P2730PIGST.

CURRENT APPLICATION NUMBER: US/09/989,732

CURRENT FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/06250

PRIOR FILING DATE: 1997-11-12

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176 GAAAGGAAGTGTTACTGCACTGTGGCTTCAAGTGTGTGATTCCT 223
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Patent No. US20020123463A1
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PRIOR FILING DATE: 1998-04-28
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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APPLICANT: Baker, Kevin P.
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Stewart, 11...
Tas. Daniel
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Patent No. US20020127576A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
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Eaton, Dan L.
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AFPLICANT: Anot, Titted. 1.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE REFERENCE: P2730P108

CURRENT APPLICATION NUMBER: US/09/990,442

CURRENT FILING DATE: 1097-06-16

PRIOR PLING DATE: 1997-06-16

PRIOR PLING DATE: 1997-10-17

PRIOR PLING DATE: 1997-11-12

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PRIOR PLING DATE: 1998-02-25

PRIOR PLING DATE: 1998-02-25
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                                                                                                                                                                                   1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                  176 GAAAGGAAGTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCCT 223
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            Length:
Matches:
Conservative:
Mismatches:
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                                                                                        Indels:
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William in Hilliams.
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Botstein, David
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                                                     Percent Similarity:
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Alignment Scores:
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R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
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R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089512

R FILING DATE: 1998-06-16

R APPLICATION NUMBER: 60/089514

PRILING DATE: 1998-06-16

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 GIACGCHGCTTCAAGTCCGATCCTCCC---CAGTGTCACACAGACCAGGACTGTCTGGGG 175
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Matches:
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CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
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Patent No. US20020132253A1
GENERAL INFORMATION:
  PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
APPLICATION NUMBER: 60/091978
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Watanabe, Colin K.
Williams, P. Mickey
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Stewart, Timothy A.
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Gerritsen, Mary E.
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R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/089947
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/089907
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LICATION NUMBER: 60/090355
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APPLICATION NUMBER: 60/090696
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091025
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Mismatches:
Indels:
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PILING DATE: 1998-07-07
PRIOR PILING DATE: 1998-07-07
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; Patent No. US20020137075A1
; GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William I.
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Paoni, Nicholas F.
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Kljavin, Ivar J.
Napier, Mary A.
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Best Local Similarity:
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RETLING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088033

R APPLICATION NUMBER: 60/088326

R FILING DATE: 1998-06-04

R FILING DATE: 1998-06-07

R FILING DATE: 1998-06-05

R FILING DATE: 1998-06-05

R APPLICATION NUMBER: 60/088202

R APPLICATION NUMBER: 60/088202

R APPLICATION NUMBER: 60/088202

R APPLICATION NUMBER: 60/088202

R APPLICATION NUMBER: 60/088202

R APPLICATION DATE: 1998-06-05 R FILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065311
R R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/066770
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/075945
R R FILING DATE: 1998-02-25
R APPLICATION NUMBER: 60/078910
R FILING DATE: 1998-03-20 R APPLICATION NUMBER: 60/087827 R FILING DATE: 1998-06-03 R APPLICATION NUMBER: 60/088021 R FILING DATE: 1998-06-04 R APPLICATION NUMBER: 60/088025 R FILING DATE: 1998-06-04 R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
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PRIOR FILING DATE: 1998-06-16
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C22
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Matches:
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                              PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091529
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091639
PRIOR PILING DATE: 1998-07-07
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Patent No. US20020137890A1
GENERAL INFORMATION:
  60/091360
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Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
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Pan, James
Paon, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Wood, William I.
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Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICATION NUMBER:
FILING DATE: 1998-07
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/04/950,456
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1999-06-25
PRIOR PELING DATE: 1998-06-26
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Gurney,Austin L.
Kljavin,Ivar J.
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Paoni, Nicholas F.
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Goddard, Audrey
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Botstein, David
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Eaton, Dan L.
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Watanabe, Colin K.

APPLICANT:

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APPLICANT: WILLIAMS P. Mickey
APPLICANT: WOOD 4 Williams P. Mickey
APPLICANT: WOOD 4 Williams P. Mickey
APPLICANT: WOOD 4 William I.
TITLE ON THWATTON WOOD 8 Encoding the Same
CURRENT FILMS ANTE: 2011.119/989,721
CURRENT FILMS ANTE: 2011.119/989,721
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RRIOR PLUCKATON WOURSE: 66/61474
RRIOR PLUCKATON WOURSE: 66/61474
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FILING DATE: 1998-06-10
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Williams, P. Mickey Wood, William I.
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PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090542

PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090557

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PRIOR FILING DATE: 1998-06-24 PRIOR FILING DATE: 1998-06-10
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PRIOR PLING DATE: 1998-06-19
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PRIOR PLING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/09045
PRIOR PRILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09045
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PRIOR PRILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/09045
PRIOR PRILING DATE: 1998-06-24
PRIOR PRILING DATE: 1998-06-24
PRIOR PRILICATION NUMBER: 60/09044
PRIOR PRILICATION NUMBER: 60/09044
PRIOR PRILICATION NUMBER: 60/0904 FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/08876
FILING DATE: 1998-06-11
FAPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 FILING DATE: 1998-06-25 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 PRIOR PRIOR

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GENERAL INFORMATION:

### APPLICANT: Young, Paul
TITLE OF INVENTION:

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REFERENCE: 692290-76

CURRENT FILING DATE: 2001-09-18

PRIOR PELICATION NUMBER: US/60/234,617

PRIOR PELICATION NUMBER: US/60/234,622

PRIOR PELILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-25

PRIOR PELILING DATE: 2000-09-26

PRIOR PELILING DATE: 2000-09-26

PRIOR PELING DATE: 2000-09-27

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 nProProAsnArgCysLeuLysAspThrAspCysProGly11eLysLysCysCysGluGl
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Mismatches:
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Matches:
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; Patent No. US20020115057A1
; GENERAL INFORMATION:
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OTHER INFORMATION: n=a,t,g or c
                                                                                                    FEATURE:
NAME/KEY: misc_feature
NCATION: (1)...(411)
OTHER INFORMATION: n=a,t,g or c
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107.00
48.00%
42.00%
32.72%
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NUMBER OF SEQ ID NOS: 2276
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                                 TYPE: DNA ORGANISM: Homo sapiens
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LENGTH: 411
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CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
RIOR FILING DATE: 2000-09-28
RIOR FILING DATE: 2000-09-28
RIOR FILING DATE: 2000-09-28
RIOR SEQ ID NOSE: 583
SOFTWARE: Patentin Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 IleargCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu 20
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Matches:
Conservative:
Mismatches:
Indels:
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                          PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR APLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PELING DATE: 1998-07-02
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112.00
53.57%
42.86%
34.25%
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Best Local Similarity:
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22 ArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlylle 41
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                                                                                                                                                                              APPLICANT: Algate, Paul A.
APPLICANT: Algate, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
CURRENT PAPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SEG ID NO 377
LENGTH: 292
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GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c5
CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT APPLICATION NUMBER: 09/866,050
PRIOR PILING DATE: 2000-05-24
PRIOR PLILNG DATE: 2000-07-25
PRIOR PLILNG DATE: 2000-07-25
PRIOR PLILNG DATE: 2000-07-25
PRIOR PLILNG DATE: 1999-04-29
PRIOR PLILNG DATE: 1999-05-14
PRIOR PLILNG DATE: 1999-05-14
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PRIOR PLILNG DATE: 1999-05-14
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Conservative:
Mismatches:
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                                                                     ; Sequence 377, Application US/0988441; Patent No. US20020119158A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 589, Application US/10152661; Publication No. US20030022835A1; GENERAL INFORMATION:
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105.00
57.14%
51.43%
32.11%
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                        US-09-884-441-377
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LENGTH: 724
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## Patent No. US20020150877A1

## GENERAL INFORMATION:
## APPLICANT: Augustus, Meena
## TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
## TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
## TITLE OF INVENTION: Sets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 CCAACAAGGNGNAACCCTTGGNAAGTNCCNAGTGANTTNTGGCCAATGTTNGATGCTNAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 CCCCCCCAATTTCTGTGAGATGGATGGCCAGTGCAAGCGTGACTTGAAGTGTTGCATGGG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 CCAACAAGGNGNAACCCTTGGNAAGTNCCNAGTGANTTNTGGCCAATGTTNGATGCTNAA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 CCCCCCCAATTCTGTGAGATGGATGGCCAGTGCAAGCGTGACTTGAAGTGTTGCATGGG 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 nProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGl 47
                                                                                                                                                                                                                                                                                                                                                                                         8 ProValSerThrLysProGlySerCysPro-IlelleLeulleArgCysAlaMetLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 ProValSerThrLysProGlySerCysPro-IlelleLeulleArgCysAlaMetLeuAs
                                Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
                                                                                                                                                                                                                                                                                                            09-833799-13B (1-57) x US-09-954-456-1987 (1-411)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
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                                                                                                                                                                                                                               Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 CATGTGTGGGAAATCCTGCGTTTCCCCT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 ySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 ySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(411)
; OTHER INFORMATION: n=a,t,g or c
US-09-967-768A-3
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42.00%
32.72%
                                3.58e-05
107.00
48.00%
42.00%
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Best Local Similarity:
                                                                                                             Percent Similarity:
Best Local Similarity:
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US-09-967-768A-3/c
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Alignment Scores:
Pred. No.:
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                                                                                                                                                                                          Query Match:
DB:
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GENERAL INFORMATION:
APPLICANT: Fenn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
ITILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO ALOSO348.19
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
US-09-864-761-1629
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SEQ ID NO 1629
LENGTH: 469
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: U5/09/664,761

CURRENT FILING DATE: 2001-05-23

PRIOR PEDICATION NUMBER: U5/09/664,761

CURRENT FILING DATE: 2000-05-20

PRIOR APPLICATION NUMBER: U5 60/207,456

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-26

PRIOR FILING DATE: 2000-06-3

PRIOR PELING DATE: 2000-09-07

PRIOR PELING DATE: 2000-09-07

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

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PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                           ; Sequence 1629, Application US/09864761
; Patent No. US20020048763A1
                                376 AAGGIGICCIGIGICACICCC 396
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ORGANISM: Homo sapiens
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Percent Similarity:
                                                                                                                   US-09-864-761-1629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE REPRENCE: 68230-72
CURRENT FILING DATE: 2001-09-28
CURRENT FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR PLILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
SOFTWARE: PALENTION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NOS: 325
SOFTWARE: PALENTIN VERSION 3.0
LENGIN 0.214
TUBDE: NAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 GTCCGAGAAAAGCAGGCACCTGCCCCAGGGGGGACATACCCAAGCTCGGCCTCTGT--- 429
                                                                                                                                                                                                                                                                                                                                                                                                                          313 AAAĊĊACCGGGAĠĠTCAAĠŦĊŦĊĊAĊĠAAĠĊĊACCGGCTGTGACCAGGGAAGGCTTAGGT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 ------GAGGACCAGTGTCAGGTGACAGCCAGTGTTCTGGCAACATGAATGC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AAGGAGGITICCIGCCCCAGGIGAACATTAACTTICCCCAGCTCGGCCTCTGTCGGGAC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 CAGTGCCAGGTGGACACGCAGTGTCCTGGCCAGATGAAATGCTGCCGCAATGGCTGTGGG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 MetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly1leLysLysCys 44
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Mismatches:
Indels:
                                                                                                                Length:
Matches:
Conservative:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 214, Application US/09967768A Patent No. US20020150877A1 GENERAL INFORMATION:
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                                                                                                                                                                43.24%
33.78%
29.97%
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                                                                                                                                                                                                    Best Local Similarity:
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  ORGANISM: Mouse
                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-967-768A-214
     ; OKGANISH: MCC.
US-10-152-661-589
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                                                                                   Alignment Scores:
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DB:
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                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
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Length:
Matches:
Conservative:
Mismatches:
Indels:
       184 TGCTGTAGCAATAGCTGTGGTCATGTCTGCAAAACTCCT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 recreradeanáciereserenereseananeere 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 CysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-833799-13B (1-57) x US-09-823-038A-29 (1-437)
                                                                     US-09-823-038A-29; Sequence 29, Application US/09823038A; Patent No. US20020058335A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/09790264 Patent No. US20020028508A1 GENERAL INFORMATION:
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41.51%
35.85%
28.90%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-823-038A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.:
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Batent No. US200200285081

GENERAL INFORMATION:

APPLICANT: HOLICEMAN.

APPLICANT: Goodearl, Andrew D.J.

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: USES

FILE REFERENCE: 07334-322001

CURRENT APPLICATION NUMBER: US/09/790,264

CURRENT FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-04-23

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

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PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

PRIOR FILING DATE: 1998-07-29

NUMBER OF SEQ ID NOS: 68
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288 CTGGTGGGCCTGTGCATTGTTGGC------TGTGTGATGATGAATTGTCAA 335
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                                                                                                                                                                                                           20 LeulleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysPro 39
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                                                                                                                                                                                                                                                                                                                                                       336 GCTGGAGAAAAİGİTİĞCAAGTCAGGCİĞİĞĞCGGCTTCİĞİGTCCCACCA 386
                                                                                                                                                                                                                                                                                                             40 GlyIleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
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Mismatches:
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                                                                     09-833799-13B (1-57) x US-09-864-761-1629 (1-469)
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Matches:
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Indels:
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                                                                                                                    4 ProvalLysGlyProvalSerThrLysPro----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mus musculus
US-09-790-264-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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Pred. No.:
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Query Match:
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GENERAL INCURARATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
FILE REPERENCE: 07334-322001
CURRENT APPLICATION NUMBER: US 09/05,64
CURRENT FILING DATE: 1998-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
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PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-04-23
PRIOR PELLING DATE: 1999-06-22
PRIOR PELING DATE: 1999-06-22
PRIOR PELLING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 09/363,630
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GENERAL INCORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Abernerly, Nevin
APPLICANT: Contust, Rene
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1037c3
CURRENT APPLICATION NUMBER: US/09/823,038A
CURRENT APPLICATION NUMBER: US/09/823,038A
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 LysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProPro--
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114
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Best Local Similarity:
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LOCATION: 1..90
NAME/KEY: CDS
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US-09-992-600A-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------AAGCCTTCACCAGAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AGTGTTGGAATTTGTGTTGATCAATGCTCAGGAGATGGATCCTGCCCTGGCAACATGAAG 219
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APPELICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PATCHILIN Ver. 2.0
SEQ ID NO 421
LENGTH: 622
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Conservative:
Mismatches:
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                            Length:
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 421, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
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40.43%
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41.51%
35.85%
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ORGANISM: Homo sapiens
US-09-925-300-421
                                                                                                                              TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                   ; LOCATION: (37)...(264)
US-09-790-264-55
                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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US-09-925-300-421
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                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                             Aliqnment Scores:
                                                                                              SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                   Query Match:
DB:
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316 AAGGAGGCTTCCTGCCCCCAGGTGAACATTAACTTTCCCCAGCTCGGCCTCTGTCGGGAC 375
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                                              348 CAGTGCCAGGTGGACAGCCAGTGTCTGGCCAGATGAATGCTGCCGCAATGGCTGTGGG 407
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Benaka, Hiroaki
APPLICANT: Fanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.02.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT APPLICATION NUMBER: US/09/924,340
FRIOR APPLICATION NUMBER: US/0305,456
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR PLILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US/02/93,574
PRIOR APPLICATION NUMBER: US/02/23,574
PRIOR APPLICATION NUMBER: US/02/23,574
PRIOR APPLICATION NUMBER: US/02/23,574
PRIOR APPLICATION NUMBER: US/02/23,574
PRIOR PILING DATE: 2001-06-15
SOFTWARE: UPACENT.
SEQ ID NOS: 112
LENGTH: 643
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/0992600A; Publication No. US20030027161A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 ; Sequence 41, Application US/09924340; Publication No. US20030027248A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 AAGGIGICCTGTGTCACTCCC 456
                                                                                                                                                     408 AAGGIGICCTGTGTCACTCCC 428
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                                                                                                         51 ---MetAlaCysPheValPro 56
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53.19%
40.43%
28.44%
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NAME/KEY: 3'TTR
LOCATION: 463..643
NAME/KEY: polyA signal
LOCATION: 607..612
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LOCATION: 607..u.c
NAME/KEY: polya site
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12 LysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsn---ProProAsn 30
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Publication No. US20030013099A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Lasek, David A.
APPLICANT: Tarpf, Agam R.
ITILE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS FILE REFERENCE: PA-0047 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SUPPLIANCE
FILE REFERENCE: 91.034.DIV
FURENT APPLICANTON: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FURENT APPLICATION WUMBER: US/09/992,600A
CURRENT APPLICATION WUMBER: US 09/924,340
FRIOR PEDITON NUMBER: US 09/924,340
FRIOR FILING DATE: 2001-08-06
FRIOR FILING DATE: 2001-08-06
FRIOR FILING DATE: 2001-08-06
FRIOR FILING DATE: 2001-08-06
FRIOR PLING DATE: 2001-08-06
FRIOR APPLICATION NUMBER: US 60/302,277
FRIOR APPLICATION NUMBER: US 60/302,277
FRIOR APPLICATION NUMBER: US 60/298,698
FRIOR PELING DATE: 2001-06-15
FRIOR PELING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
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FRIOR FILING DATE: UP ONCE: 114
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ---MetAlaCysPheValPro 56
APPLICANT: Benjanin, Stephane
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LOCATION: 463..643
FABTURE:
NAME/KEY: polyA signal
LOCATION: 607..612
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; LOCATION: 628..643
US-09-992-600A-41
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Best Local Similarity:
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LOCATION: 91..462
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LOCATION: 1..90
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LENGTH: 643
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FILE REFERENCE:
GENERAL SETS
FILE REFERENCE:
GENERAL APPLICATION NUMBER:
US/09/954,456
CURRENT FILING DATE:
2001-09-18
FRIOR APPLICATION NUMBER:
US/60/233,617
FRIOR APPLICATION NUMBER:
US/60/234,052
FRIOR APPLICATION NUMBER:
US/60/234,923
FRIOR PELING DATE:
S000-09-26
FRIOR APPLICATION NUMBER:
US/60/235,637
FRIOR PELING DATE:
S000-09-26
FRIOR APPLICATION NUMBER:
US/60/235,637
FRIOR PELING DATE:
S000-09-26
FRIOR APPLICATION NUMBER:
US/60/235,711
FRIOR APPLICATION NUMBER:
US/60/235,711
FRIOR APPLICATION NUMBER:
US/60/235,711
FRIOR APPLICATION NUMBER:
US/60/235,731
FRIOR PELING DATE:
S000-09-26
FRIOR APPLICATION NUMBER:
US/60/235,840
FRIOR FILING DATE:
US/60/235,863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471 AAGGAGGTTCCTGCCCCCAGGTGAACATTAACTTTCCCCAGCTCGGCCTCTGTCGGGAC
                                                                                                                                                                                                                                                                                                                    | NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20030013099A1 1383215.32
| US-10-093-766-57
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/10/093,766
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 57
LENGTH: 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 AAGGTGTCCTGTCACTCC 611
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93.00
53.19%
40.43%
28.44%
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-09-954-456-319
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
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                                                                                                                                                                  595 ------GAAAGCTGCGAAGTTGACAATGAGTGCTCTGGGGTGAAGAATGTGT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VallysGlyProValSerThrLys-----ProGlySerCysProllelleLeulle 21
26 LeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCys
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/09852797
Sequence 34, Application US/09852797
Sequence 34, Application US/09852797
GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT APPLICATION NUMBER: 00/265,583
PRIOR APPLICATION NUMBER: 00/265,583
PRIOR PILING DATE: 1001-02.02
PRIOR FILING DATE: 1998-09.11
PRIOR FILING DATE: 1998-09.11
PRIOR FILING DATE: 1998-09.12
PRIOR PILING DATE: 1997-03.14
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Mismatches:
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                                                                                                                                                                                                                                                                                                         643 rcgaargggrigigacacaccrgrcaagraccaag 678
                                                                                                                                                                                                                                           46 GluGlySerCysGlyMetAlaCysPheValProGln 57
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US-09-852-797-34
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JAPPLICART: Young, Pau;

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

CURRENT FILING DATE: 2001-09-18

PRIOR PELING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-25

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PRIOR PELING DATE: 2000-09-27
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Conservative:
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Matches:
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PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1230, Application US/09954456 Patent No. US20020115057A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity:
Query Match:
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                                                              Alignment Scores:
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85 GTCCAGGGACCTGGTCTGATTGGTTATTTCCCAGGAGATGTCCCCAAAATCAGAGAA 144
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Conservative:
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202 AAGAAGTGTTGTCTTCAGCTGCGGAAAAATGT 237
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Sequence 34, Application US/09852659A

Patent No. US20020077287A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins
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                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: PZ003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
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PRIOR PELING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-14
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PRIOR PELING DATE: 1997-05-30
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PRIOR PELING DATE: 1997-09-05
PRIOR PELING DATE: 1997-09-05
PRIOR PELING DATE: 1997-06-06
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PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN VET: 2.0
                                                                 US-09-853-161-34
; Sequence 34, Application US/09853161; Patent No. US20020076756A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-853-161-34
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LENGTH: 753
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Patent No. US20020172994A1
GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PS003P2
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-12
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FILE REFRENCE: PZ003.P4

CURRENT PELLICATION NUMBER: US/09/852,659A

CURRENT FILING DATE: 2001-05-11

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 1908-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR PELLING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR APPLICATION NUMBER: PC7/US98/04858

PRIOR PELLING DATE: 1998-03-12

PRIOR PELLING DATE: 1997-03-14

PRIOR PELLING DATE: 1997-03-14

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Best Local Similarity:
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US-09-852-797-50
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85 GTCCAGGGACCTGGTCTGACTGATTGGTTATTTCCCAGGAGATGTCCCAAAATCAGAGAA 144
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Mismatches:
Indels:
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Matches:
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PRIOR PELING DATE: 2001-02-02
PRIOR PELING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 1998-09-11
PRIOR PILING DATE: 1998-09-11
PRIOR PLING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR PELING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,100
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR APPLICATION NUMBER: 60/048,100
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CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
                     PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/040,710

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR PILING DATE: 1997-05-30

PRIOR PILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR PILING DATE: 1997-05-30

PRIOR PILING DATE: 1997-05-30

PRIOR PILING DATE: 1997-05-30

PRIOR PILING DATE: 1997-05-05

PRIOR PAPLICATION NUMBER: 60/048,970

PRIOR PLING DATE: 1997-06-05

PRIOR PLING DATE: 1997-06-06

PRIOR PLING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR PILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 50

LENGTH: 783
APPLICATION NUMBER: 60/040,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50, Application US/09853161 Patent No. US20020076756A1
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; ORGANISM: Homo sapiens
US-09-852-797-50
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Pred. No.:
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85 GICCAGGGACCIGGICIGACIGAIIGGITAIIICCCAGGAGAIGICCCAAAAICAGAGAA 144
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Sequence 50, Application US/09852659A

Patent No. US20020077287A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 2001-05-11

PRIOR FILING DATE: 1090-11

PRIOR FILING DATE: 1990-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-09-11

PRIOR FILING DATE: 1998-03-12

PRIOR FILING DATE: 1998-03-12

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-03-14

PRIOR FILING DATE: 1997-05-30

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PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR PAPLICATION NUMBER: 60/048,100

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

PRIOR FILING DATE: 1997-05-30

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PRIOR FILING DATE: 1997-05-30
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Mismatches:
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                    PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR PELING DATE: 1997-05-30
PRIOR PILING DATE: 1997-09-05
PRIOR PILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SEG ID NO 50
LENGTH: 783
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PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
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PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-05-30
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COGGANISM: Homo sapiens
US-09-853-161-50
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Best Local Similarity:
Query Match:
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85 GTCCAGGGACCTGGTCTGATTGGTTATTTCCCAGGAGATGTCCCAAATCAGAGAA 144
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21
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Matches:
Conservative:
Mismatches:
Indels:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPULICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT FILING DATE: 2001-05-11
PRIOR FLUING DATE: 2001-05-13
PRIOR FLUING DATE: 1998-09-11
PRIOR FLUING DATE: 1998-09-11
PRIOR FLUING DATE: 1998-03-12
PRIOR FLUING DATE: 1998-03-12
PRIOR FLUING DATE: 1998-03-12
PRIOR FLUING DATE: 1997-03-14
PRIOR FLUING DATE: 1997-03-14
PRIOR FLUING DATE: 1997-03-14
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PRIOR FLUING DATE: 1997-05-30
PRIOR FLUING DATE: 1997-05-30
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PRIOR FLUING DATE: 1997-05-30
PRIOR FLUING DATE: 1997-05-30
PRIOR FLUING DATE: 1997-10-10-10
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44.23%
40.38%
25.99%
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 50
LENGTH: 783
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SEQ ID NO 121
LENGTH: 354
                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
US-09-852-659A-50
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Best Local Similarity:
Query Match:
DB:
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Alignment Scores:

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APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs FILE REPREBNCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT PILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 747

LENGTH: 334
                                                                                                                                                                                                                                                                                                                                         100 AAGGACAGACAATGCCAGGACAACAAGAAGTGTTGTGTCTTCAGCTGCGGAAAAAATGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 AGCCCGCCGCGGGAGCGCTTCATGTTGCGGAAATACTGCCCCCAGCGCTGCGGGGCCGGCG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 AAGAAGCCATTGGCCGGGCCCATTTCCGCCAAGGAAGGCTCATCGGGGAAGGAGACCCTC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 GGGAGATGTCCCAAAATCAGAGAATGTGAA---TTCCAAGAAAGGGATGTGTGTAACA 99
                                                                                                                                                                                                                                                                                                 34 LysaspThraspCysProGlylleLysLysCysCysGluGlySerCysGlyMetalaCys 53
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                                                                                                                                                                                                       14 GlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsnArgCysLeu 33
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20
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21
13
                     Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
Mismatches:
Indels:
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; Patent No. US20020132090A1
; GENERAL INFORMATION:
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GENERAL INFORMATION: DARREL INFORMATION: DARREL INFORMATION: DARREL CONKIN, DARRELL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(334)
CSATION: INFORMATION: n = A,T,C or
US-09-833-381-747
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78.50
45.16%
32.26%
24.01%
0.064
80.50
45.00%
42.50%
24.62%
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Best Local Similarity:
Query Match:
                                            Percent Similarity:
Best Local Similarity:
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Pred. No.:
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                                                                                         Query Match:
Pred. No.:
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439 TTGCTGCCAGGGCAGGCAGCCGGGGGGGGGGGGCCCCAACCAGCTCAGCCCCAACCTG 498
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TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
FILE REFERENCE: 00-25
CURRENT APPLICATION NUMBER: US/09/819,136
CURRENT FILING DATE: 2001-03-27
FRIOR APPLICATION NUMBER: US 60/193,642
FRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1.
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Matches:
Conservative:
Mismatches:
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Patent No. US20020102607A1
GENERAL INFORMATION:
APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
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APPLICANT: Shen, Greg S.
TITLE OF INVENTION: I-Superfamily Conotoxins FILE REFERENCE: 2114-238
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US 60/29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR FILING DATE: 2000-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GluProValLysGlyProValSerThrLysProGly---
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PPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
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74.50
36.26%
26.37%
22.78%
                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (376)...(2022)
                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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Mismatches:
Indels:
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APPLICANT: University of Utah Research Foundation
APPLICANT: Cognetix, Inc.
APPLICANT: Walker, Craig S.
APPLICANT: Shetty, Reshma
APPLICANT: Jimenez, Elsie C.
APPLICANT: McIncash, J. Michael
APPLICANT: Olivera, Baldomero M.
APPLICANT: Watkins, Maren
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CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT APPLICATION NUMBER: US/09/894,882
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/243,410
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-37
PRIOR FILING DATE: 2000-11-48
PRIOR APPLICATION NUMBER: US 60/245,581
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR APPLICATION NUMBER: US 60/247,714
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
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Matches:
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                     PRIOR FILING DATE: 2000-11-14
PRIOR PILING DATE: 2000-11-18
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 506
SOFTWARE: Patentin version 3.0
SEQ ID NO 240
LENGTH: 243
PRIOR APPLICATION NUMBER: US 60/247,714
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Shen, Greg S.
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54.17%
37.50%
22.48%
                                                                                                                                                                                                         TYPE: DNA; Conus emaciatus US-09-894-882-240
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LENGTH: 243
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Pred. No.:

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TITLE OF INVENTION: Methods For Monitoring Multiple Gene
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Best Local Similarity:
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Query Match:
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LENGTH: 2937
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LENGTH: 753
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APPLICANT: Olga Bandman

TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US

CURRENT APPLICATION NUMBER: US/10/044,090

CURRENT APPLICATION NUMBER: 2002-01-09

NUMBER OF SEQ ID NOS: 850

SOFTWARE: PERL PROGram
                                                                                                                                                                                                15 SerCysProlleIleLeuileArgCysAla---MetLeuAsnProProAsnArgCysLeu 33
                                                                                                                                                                              34 LysAsp---ThrAspCysProGlyIle------LysLysCysCysGluGly 47
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                                                                                                                                 25 AGCTGTTTCCTACTGGTCATCGTTTGTCTGAACTTGATTGTGTTATCAATGCCTGCTAC
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OTHER INFORMATION: Incyte ID No. US20020137081A1 198795.2
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            Conservative:
Mismatches:
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Mismatches:
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                                                                                    09-833799-13B (1-57) x US-09-894-882-249 (1-243)
 Matches:
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Matches:
                                            Indels:
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; Sequence 2288, Application US/09974300
; Patent No. US20020146721A1
; PALERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
                                                                                                                                                                                                                                                                                                                                   Sequence 750, Application US/10044090 Patent No. US20020137081A1
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145 ACATGCAGATTTCCGTGTTACGTT 168
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71.00
55.81$
32.56$
21.71$
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ORGANISM: Homo sapiens
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         Percent Similarity:
Best Local Similarity:
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LOCATION: 106
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LENGTH: 3836
                                         Query Match:
DB:
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2355 AGCTGCCCCACAGGAAGCTGTTCCATCCTTCAATTGCGT-----CATAATCGGCT 2305
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Sequence 661, Application US/09910943

Parent No. US20020081610A1

GENERAL INFORMATION:
APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REPERBNCE: 7529/16148U3.
CURRENT APPLICATION NUMBER: US/09/910,943

CURRENT FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 742

SOFTWARE: Patentin version 3.1
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Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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TITLE OF INVENTION: EXPRESSION FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT TILING DATE: 2001-10.05
PRIOR PLICATION NUMBER: 09/680,598
PRIOR PILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
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Gaps:
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LOCATION: (1). (753)
OTHER INFORMATION: n may be a or g
                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2288
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37.25%
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TYPE: DNA
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; Sequence 18387, Application US/09864761
; Sequence 18387, Application US/09864761
; Fatert No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Rank, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REPRENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 261507 decadececececedarices as as as a series as a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a series and a se
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1 AlaGluProValLys-----GlyProValSerThrLysProGly-SerCysPr 17
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                                                                                                                                                                                                                                                        475 CAGACTIGGAATITICCAACTGGAAAGAGCIGIGGAAAGCAICAAAACTGICCIGGC 418
                                                                                                                                                                21 eArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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CURRENT FILING DATE: 2001-08-21

PRIOR PELING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-34

PRIOR PLING DATE: 2001-01-34

PRIOR APPLICATION NUMBER: 09/804076

PRIOR PLING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: 09/8026314

PRIOR PLING DATE: 2001-03-13

PRIOR PLING DATE: 2001-03-13
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Mismatches:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-933-267A-1/c
; Sequence 1, Application US/09933267A
; Patent No. US20020123095A1
; GENERAL INFORMATION:
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CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
CTHER INFORMATION: EXPRESSED IN BORE MARROW, SIGNAL = 1.1
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
CTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
CTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
CTHER INFORMATION: MITT: B1910609.1, EVALUE 5.00e-78
CTHER INFORMATION: WISSPROT HIT: 046655, EVALUE 5.00e-05
US-09-864-761-18387
                                          PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-09-03
PRIOR PILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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Query Match:
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Sequence 225, Application US/09962832
Patent No. US20020110821A1
Sequence 225, Application US/09962832
Patent No. US20020110821A1
SAPELICANT: EDNEY Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatun TITLE OF INVENTION: Sets
FILE REFERENCE: 669290-74
CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
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EXPRESSED IN PLACENTA, SIGNAL = 1.6
EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
EXPRESSED IN BRAIN, SIGNAL = 1.4
EXPRESSED IN BRAIN, SIGNAL = 1.4
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SEQ ID NO 12659
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
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PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117.
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OTHER INFORMATION: EXPRESSED IN LUNG,
OTHER INFORMATION: EXPRESSED IN PLACE
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-962-832-225/c
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Sequence 12659, Application US/09864761

Patent No. US20020048763A1

GENERAL INPORMATION:

APPLICANT: Pana. Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR PELING DATE: 2000-06-26

PRIOR PELING DATE: 2000-06-06

PRIOR PELING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-07

PRIOR FILING DATE: 2001-01-07

PRIOR FILING DATE: 2001-01-07
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                                                     Sequence 198, Application US/09884441

Barent No. US20020119158A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: ONGOSITIONS OF OVARIAN CANCER FILE REFERENCE: 210121.46207
CURRENT APPLICATION NUMBER: US/09/884,441

CURRENT FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
Indels:
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Matches:
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OTHER INFORMATION: n = A,T,C or G
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69.00
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37.50%
21.10%
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                          US-09-884-441-198/c
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24 AlametLeuAsnProProAsn----ArgCysLeuLysAspThrAspCysProGly1le 41
                                     Db 291916 ccraidirroccagggcrridddaiddcicarggccccagccccidccrcdriroccaA 291973
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--CysPheValProGln
                                                                                                                                                                                                                                                                                                       APPLICANT: CHAIL, GERUL U.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1040-104
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-16
NUMBER OF SEQ ID NOS: 14110
SCOFUTANE: FRAESEQ FOR WINGOWS VERSION 4.0
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Mismatches:
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                                                                                     RESULT 71
US-09-815-242-7863/c
; Sequence 7863, Application US/09815242
; Patent No. US2002061569A1
; GENERAL INFORMATION:
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US-09-891-216-6/c
; Sequence 6, Application US/09891216
        43 sCysCysGluGlySerCysGlyMetAla-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W. APPLICANT: Trawick, John D. APPLICANT: Carr, Grant J. APPLICANT: Carr, Grant J.
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34.69%
20.18%
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APPLICANT: Ebner. Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE REPERENCE: 689290-74
CURRENT APPLICATION NUMBER: US/69/235,077
PRIOR PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.0
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Matches:
Conservative:
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Matches:
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    PRIOR FILING DATE: 2000-09-25
PRIOR PEDLICATION NUMBER: US660/235,280
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.0
SEQ ID NO 225
LENGTH: 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 154, Application US/09962832 Patent No. US20020110821A1 GENERAL INFORMATION:
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US-09-962-832-154
                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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LENGTH: 302250
                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                      TYPE: DNA
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6056 GAGTGTGTCGCCCTTCCCGGCTCTTGCTCCTGGTACCTGTCAGAATTTGGAGGATCC 6115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 IleLysLysCysCysGlu------49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
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; OTHER INFORMATION: Incyte ID No. US20020156263A1 1098479.1
US-09-974-298-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER FILE REFERENCE: PA-0037 P CURRENT APPLICATION NUMBER: US/09/974,298 CURRENT FILING DATE: 2001-10-04 PRIOR APPLICATION NUMBER: 60/238,331 PRIOR FILING DATE: 2000-05-10 NUMBER OF SEQ ID NOS: 194 SOFTWARE: PERL PROGram SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                              Length:
  PRIOR APPLICATION NUMBER: US/60/235,863
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Patent No. US20020156263A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 --- GlyMetAlaCysPheValPro 56
                          PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 702
                                                                                                                                                                                                                                                                                                                                  66.00
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CRGANISM: Homo sapiens
US-09-954-456-702
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TITLE OF INVENTION:

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sete

TITLE OF INVENTION: Sete

TITLE OF INVENTION: Sete

TITLE OF INVENTION: Sete

CURRENT PAPLICATION NUMBER: US/09/954,456

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

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PRIOR PRIOR DATE: 2000-09-26

PRIOR PRIOR DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,711

PRIOR PRIOR DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,720

PRIOR APPLICATION NUMBER: US/60/235,720

PRIOR PRIOR DATE: 2000-09-27

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                    GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human
TITLE OF INVENTION: Phosphodisterase-Like Enzyme
TITLE OF INVENTION: Phosphodisterase-Like Enzyme
TITLE OF INVENTION: Phosphodisterase-Like Enzyme
TITLE OF INVENTION: 20273.00511
CURRENT APPLICATION NUMBER: US/09/891,216
CURRENT FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/293,221
PRIOR FILING DATE: 2001-05-25
PRIOR PLICATION NUMBER: QS 00/293,221
PRIOR PLICATION NUMBER: QS 00/293,221
PRIOR PLICATION NUMBER: QS 00/293,221
PRIOR PLICATION NUMBER: QS 00/293,221
PRIOR PRIOR APPLICATION NUMBER: QS 00/293,221
SROFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
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Patent No. US20020115057A1
GENERAL INFORMATION:
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Patent No. US20020103120A1
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US-09-891-216-6
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Sequence 47, Application US/10044090
Sequence 47, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT PILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 47
LENGTH: 10284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6056 GAGTGTCGCCCTTCCCGGCTCTTGCTCTCCTGGTACCTGTCAGAATTTGGAGGATCC 6115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6116 TTCAGATGC----ATCTGTCCCCCAGGGTATGAAGTAAAAAGCGAGAACTGCATTGAT 6169
                                                                                                      6170 ATAAATGAATGTGATGAAGATCCCAACATTTGTCTTTTTGGTTCCTGTACTAATACTCCA 6229
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21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                           ------GlySerCys------ 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
COTHER INFORMATION: Incyte ID No. US20020137081A1 1098479.1
US-10-044-090-47
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Matches:
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Job time : 181 secs
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                                                                           41 IleLysLysCysCysGlu---
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Best Local Similarity:
Query Match:
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February 15, 2003, 21	:14:47 ; Search time 704.5 Seconds (without alignments) 8509.834 Million cell updates/sec
Title: 09-833799-13A Perfect score: 206 Sequence: 1 AATTCGAGCTCGGTACCATA	AGTTTCGTTCCACAATAAIAG 206
Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.	0.
Searched: 2054640 seqs, 14551402878	878 residues
Total number of hits satisfying chosen	1 parameters: 4109280
Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 sum	summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	A31086 A31087	E16036 I96047		AX397178 AX041087		A31090	1/4318 BC010952	196048	HUMELAFIN	AX334316	HUMPREELAS		30 68		A31088	1201				7	12					-	10	A310/8 AB003282	PIGWAPE	AB011010 PIGWAPC	AB003285			AC006054	ACU9664/ PIGALP	MMU88	MMU94	MMU73	AC1106	AC1006/9	AL136380	AC1161	AF002 A1.6628	ALS90429	AC021992	HS319F24 AC104349	
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AC126796 Mus muscu
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AC092960 F
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AC117109
AC006377
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AC116099
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AC108282 B
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AC004054 B
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AC123297
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AC012181
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AC004054
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                 AC126796
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## ALIGNMENTS

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1 (bases 1 to 206)
Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D. Polypeptides and polypeptide analogues with inhibitory activity against human elasteas Patent: EP 0402068-A 27 12-DEC-1990; IMPERIAL CHEMICAL INDUSTRIES PLC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTAAGCCAGGITCTTGICCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTA 60
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/db_xref="taxon:32630"
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                                                  DNA fragment from patent EP0402068.
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ELAFINS-EXPRESSION VECTOR AND PRODUCTION OF ELAFINS BY UTILIZING
THE SAME
PATENT: JP 1998127292-A 1 19-MAY-1998;
TSUMURA & CO
OS Pichia pastoris
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Saccharomycetales; Saccharomycetaceae; Pichia.
1 (bases 1 to 8598)
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                                  121 GTIGITIGAAGGACACIGATIGICCAGGIATCAAAAAGIGCIGIGAAAGGITCCIGCGGIA 180
61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
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45 c 47 g
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artificial sequences.
1 (bases 1 to 206)
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Sequence 1393 from Patent WO0212328.
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49 c 47 g
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                                    TANIYAMA MITSUE, YAMAMOTO TAKASHI, OKAWA NORIYUKI, PI
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1 (bases 1 to 177)

1 shima, Y., Okawa, N., Yoshida, M., Amagaya, S. and Kaji, A. Elafin derivative
Patent: US 5734014-A 3 31-MAR-1998;

Location/Qualifiers
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                                                                                                                                                                                                                                                              /product='improved Pichia elafin'
replace(1276. .1278,'atg')
/note='native Pichia elafin'.
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/Conne='pPIC9/ELF25L'
949. .1377
/product='improved Pichia elafin'
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61.7%; Score 127; DB 6; Length 8598;
Best Local Similarity 82.9%; Pred. No. 9.1e-29;
Matches 145; Conservative 0; Mismatches 30; Indels
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/organism="Pichia pastoris"
/db_xref="taxon:4922"
/ 2025 c 1920 g 2347 t
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Sequence 3 from patent US 5734014.
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JP 1998127292-A/1
19-MAY-1998
31-OCT-1996 JP 1996304233
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                                                                       C12R1:84),
PC (C12P21/02,C12R1:84);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
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82.3%;
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PAT 01-DEC-1998
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                 90 ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT 149
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90 ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT
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1 (bases 1 to 177)
1 (bases 1 to 177)
1 ishima,Y., Okawa,N., Yoshida,M., Amagaya,S. and Kaji,A.
Blafin derivative
Patent: US 5734014-A 7 31-MAR-1998;
Location/Qualifiers
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Query Match

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FEATURES

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/evidence-experimental
/podduct="skin-derived antileukoproteinase"
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/db_xref="g1:28712";
/db_xref="sw18S-PROT: P19957"
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DPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic construct
artificial sequences.
1 (bases 1 to 504)
Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D.
Polypeptides and polypeptide analogues with inhibitory activity
against human elastase
Patent: EP 0402068-A 31 12-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 240
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                 keratinocytes. Purification, cDNA sequence, and evidence for transglutaminase cross-linking
J. Biol. Chem. 268 (16), 12028-12032 (1993)
93280175
                                                                                                                                                                                                       Submitted (20-NOV-1992) Molhuizen H.O.F., Academic Hospital,
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SKALP/elafin: an elastase inhibitor from cultured human
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/function="proteinase inhibitor"
142 c 119 g 115 t
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Location/Qualifiers
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81.0%; Pred. No. 5.4e-28;
iive 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="proteinase inhibitor"
                                                                                                                                                                                                                                                                                                                                                                          /cell_type="keratinocyte"
/clone_lib="HL1110b Clonetech"
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A31090
                                                                                                                                                                                                                                                                                                           sapiens"
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/db_xref="taxon:9606"
/clone="pGESKA"
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Molhuizen, H.O.F.
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SOURCE
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1 (bases 1 to 434)
Wang,T. and Dillon,D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 TGATICGTIGCGCTAIGTIAAACCCACCIAACCGTIGTITGAAGGACACIGAITGTCCAG 147
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                                                                                               28 ATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCT 87
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Molhuizen, H.O., Alkemade, H.A., Zeeuwen, P.L., de Jongh, G.J., Wieringa, B. and Schalkwijk, J.
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  Length 480;
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H.sapiens encoding skin-derived antileukoproteinase.
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Score 125.2; DB 6;
Pred. No. 3.5e-28;
0; Mismatches 34;
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81.0%;
    60.8%;
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Query Match

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BASE COUNT ORIGIN

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RESULT 8

ORGANISM

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REFERENCE AUTHORS

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Gaps

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PAT 21-AUG-1995

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/trānslation="MRASSFLIVVVFLIAGTLVLEAAVTGVPVKGQDTVKGRVPFNGQ
DPVKGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
KCCEGSCGMACFVPQ"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505786. Location/Qualifiers
                                                                                                                                                                                                                                              cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadangesystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                   Direct Submission
Submitted (13-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26...379
/codon_start=1
/product="Similar to protease inhibitor 3, skin-derived
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            Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Strausberg,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="Brain, glioblastoma"
/clone_lib="NIH_MGC_57"
/lab_host="DH10B"
                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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81.0%; Pred. No. 5.3e-28;
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/organism="Homo sapiens"
/db xref="taxon:9606"
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/db_xref="GI:15012095"
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                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                           156 AAGCGCAAGACCAATCAAAGGTCCACTCCACTAAGCCTGGCTGCCCCATTATCT 215
                                                                                                                                                                                                                                                                                                                    88 TGATTCGTTGCGCTAIGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                       Gaps
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Sager.R., Zou,Z., Lee,S.Whan. and Tomasetto,C.Laure. Cancer diagnosis using nucleic acid hybridization Patent: Location/Qualifiers
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Pred. No. 5.3e-28;
0; Mismatches 34; Indels
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                                                                                                                                                                                                       34; Indels
                                                                                                                                                                . 9
                                           1. .504
/organism="synthetic construct"
                                                                                                                                                            Score 124.6; DB 6
Pred. No. 5.4e-28;
0; Mismatches 34
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IMPERIAL CHEMICAL INDUSTRIES PLC Location/Qualifiers
                                                                              /db_xref="taxon:32630"
152 c 120 g
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167 c 130 g
                                                                                                                                                            60.5%;
81.0%;
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Best Local Similarity 81.0%;
Matches 145; Conservative
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                                                                                                                                                                                                 Matches 145; Conservative
                                                                                                                                                                              Best Local Similarity
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Gaps

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Submitted (01-SEP-1992) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences, Ookayama, Meguro-ku, Tokyo 152, Japan (Tel:03-3726-1111(ex.2226), Fax:03-3729-0335) Submitted (01-SEP-1992) to DDBJ by:
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primary structure of the human elafin precursor preproelafin deduced from the nucleotide sequence of its gene and the presence of unique repetitive sequences in the prosegment Biochem. Biophys. Res. Commun. 185 (1), 240-245 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1878)
SaheKi,T., Ito,F., Hagiwara,H., Saito,Y., Kuroki,J., Tachibana,S. and Hirose,S.
                                                                                                                                                                                                                                                                                                                           90 ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT 149
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elafin; elastase inhibitor.
Homo sapiens (library: lambda EMBL) DNA, clone lambda hI-Gl.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  150 ATCAAAAAGIGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAAT 204
1 (bases 1 to 177)
Ishima,Y., Okawa,N., Yoshida,M., Amagaya,S. and Kaji,A.
Elafin derivative
Patent: US 5734014-A 5 31-MAR-1998;
Location/Qualifiers
                                                                                                                                                                                 DB 6; Length 177;
                                                                                                                                                                                                                     32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                 Score 123.8; DB 6 Pred. No. 9.7e-28;
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/clone_lib="lambda EMBL"
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/codon_start=1
/product="preproelafin"
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Tokyo Institute of Technology
Ookayama, Meguroku
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                                                                                                         /organism="unknown"
                                                                                                                                48 g
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81.7%;
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/number=1
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HUMELAFIN
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/protein id="BAA02441.1"
/db_xref="G1:219615"
/translation="WRASSFLIVVVFLIAGTLVLEAAVTGVPVKGQDTVKGRVPFNGQ
/pvkGQVSVKGQDKVKAQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                   Query Match 59.8%; Score 123.2; DB 9; Length 1878; Best Local Similarity 81.2%; Pred. No. 1.4e-27;
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0; Mismatches 33;
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/db_xref="taxon:9606"
-537 c 603 g 572
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/product="elafin"
1185. .1460
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81.2%;
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/translation="massfplivvyPliagTlvLzaavTgVPVKGQDTVKGRVPFNGQ
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KCCEGSCGMACFVPQ"
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pre-elafin=elastase-specific inhibitor (human, placental, Genomic,
2309 nt).
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1 (bases 1 to 2309)
Sallenave, J.M. and Silva, A.
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join(517. :595,1453. .1727)
/gene="pre-elafin"
/note="elastase-specific inhibitor; This sequence comes
/note="elafin has been sequenced at the protein level;
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Am. J. Respir. Cell Mol. Biol. 8 (4), 439-445 (1993)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2309;
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Pred. No. 1.4e-27;
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join(398. .595,1453. .1727,1962.
517. .1727
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                                                                    /product="elafin precursor"
/protein_id="AAA36483.1"
/db_xref="GI:190338"
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/number=2
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/number=2
1729. .1961
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Best Local Similarity 81.2%;
Matches 143; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sallenave, J. M. and Silva, A.
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join(517. .595,1453. .1727)
/function="elastase-specific proteinase inhibitor"
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Avalon Pharmaceuticals (US)
Location/Qualifiers
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                                                                  AX334316 2309 bp DI Sequence 4825 from Patent WO0194629.
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/db_xref="taxon:9606"
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/number=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submitted (139-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, Cubmitted (139-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestedsanger.ac.uk
On Nov 27, 2000 this sequence version replaced gi:10198636.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Bm:, SMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information the their/Www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 mapping group. Purther information can be found at http://www.sanger.ac.uk/HGP/Chtz0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPI-177H20 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RPI-172H20 is at 9947 in this sequence. The true left end of clone RPI-3012 is at 28594 in this sequence. The true right end of clone RPI-21D12 is at 100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred
                                                                                                                            /translation="MRASSFLIVVVFLIAGTLVLEAAVTGVPVKGQDTVKGRVPFNGQ
DPVKGQVSVKGQDKVKAQEFVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSJ172H20 DNA linear PRI 07-APR-2001 Human DNA sequence from clone RPI-172H20 on chromosome 20q12-13.12 Contains SEMG1 and SEMG2 genes for semenogelin I and II, the PI3 gene for procease inhibitor 3, skin-derived (SKALP), ESTS, STSS and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1552 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGATTCGTTGCGCTATGTTAAACCCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1672 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGA 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAA 203
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                                                                                                                                                                                                                                                                                                                                             59.8%; Score 123.2; DB 9; Length 2309; 81.2%; Pred. No. 1.4e-27;
                                                                                                                                                                                                                                         2 others
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
/codon_start=1
/product="pre-elafin"
/protein_id="AAB26371.1"
/db_xref="G1:299841"
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HTG; PI3; SEMG1; SEMG2; SKALP.
                                                                                                                                                                                                                                      603 g
                                                                                                                                                                                                      KCCEGSCGMACFVPQ"
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                                                                                                                                                                                                                                         537 C
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                                                                                                                                                                                                                                                                                                                                                                                Sest Local Similarity
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AUTHORS
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KEYWORDS
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note="Charlie2 repeat: matches 3534. .3727 of consensus"
                problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPI-172H20 is from the library RPC-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MB1 repeat: matches 5696. .6172 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548. .6731
note="L1MC4 repeat: matches 7650. .7849 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1MA8 repeat: matches 4484. .6153 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note≈"AluSg/x repeat: matches 136. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MB1 repeat: matches 5294. .6159 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1M3e repeat: matches 22. .1826 of consensus"
10656. .10979
'note="MER74A repeat: matches 248. .557 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2989. .3136
/note="LiM4 repeat: matches 3850. .3998 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="HAL1 repeat: matches 1501. .1692 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .049. .6158 note="MER20 repeat: matches 109. .218 of consensus"
quality >= 30); an attempt was made to resolve all sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LTR16B repeat: matches 2. .461 of consensus"
1973. .12160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160. .6228
/note="L2 repeat: matches 2021. .2087 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="FLAM_A repeat: matches 1. .122 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .286. .6466 -
note="L2 repeat: matches 2329. .2497 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="MER20 repeat: matches 7. .218 cf consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluSx repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     001. .2042
note="21 copies 2 mer ta 83% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: STS: Em:GO8051"
14337. .14396
/note="30 copies 2 mer ct 75% conserved"
14492. .17136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="16 copies 2 mer ta 84% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               965. .5002
note="19 copies 2 mer gt 94% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="18 copies 2 mer at 80% conserved"
                                                                                                                                                                                                                                                                                                                                                          complement(1. .100)
/note="match: STS: Em:HS211D128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2469. .2951)
/note="match: GSS: Em:AQ809877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="match: GSS: Em:AQ386436"
                                                                                                                                                                                                                           'organism="Homo sapiens"
                                                                                                                                                                                                                                                   /db xref="taxon:9606"
                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                      /chromosome="20"
/map="q12-13.12"
/clone="RP1-172H20"
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                                                                                                                                                        VECTOR: pCYPAC2.
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/note="L1ME3A repeat: matches 5388. .5937 of consensus"
complement (48203. .48496)
/note="match: GSS: Em:AQ275745"
48638. .48679
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15840. .45956
note="LIME repeat: matches 5530. .5647 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="LlM4c repeat: matches 1312. .1666 of consensus" 39261. .42088 /note="LlPA1s repeat: matches 671. .3485 of consensus" 42057. .43098 /note="LlPA5_repeat: matches 5104. .6143 of consensus" 40cte="LlPA5_repeat: matches 5104. .6143 of consensus"
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46916. .47210
                                                                                           /note="L1 repeat: matches 4299. .4610 of consensus"
17898. .18682
/note="lim1 repeat: matches -1390. .-578 of consensus"
19077. .19213
/note="Lim2 repeat: matches 5694. .5824 of consensus"
20761. .20831
/note="Lim4b repeat: matches -259. .-184 of consensus"
                                                                                                                                                                                                                                                                    20653. .21014
/note="LiMA9 repeat: matches 6102. .6270 of consensus"
21044. .21573
/note="LiMAb repeat: matches -263. .330 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31318. .31729
/note="THENC repeat: matches 1. .371 of consensus"
31730. .31886
/note="LiM1 repeat: matches 859. .987 of consensus"
33209. .34261
/note="LiM3d repeat: matches 859. .1833 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74232. .34942
/note="LiM1 repeat: matches 1560. .2657 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="LIME repeat: matches 5521. .5793 of consensus"
46828. .46915
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 1. .309 of consensus"
25460. 25629
27610. 27639
27612. .27639
                                                                                                                                                                                                                                                                                                                                                                          21634. .21829
/note="LlM4b repeat: matches 330. .524 of consensus"
22891. .23199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1 repeat: matches 4912. .5038 of consensus"
71434. .37469
710te="L1P repeat: matches 2850. .2885 of consensus"
38377. .39183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.06="14_Copies 2 mer ac 100% conserved"
27655. .27986
7.06="LM3 repeat: matches 202. .531 of consensus"
28959. .29336
7.06="LIM1 repeat: matches 469. .859 of consensus"
7.06="THEC repeat: matches 1. .371 of consensus"
29712. .3337
7.06="THEIC repeat: matches 1. .371 of consensus"
29712. .31317
7.060="THEIC repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34941. 36117
hote="11" repeat: matches 3935. .5142 of consensus" 3618. .36412
/note="HERVL repeat: matches 4. .2665 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3780 of consensus"
                       77140. .17589
//hote="MLT2B repeat: matches 1. .444 of consensus"
77590. .17899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluJo repeat: matches 9. .292 of consensus"
36430. .37302
"note="L1 repeat: matches 2905. .3780 of consensus
37299. .37425
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47211. .47769
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46492. .46761
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                                                                                              'product="dJ172H20.3 (protease inhibitor 3, skin-derived
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synthetic construct
artificial sequences.
1 (Bases 1 to 347)
Christophers,E., Schroder,J.M., Pioli,D., Wiedow,O. and Edge,M.D.
Polypeptides and polypeptide analogues with inhibitory activity
against human elastase
Patent: EP 0402068-A 30 12-DEC-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     50574 AAGCGCAAAGAGCCAGTCAAAAGGTCCCAGTCTAAGCCTGGCTCCTGCCCCATTATCT 50633
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: cDNAs: Em:Z18538 Em:AJ223218 Em:AJ223216
match: BSTs: Em:AAS2757 Em:AAS83567 Em:AAS82866"
/evidence=not experimental
                                                                                                                                                                                                                                                                                                                                                                                            88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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                                          join(49535. .49615,50475. .50750,50984.
/gene="PI3"
/note="21 copies 2 mer ac 97% conserved'
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80.2%; Pred. No. 1.7e-27;
iive 2; Mismatches 33;
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/organism="synthetic construct"
/db_xref="taxon:32630"
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DEFINITION Sequence 11 from patent US 5688641.
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                    49535. .51104
/gene="PI3"
                                                                                                                                                                                                                                Query Match 59.8%;
Best Local Similarity 81.2%;
Matches 143; Conservative
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Best Local Similarity 80.2
Matches 142; Conservative
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nomenclature
J. Biol. Chem. 272 (33), 20471-20478 (1997)
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J. Biol. Chem. 268 (16), 12028-12032 (1993)
93280175
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|db_xref="G1:2764786"
|db_xref="SPTREMBL:046625"
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db xref="taxon:9913"
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Zeeuwen, P.L.J.M.
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(h. [bases 1 to 171])

Christophers,E., Schroder,J.M., Pioli,D., Wiedow,O. and Edge,M.D. Polypeptides and polypeptide analogues with inhibitory activity against human elastase
Patent: EP 0402068-A 29 12-DEC-1990;
IMPERIAL CHEMICAL INDUSTRIES PLC
                                                                                                                                                                                                                                                                                                                                                              88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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Sager, F., Zou,Z., Lee,S.Whan. and Tomasetto,C.Laure.
Cancer diagnosis using nucleic acid hybridization
Patent: US 5688641-A 11 18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 ATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACA 199
                                                                                                                                                                                                                                         Score 121; DB 6; Length 321;
Pred. No. 7.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                        148 GTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCC 196
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/db_xref="taxon:32630"
51 c 42 g 40 t
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Pred. No. 8.3e-27;
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illarity 81.2%;
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              I74313.1 GI:3010454
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Matches 139; Conservative
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Zeeuwen, P. L., Hendriks, W., de Jong, W.W. and Schalkwijk, J.
Identification and sequence analysis of two new members of the SKALP/elafin and SPAI-2 gene family. Bacchemical properties of the transglutaminase substrate motif and suggestions for a new
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                AJ223216.1 GI:2764785
bTrappin-2 gene; proteinase inhibitor, putative; transglutaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-JAN-1998) Zeeuwen P.L.J.M., Dermatology, University Hospital Nijmegen, PO BOX 9101, 6500 HB Nijmegen, THE NETHERLANDS
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Molhuizen,H.O., Alkemade,H.A., Zeeuwen,P.L., de Jongh,G.J.,
Wieringa,B. and Schalkwijk,J.
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Tamechika, I., Itakura, M., Saruta, Y., Furukawa, M., Kato, A.,
Tachibana, S. and Hirose, S.
DOLZZZZZI6 BOS TAURA DE MRNA Linear MAM L
BOS TAURUS MRNA for putative bTrappin-2 protein, partial.
AJ223216
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/db_xref="G1:1228058"
/tanslat_ion="MRSRSFLVLVVVFLICGTLVAQAAGRIRRPKGKGTKKILALVKG
QGPYRGKDQYKGQGPYKGQDLGKSQDPVKAQLPDKGQDLGKGEDSYKGQDPFKAQLPD
KLQDPVKAQPAIKRLILLTKPGSCPRILIRCLMVNPPNRCLSDAQCPGLKKCCEGFCG
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Tamechika,I., Itakura,M., Saruta,Y., Furukawa,M., Kato,A.,
Tachibana,S. and Hirose,S.
Accelerated evolution in inhibitor domains of porcine elafin family
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Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                    235 CAAGGCCGAATCGGAGGTCCACTCCTCACTAAGCCTGGGTCCTGCCCCAGGGTTCTGATC 294
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1. Grganism="Sus scrofa"
/db xref="taxon:9823"
/clone="lambda WAP-1"
<lone="lb="EMBL SP6/T7"
/number=1
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/note="SINE (PRE-1)"
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/product="elafin"
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/number=1
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3 (bases 1 to 3693)
Hirose,S.
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AB003281 1128 bp DNA linear MAM 26-MAY-1999
Phacochoerus aethiopicus gene for elafin (trappin-2), partial cds.
AB003281
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Phacochoerus aethiopicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Phacochoerus.
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Patent: EP 0402068-A 22 12-DEC-1990;
IMPERIAL CHEMICAL INDEFRIES PLC
Location/Qualifiers
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oligonucleotide ELIS from patent EP0402068.
A31082
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/db_xref="taxon:32630"
__14 c __18 g __23 t
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/note="TG repeat"
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Pig mRNA for elafin family member protein, complete cds.
D50322
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KAQLPDKGQDLGKGEDSVKGQDPIKAQLPDKVQDPVKAQPAIKRLILLTKPGSCPRIL
IRCMMVNPPNRCLSDAQCPGVKKCCGGFCGKECLNPR"
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Tachibana, S. and Hirose, S.
Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                        Submitted (21-APR-1997) Shigehisa Hirose, Tokyo Institute of rechnology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (B-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                        Furutani, Y., Kato, A., Yasue, H., Alexander, L.J., Beattie, C.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furutani, Y., Kato, A., Yasue, H., Alexander, L.J., Beattie, C.W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 TACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                     niversity of the trappin multigene family in the Suidae J. Biochem. 124 (3), 491-502 (1998)
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/db xref="taxon:85517"
<211. .632
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elafin family member protein.
Sus scrofa cDNA to mRNA, clone:WAP-5.
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                                                                                                                                                                        Direct Submission
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PRILIRCLMVNPPNRCLSDAQCPGVKKCCEGFCGKDCMDPK"
Direct Submission
Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8801, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
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Tamechika,I., Itakura,M., Saruta,Y., Furukawa,M., Kato,A.,
Tachibana,S. and Hirose,S.
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Journal of Biological Chemistry (1996) In press
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111 c 124 g
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/codon_start=2
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VKGQDRVKGRGPVKGPVSTKPGSCPNILIRCAMLNPPNRCLKDTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="unnamed"
/function="transglutaminase substrate, putative proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="sTrappin-2"
/function="transglutaminase substrate, putative proteinase
                                                                                                                                                                                                 Tobases 1 to 270)
Zeeuwen, P. L., Hendriks, W., de Jong, W.W. and Schalkwijk, J.
Identification and sequence analysis of two new members of the SKALP/elafin and SPAI-2 gene family. Biochemical properties of the transglutaminase substrate motif and suggestions for a new
                 Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 270)
Zeeuwen, P. L. J. M.
                                                                                                                                         Direct Submission
Submitted (06-JAN-1998) Zeeuwen P.L.J.M., Dermatology, University
Hospital Nijmegen, PO BOX 9101, 6500 HB Nijmegen, THE NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (bases 1 to 270)
Molhuizen, H.O., Alkemade, H.A., Zeeuwen, P.L., de Jongh, G.J., Wieringa, B. and Schalkwijk, J.
SKALP/elafin: an elastase inhibitor from cultured human keratinocytes. Purification, cDNA sequence, and evidence for transglutaminase cross-linking
J. Biol. Chem. 268 (16), 12028-12032 (1993)
                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 270)
Tamechika, I., Itakura, M., Saruta, Y., Furukawa, M., Kato, A.,
Tachibana, S. and Hirose, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 TGATICGTIGCGCTATGTTAAACCCACCTAACCGTIGTTIGAAGGACACTGATIG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 272 (33), 20471-20478 (1997) 97400522
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/gene="sTrappin-2"
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| db_xxef="GG:120938.1"
| translation="PRGKGTRKTLALVKGGEPVRGKDQVKGGGPVKGODLGKSQDPV
| kAQLPDKGQDPVKAQPAIKRLILLTKPGSCPRILIRCLMVNPPNRCLSDAQCPGVKKC
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                                                                                                                                       Direct Submission
Submitted (23-FBB-1996) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteinase inhibitor; putative; sTrappin-2 gene; transglutaminase substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /function="elastase specific inhibitor"
/note="Mature protein has a characteristic
disulfide-linked structure called four disulfide core or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 ACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAAC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 CGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 AGGIGTITGAGIGATGCTCAGIGCCCAGGGGTCAAGAAGIGCTGTGAAGGCTITTGCGGG 534
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On Apr 29, 1997 this sequence version replaced gi:1209380.
Sequence updated (21-Apr-1997).
Location/Qualifiers
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                   Evolution of the trappin multigene family in the Suidae J. Biochem. 124 (3), 491-502 (1998)
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/product="elafin homolog"
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/organism="Sus scrofa"
/db_xref="taxon:9823"
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1010. .>1034
/note="PCR primer"
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/note="PCR primer"
209. .559
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/note="exon2 part"
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Matches 100; Conservative
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  Hirose, S.
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Furutani, Y., Kato, A., Yasue, H., Alexander, L.J., Beattie, C.W. and
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                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pecari tajacu"
/db_xref="taxon:9829"
<212. .675
                                                       1169 bp
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                                                                                                                                          Pecari tajacu
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attificial sequences.

(bases 1 to 68)
Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D.
Polypeptides and polypeptide analogues with inhibitory activity
against human elastase
Patent: EP 0402068-A 20 12-DEC-1990,
IMPERIAL CHEMICAL INDUSTRIES PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 69 TICTIGECCIATTATCTIGATICGTIGGCGCTATGTIAAAACCCACCTAACCGTIGTITGAA 10
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                                                             69 bp DNA oligonucleotide ELI4 from patent BP0402068.
A31081
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/db_xref="taxon:32630"
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LPRRKPGFCPMIKIRCALFNPPNRCLTDAGCPGARKCCIGSCGKACLNPVR"
MAM 26-MAY-1999
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Hippopotamidae, Hippopotamus.
                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Tayassuidae, Pecari.
                                                                                                                                                                                                                                                                                                                                                                                  Furutani, Y., Kato, A., Yasue, H., Alexander, L.J., Beattie, C.W. and
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Hippopotamus amphibius gene for trappin, partial cds.
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linear
                                Pecari tajacu gene for trappin, partial cds.
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Pred. No. 2.5e-10;
0; Mismatches 42;
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95; Conservative
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                                                                                                               RESULT 34
PIGSPAI2S2
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                                                                                            Submitted (21-APR-1997) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shiros@bio.titech.ac.jp, Tel:045-924-5726,
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1 (bases 1 to 71)

Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D. Polypeptides and polypeptide analogues with inhibitory activity against human elastase
Patent: EP 0402068-A 24 12-DEC-1990;
IMPERIAL CHEMICAL INDUGIRIES PLC
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Evolution of the trappin multigene family in the Suidae J. Biochem. 124 (3), 491-502 (1998) 98391820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 TGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTT 190
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A31083
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                                              2 (bases 1 to 734)
Hirose, S.
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Best Local Similarity 100.0
Marches 67, Conservative
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                                                                                  Direct Submission
                                                                                                                                                               Fax: 045-924-5824)
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SOURCE
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Submitted (27-SEP-1993) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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TIGHTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACA 12
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Yoshimoto,T., Ghoneim,M.A., Nara,K., Kato,A., Suzuki,Y.,
Furukawa,M. and Tachibana,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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Submitted (27-Sep-1993) to DDBJ by:
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Tokyo Institute of Technology
4259 Nagatsuta-cho, Midori-ku
Yokohama, Kanagawa 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porcine DNA for SPAI-2, exon 2. D17755
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Location/Qualifiers
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61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120

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140 TTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACA 199

09-833799-13a.rge

MAM 01-FEB-2000

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VKGHBPVEGQDPVNAQLPDKXQQDPVKAQPAVPGRFLLSKRGHCPRILFRCPLSNPSN

KCWRDYDCPGVKKCCEGFCGKDCLYPK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Technology, Department of Biological Sciences, Ookayama, Meguro-ku, Tokyo 152, Japan (Tel:81-3-3726-1111, Fax:81-3-3729-0335) on or before Mar 17, 1999 this sequence version replaced gi:2078450, gi:1054611, gi:2077950.
D17753:Submitted (27-Sep-1993) to DDBJ by:Shigehisa Hirose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning, characterization, and tissue distribution of porcine SPAI, a protein with a transglutaminase substrate domain and the WAP
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (sites)
                                                                                                                                                                                                                                                     APAI-2; preproSPAI-2; proSPAI-2; SPAI-2.
Sus scrofa cell_line:NM514 cDNA to mRNA, clone_lib:lambda gt10.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-FEB-1996) Shigehisa Hirose, Tokyo Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                     Kuroki,J., Hosoya,T., Itakura,M., Hirose,S., Tamechika,I.,
Yoshimoto,T., Ghoneim,M.A., Nara,K., Kato,A., Suzuki,Y.,
Furukawa,M. and Tachibana,S.
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                                                                                                                               789 bp mRNA line.
Sus scrofa mRNA for preproSPAI-2, complete cds.
D83667 D17753
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0; Mismatches 48
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/ceIl line="NM514"
/clone_lib="lambda gt10"
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439. 621
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1. .789
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        548 AGGATTGTTTGTATCCCAAGTGA 570
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215 c
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Matches 95; Conservative
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polyA_signal
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                                                                                                                                                                                                 ACCESSION
VERSION
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JOURNAL
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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A31078.1 GI:1249292
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oligonucleotide ELI2 from patent EP0402068.
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/db_xref="taxon:32630"
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ESPGPVWETLIDIGQDPVKGQDPVKGQDPVKGQDPVKGQDLVKSQDBVYAELPDIGQD
VVKGHEPVEGQDPVNAQLPDKVQDPVKAQPAVPGRFLLSKRGHCPRILFRCPLSNPSN
KCWRDYDCPGVKKCCEGFCGKDCLYPK"
                                               MAM 14-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                      Sus scrofa DNA, clone_lib:EMBL SP6/T7 clone:lambda WAP-2.
Sus scrofa
                                               linear
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                                               DNA
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join(629. .710,1552. .2033)</pre>
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/db_xref="taxon:9823"
/clone="lambda WAP-2"
/clone=lib="EMBL SP6/T7"
                                          Pig DNA for SPAI-2, complete cds. D50320
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/db_xref="GI:1228060"
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/evidence=experimental
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1 (bases 1 to 64)
Christophers, E., Schroder, J.M., Pioli, D., Wiedow, O. and Edge, M.D.
christophers polypeptide analogues with inhibitory activity
against human elastase ase
Patent: EP 0402068-A 18 12-DEC-1990;
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                                                                                                                                                                                                                                                                                                                          1951 AGTGTTGGAGAGATTATGACTGTCCAGGGGTCAAGAAGTGCTGTGAAGGCTTTTGCGGGA 2010
                                                                                                                                                                                                          1891 chaagcergeccachecchaegahrehrhrechiecececheaecaarecerehaea 1950
                                                                                                                                             61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
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Query Match 32.1%; Score 66.2; DB 4; Length 3782; Best Local Similarity 66.4%; Pred. No. 7.7e-10; Matches 95; Conservative 0; Mismatches 48; Indels 0
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UNKSQDPVKAELPDIGQDVVKQDPVKKGDLVKSQDPVTAELPDIGQDVVKGQDPVKG
QDLVKSQDPVTAELPDIGQDVVKGHEPVEGQDPINAQIPDKVQDPIKAQPAVGGLLFI
SKRGRCPWILLRCPLANPSNKCWRDYDCPGVKKCCEGFCGKOCLYPK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-APR-1997) Shigehisa Hirose, Tokyo Institute of rechnology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furutani,Y., Kato,A., Yasue,H. and Hirose,S. (Very Recent) evolution in suidae of the trappin multigene family with unusually conserved intron sequences
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Phacochoerus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB003282 1325 bp DNA linear MAM 26-MAY-1
Phacochoerus aethiopicus gene for SPAI (trappin-1), partial cds.
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                                                                                                                                                          Length 64;
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                                                        /organism="synthetic construct"
                                                                                                                                                        31.1%; Score 64; DB 6;
100.0%; Pred. No. 4e-09;
tive 0; Mismatches 0
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/product="SPAI (trappin-1)"
/protein_id="BAA77826.1"
/db_xref="G1:4887640"
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IMPERIAL CHEMICAL INDUSTRIES PLC
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Phacochoerus aethiopicus
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Tamechika,I., Itakura,M., Saruta,Y., Furukawa,M., Kato,A.,
Tachibana,S. and Hirose,S.
Accelerated evolution in inhibitor domains of porcine elafin family
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/product="elafin family member protein"
/protein_id="BAA0888.1"
/db_xref="G1:1864016"
/translation="MRSRSFLVLVAVFLICETLVAQRPEKIRGPKGQGQDPVEGQDQD
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PVGGDPVNAQLPDKVQDPVKAQPPVQGRLLHYKPGLCPWIFLRCPLPKPPNKCWRDS
HCPGVMKCCEGFCGNECSYPR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Technology, Department of Biological Sciences, 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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686 CTAAGCGTGGCCGCTTGGATTCTTCTCCGTTGCCCGCTGGCCAATCCTTAACA 745
                                                                121 GTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGGTA 180
                                                                                                     746 AGTÉTTGGAGAGATTATGACTGTCCAGGGGTCAAGAAGTGCTGTGAAGCCTTTTGCGGGA 805
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Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of
                                                                                                                                                                                                                                                                                                              Pig mRNA for elafin family member protein, complete cds. D50323
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/clone="WAP-4"
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/product="unnamed"
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'note="PCR primer"
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AUTHORS
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/product="Trappin-6"
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/db_xref="GI:313274"
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AGGLPFKRGLCPRVRIHCNLWNPPNQCWRDAHCPGAKKCCEGFCGKTCMNPR"
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Submitted (10-FEB-1998) Shigehisa Hirose, Tokyo Institute of
Submitted (10-FEB-1998) Shigehisa Hirose, Tokyo Institute of
Echnology, Department of Biological Sciences; 4259 Nagatsuta-cho,
Midori-ku, Yokohama, Kanagawa 226-8501, Japan
(E-mail:shirose@bio.titech.ac.jp, Tel:+81-45-924-5726,
Pax:+81-45-924-5824)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Furutani,Y., Kato,A., Yasue,H., Alexander,L.J., Beattie,C.W. and
                                                                                                                                        419 TAAGCCTGGCCTCTGCCCTTGGATTTTTTACGTTGCCCGCTGCCCAAACCTCCTAACAA 478
                                                                                                                                                                      122 TTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTAT 181
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J. Biochem. 124 (3), 491-502 (1998)
98391820
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                                              Length 578;
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                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                      Bos taurus gene for Trappin-6, partial cds. AB011010
                                            Score 60.4; DB 4;
Pred. No. 5.1e-08;
0; Mismatches 51;
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/organism="Bos taurus"
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<1. .36
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                                              29.3%;
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Hirose, S.
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Best Local Similarity 61.7
Matches 87; Conservative
                                                                           91; Conservative
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Bos taurus DNA.
Bos taurus
                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                           RESULT 42
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9670 bp DNA linear MAM 14-APR-2000
Pig DNA for elafin family member protein, complete cds.
D50321
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BGQGPvVKvEILDIGQDLVKGQDPVEGODPVKAQLPDKVQDPVKAQPPIQGGFLFPKPG
VCPKIIFCPLVNPPIKCWRDSHCFGVKKCCPSLCGKGCVTPR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirose, S.
Direct Submission
Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of Submitted (18-APR-1995) Shigehisa Hirose, Tokyo Institute of Technology, Department of Biological Sciences; 4259 Nagatsuta-cho, Midori-ku, Yokohama, Kanagawa 226-8501, Japan (E-mail:shirose@bio.titech.ac.jp, Tel:045-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
189 AAGCGTGGCTTATGCCCCCAGGGTTCGGATCCACTGCAACTTGTGGAATCCCCCTAACCAG 248
                                                    TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                     249 rGTTGGAGAGATGCTCACTGCCCAGGGGCCAAGAAGTGCTGTGAAGGCTTTTGTGGGAAG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . barcas,
Tamechika,I., Itakura,M., Saruta,Y., Furukawa,M., Kato,A.,
Tachibana,S. and Hirose,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                elafin family member protein.
Sus scrofa DNA, clone_lib:EMBL SP6/T7 clone:lambda WAP-3.
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/producis="elafin family member protein"
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96215132
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join(629. .710,1552. .1904)</pre>
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/db xref="taxon:9823"
/clone="lambda WAP-3"
/clone lib="EMBL SP6/T7"
<1. .710
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1722. .1901
/product="unnamed"
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                                                                                                                                                                                                           309 Accrerateranda 329
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'note="SINE
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Hirose, S.
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/number=1
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PAT 29-SEP-1999

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AB042257

AB042257

Cavia porcellus mRNA for caltrin-like protein II, complete cds.
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Sugiyyama, T., Kamimura,T., Masuda,K., Okada,M., Ohtsuka,E.,
Imaizumi,A., Matanabe,K., Suga,T., Matsumoto,Y. and Takeuchi,A.
Elastase inhibitory polypeptide and process for production thereof
by recombinant gene technology
Patent: US 5851983.A S. 22-DEC-1998;
Location/Qualifiers
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Furucani,Y. and Hirose,S.

Direct Submission

Submitted (26-APR-2000) Shigehisa Hirose, Tokyo Institute of
Technology, Department of Bioscience; Nagatudacho4259 Midori-ku,
Yokohama, Kanagawa 226-8501, Japan
(E-mailshirose@bio.titech.ac.jp, Tel:81-45-924-5726,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Purification and structure of caltrin-like proteins from seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCG 121
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J. Biol. Chem. 265 (12), 6854-6859 (1990)
90216715
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Sequence 5 from patent US 5851983.
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Evolution of caltrin-like protein
Unpublished
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               535 AGTCCTGTGCGGATCCCCGGTAAGA 559
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55.6%;
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AB042257
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                               1789 TTATCTTTTGCCCGCTGGTCAATCCCCCTATCAAGTGTTGGAGAGATTCTCACTGCCCAG 1848
                                                                                                                                                                                                                                                                        88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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                                                                                                                                                   Score 43.4; DB 4; Length 3670;
Pred. No. 0.0097;
0; Mismatches 41; Indels 0;
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Pred. No. 0.017;
0; Mismatches 54; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                   148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGGTTTCGTTCC 196
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Sus scrofa gene for elafin homolog, partial cds.
AB003285
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COUNT 774 a 951 c 1131 g
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Matches 68; Conserv
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***, 29 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                             /note="antileukoproteinase repeat homology #label ALP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 CGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGT 179
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                                                                                                                                                                                                                                                                                                                                                                                                                    104 AATAGGCCTGGTTCCTGTCCCCGGGTTATGATATACTGCCCGGCAAGGCATCCTCCCAAC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AAGTGCACGAGTGATTATGACTGCCCAAAGCCTCAGAAGTGCTGCCCAGGCTACTGCGGG 223
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17. .247
                                                                                                                                                                                     /product="unnamed"
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110. .247
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organism="Cavia porcellus"
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                db_xref="taxon:10141"
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/note="WAP. domain"
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HTG; HTGS_PHASE1.
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Matches 78; Conservative
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Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Maedor, M., Mai, G., Merzker, M., Miner, G., Minchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Pace, A., Pace, A., Payton, B., Peerry, J., Perez, L., Peters, E., Pace, A., Pace, A., Payton, B., Li, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Soct, G., Shen, H., Shoosherari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, Y., Usmani, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wulliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 204225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 26, 2002 this sequence version replaced gi:21954968.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length
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3121: gap of unknown length
4764: contig of 1643 bp in length
4864: gap of unknown length
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1373: gap of unknown length
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5869: contig of 1005 bp in length
5969: gap of unknown length
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Contact: hgsc-help@bcm.tmc.edu
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14608: gap of
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Worley, K.C.
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<code>SEQUENCING</code> READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 \,
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              AC006054.2 GI:4557048
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                                         Homo sapiens.
                                                     Homo sapiens
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 AC006054
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Homo sapiens Xq28 BAC GSI-382P7 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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contig of 23326 bp in length.
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contig of 10808 bp in length
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/clone="CH230-170K14"
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STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3189-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases I to 143738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 6 (bases I to 143738) Worley, K.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (31-MAR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                    Chen, Z.,
                                                                                                                           Muzny, D., Arenson, A.D., Bouck, J., Brundage, E., Bunac, C., Chen, Z. Di, W., Ding, Y., Dugan, S., Durbin, J., Forcum, J., Garcia, C., Gorrell, J.H., Gorrell, L.L., Hernandez, J., Jackson, L., Kondejewski, N., Leal, B., Lichtarge, O., Liu, W., Logan, O., Lu, J., Martinez, C., Oswal, G., Pampell, L.R., Parish, B.J., Perez, L., Rashid, N.D., Rives, C., Scherer, S.E., Shen, H., Simon, M., Vo, O., Williamson, A., Worley, K.C., Yu, W., Zhou, X., Nelson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Overlapping clones are noted at the beginning and end of the Features listing.
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reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Pepprts of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation. html.

## QUALSTAT-REPORT------

142753 0.000121373 0.0449448 143738 ---- Summary Statistics -----Phrap values in estimate:
Average error rate (BCM-Phrap estimate):
Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus: Contig length:

acttggtgca (a) ggaaaatatt atttctctga (t) gatcactgat ttaaaccaaa (t) aaaaaacttca Edited+Context -- Consensus changing edits Original+Context acttggtgca (n) ggaaaatatt atttctctga (n) gatcactgat ttaaaccaaa (n) aaaaacttca Position 28154 114564

35 30 ------ Distribution of Quality < 40 Bases 15 20 25 Phrap Value Range 10 S 700 500 400 300 200 100 # bases

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complement (4994..5058)
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complement(2833. .2856) /clone="RPCI11-382P7" 1.01 qxfo. cocation/Qualifiers complement(1. .431)
/rpt family="L1P" .143738 1.01 Version: repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region FEATURES

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ement(2500)
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26728. .28079
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ement /100
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ement/1000
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14636. .14789
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27846. .27960
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17.23
Best Local Similarity 66.2
Matches 51, Conservative

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44303 AIGICTCCATTITITAAAGAACCAATIGCAAGICTAAIGAGIACTAGICCTAGITCTGGI 44244 77 18 ATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGT g ઠે

78 CCTATTATCTTGATTCG 94 ò

44243 CCTACTTTGGTGATTTG 44227

ACO96647.1 GI:15668086 DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 49 AC096647 LOCUS

Homo sapiens

1 (bases 1 to 146935) Sulston, J.E. and Waterston, R.

AUTHORS TITLE

REFERENCE

MEDLINE JOURNAL PUBMED REFERENCE AUTHORS

Homo sapiens

ORGANISM

(bases 1 to 146935)

(bases 1 to 146935)

TITLE

Waterston, R.H.

AUTHORS JOURNAL

REFERENCE

(bases 1 to 146935)

REFERENCE AUTHORS JOURNAL

USA

Direct Submission

COMMENT

Waterston, R. 63108,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01 MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 19, 2001 this sequence version replaced gi:8072447.
                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping information for this clone was provided by Dr. John D. Webherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanses, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          all regions were doubte stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP11-40315. Actual start of
this clone is at base position 1 of RP11-2G16; actual end is at
base position 146935 of RP11-2G16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
                                                                                                                                                                                             Nguyen,C., Abbott,A., Dignan,G., Doebber,A. and Boyer,B. The sequence of Homo sapiens BAC clone RP11-2G16 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                      Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H_NH0002G16
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Drafting Center: WIBR

MAPPING INFORMATION:

restriction digest.

SOURCE INFORMATION:

Center code: WUGSC

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FEATURES

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Mus musculus secretory leukocyte protease inhibitor mRNA, complete
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Zitnik, R.J., Zhang, J., Kashem, M.A., Kohno, T., Lyons, D.E., Wright, C.D., Rosen, E., Goldberg, I. and Hayday, A.C.
The cloning and characterization of a murine secretory leukocyte protease inhibitor cDNA
Biochem. Biophys. Res. Commun. 232 (3), 687-697 (1997)
              Sus scrofa
Bukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
1 (bases 1 to 600)
Framer, S.J., Fliss, A.E. and Simmen, R.C.
Complementary DNA cloning and regulation of expression of the
messenger RNA encoding a pregnancy-associated porcine uterine
protein related to human antileukoproteinase
MOI. Endocrinol. 4 (8), 1095-1104 (1990)
2293019
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Matches 72; Conservative 0; Mismatches 62; Indels
Porcine uterus. cDNA to mRNA, clone pALP.
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/rpt family=12
31720. .33118
/rpt family="L1"
33111. .33144
/rpt family="AT_rich"
            /rpt_family="Alu"
25863. .25922
/rpt_family="AT_rich"
25895. .26547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [. .35634
family="AT_rich"
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/rpt_family="T-rich"
                                                                                                                                                                                                                              /rpt_family="MaLR"
28425. .28453
/rpt_family="(T)n"
28605. .29988
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39515. .39924
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1000. .31073
rpt_family="MaLR"
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family="ERV1"
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8150. .28424
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/spt family="L1"
/35401. 3811
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26649. 27752
/rpt_family="L1"
27759. 28143
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family="MaLR"
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38095. .38245
/rpt_family="L1"
38267. .39514
                                                                                                                                                                                                                                                                                                                                   'rpt_family="Alu"
10260. .30999
                                                                                                                                                                                                                                                                                                                                                                                                                                            family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .38116
family="L1"
                                                                                    rpt_family="L1"
:6552. .26649
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 25582. .25877
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1079.
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560<u>1</u>.
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1330.
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Matches 70; Conserv
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PIGALP
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ROD 07-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chui, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawar Bandoh, Anna-Lisa Prabhu, Parvaneh Saedii, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                           51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGTATGTTAAAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
MNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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                                                                                                                                                                                                                                                                                                                   Length 682;
          /product="secretory leukoprotease inhibitor"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                George Yang, Scott Zuyderduyn, Marco Marra.
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/clone="MGC:41142 IMAGE:1513866"
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                                                                                                                                                                                                                                                                                                                16.8%; Score 34.6; DE 53.3%; Pred. No. 5.4;
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                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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1 (bases 1 to 894)
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LKLEKPQCRTDWECPGKQRCCQDACGSKCVNPVPIRKPVWRKPGRCVKTQARCMMLNP
PNVCQRDGQCDGKYKCCEGICGKVCLPPM"
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Abe,T., Tominaga,Y., Kikuchi,T., Watanabe,A., Satoh,K., Watanabe,Y. and Nukiwa,T.
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and Nukiwa,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMU94341 682 bp mRNA linear ROD 29-OCT-1997
Mus musculus secretory leukoprotease inhibitor mRNA, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Tohoku University, 4-1 Seiryomachi, Aoba-ku, Sendai 980-77, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacterial pneumonia causes augmented expression of the secretory leukoprotease inhibitor gene in the murine lung Am. J. Respir. Crit. Care Med. 156 (4 Pt 1), 1235-1240 (1997) 98011992
Zitnik,R.J., Zhang,J., Kashem,M.A., Kohno,T., Lyons,D.E.,
Wright,C.D., Rosen,E., Goldberg,I. and Hayday,A.C.
Direct Submission
Submitted (31-JAN-1997) Internal Medicine, Yale University, 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 CCAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAACTCAGGCAAGATGTATGATGCTTAAC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
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                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="secretory leukocyte protease inhibitor"
/protein_id="AAC53140.1"
/db_refe="GI:1945383"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 671;
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                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/cell line="ras-transformed 3T3 cells"
13. .408
                                                                                                                                                                                                                                                                                                                                                                        function="serine protease inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="B6CBA [C57Black/6 x CBA]"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34.6; DB 10;
Pred. No. 5.4;
                                                                                                                               Cedar Street, New Haven, CT 06520, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match
Local Similarity 53.3%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="lung"
14. .409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 ATATGTGGGAAAGTCTG 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                              1. .671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus.
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   AUTHORS
                                                                                                  JOURNAL
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/db_xref="G1:1763263"
/db_xref="G1:1763263"
/Ltanslation="MKSCGLIPFTVILALGILAPWTVEGGKNDAIKIGACPAKKPAQC
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PNVCQRDGQCDGKYKCCEGICGKVCLPPPM"
                                                                                                          | codon_start=1
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| product==secretory leukocyte protease inhibitor"
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| PNVCQRDGQCDGKYKCCEGICGKVCLPPM"
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Mus musculus secretory leukocyte protease inhibitor mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                479 CCAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGTATGATGCTTAAC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 CCTCCCAATGTCTGCCAGAGGGACGGCAGTGTGACGGCAAATACAAGTGCTGTGAGGGT 598
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Ding,A., Jin,F.-Y. and Nathan,C.F.
Direct Submission
Submitted (01-007-1996) Medicine, Cornell University Medical
College, 1300 York Ave. Box 57, New York, NY 10021, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jin, F.Y., Nathan, C., Radzioch, D. and Ding, A. Secretory leukocyte procease inhibitor: a macrophage product induced by and antagonistic to bacterial lipopolysaccharide cell 88 (3), 417-426 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="secretory leukocyte protease inhibitor"
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0
                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 894;
                                                                                                                                                                                                                                                                                                                                                                                                            64; Indels
/tissue_type="Mammary gland, lactating
/clone_lib="Soares_mammary_gland_NMLMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="serine protease inhibitor"
                                                                                                                                                                                                                                                                                                                                                               Match 16.8%; Score 34.6; DE Local Similarity 53.3%; Pred. No. 5.4;
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                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                  /note="Vector: pT7T3D-Pac'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/cell line="RAW 264.7"
/cell type="macrophage"
447. 842
                                                                                                                                                                                                                                                                                          233 g
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                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U73004.1 GI:1763262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 TCCTGCGGTATGGCTTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    599 ATATGTGGGAAAGTCTG 615
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                                                                                         .631
                                                                                                                                                                                                                                                                                                                                                                                                            73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus.
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TITLE
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JOURNAL
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MMU73004
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To (bases 1 to 156460)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Burbar, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, M.C., Carron, T.F., Carter, M., Erown, E., Brown, M., Bryant, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Charezo, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Carron, T.F., Carter, M., Day, Carroll, L., Daderich, D.A., Davila, M.L., Day, Carroll, L., Dathorne, S.R., Durbin, K.J., Davaris, C., Day, Carroll, L., Ding, Y., Durbin, R., J., Davaris, C., Day, Carroll, L., Ding, Y., Durbin, R., J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C. Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggo, N., Folle, S., Hamilton, K., Harris, G., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jai, Y., Johnson, R., Hull, M., Louis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Louisegd, H., Lozado, K.J., Lui, Y., Lucter, R., Martinde, A., Martinez, E., Martinez, E., Martiney, E., Martine, E., Martiney, E., Martin, E., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus clone CH230-197B1, *** SEQUENCING IN PROGRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                        51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAAC 110
                                                                                                                                                                                                                                                                                111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
                                                                                                                                                                                                                                                                                                                                                   750 ccrcccaarercreccadaggacggcagrergacggcaarracaagrergreaggr 809
                                                                                                                                                                                                          690 ccaciciogadgadaccidagagadaracacaaaacrcagacaagaigiargaraciraac 749
                                                                         Gaps
                                                                      ;
0
   Length 1123;
                                                                      64; Indels
Score 34.6; DB 10;
Pred. No. 5.4;
0; Mismatches 64;
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   16.8%;
53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                171 TCCTGCGGTATGGCTTG 187
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                                                                         Conservative
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   Query Match
Best Local Similarity
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AC110686
                                                                         Matches
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AUTHORS TITLE JOURNAL

JOURNAL REFERENCE

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

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                                                                         Direct Submission

Submitted (15-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

S Worley, K.C.

Direct Submission

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 12, 2002 this sequence version replaced gi:18767289.

Center: Baylor College of Medicine
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NOTE: This is a 'working draft' sequence. It currently consists of 81 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap, version 0.990329 consensus quality: 89134 bases at least Q40 Consensus quality: 94194 bases at least Q30 Consensus quality: 97800 bases at least Q20
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Mus musculus clone RP23-16701, LOW-PASS SEQUENCE SAMPLING.
AC100679
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 61448)
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 TGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCC 173
82496: gap of unknown length
83902: contig of 1406 bp in length
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                                                                                              Score 34.2; Dl
Pred. No. 6.6;
                                                                                                                                                              0; Mismatches
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Best Local Similarity
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AC100679/c
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AUTHORS
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* NOTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Buns of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                       71: gap of 100 bp 6382: contig of 711 bp in length 82: gap of 100 bp 722 bp in length 64: gap of 100 bp 8027: contig of 723 bp in length 27: gap of 100 bp
                                                                                                                                                693 792: gap of 100 bp 793 1505: contig of 713 bp in length 1506 1605: gap of 100 bp 1606 2326: contig of 721 bp in length 2327 2426: gap of 100 bp 2427 3168: contig of 742 bp in length 2427 3168: contig of 742 bp in length
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contig of 700 bp
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contig of 702 bp
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5571: cor
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9663: cor
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4780: co
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6382: co
                                                                                                                                                                                                                                                                                                                                                                              8127: gap of
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7204: co
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15 25815: contig of 701 bp in length
16 25915: gap of 100 bp
16 26595: contig of 680 bp in length
18 26595: contig of 680 bp in length
19 27403: contig of 708 bp in length
19 38224: contig of 708 bp in length
19 38224: contig of 721 bp in length
19 28224: contig of 721 bp in length
19 28224: gap of 100 bp
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: contig of 715 bp in length
ap of 100 bp.

: contig of 713 bp in length
ap of 100 bp.
: contig of 716 bp in length
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56: gap of 100 bp
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41188: contig of 682 bp in length
41288: gap of 100 bp
41941: contig of 653 bp in length
42041: gap of 100 bp
42711: contig of 670 bp in length
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48417: con
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54078: cont
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Mus musculus chromosome X clone RP23-405E21, *** SEQUENCING IN A PROCRESS ***, 9 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (09-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 15, 2002 this sequence version replaced gi:21998201.
                                                                                                                                                                                                                                                                           81 ATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGAT 140
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAF4; version 4.5
Chemistry: Dye-terminator; 16% of reads
Chemistry: Dye-terminator Big Dye; 83% of reads
Consensus quality: 250716 bases at least Q40
Consensus quality: 252116 bases at least Q40
Consensus quality: 253330 bases at least Q20
Insert size: 254036; sum-of-contigs
Insert size: 193899; 9.8% error; agarose-fp
Quality coverage: 10.38x in Q20 bases; sum-of-contigs Quality
coverage: 15.09x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL671891.10 GI:22265400
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                   Db 45637 Trigicascandaardaricicricarcricarcricaarrcacrircicaacri 45584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                  141 TGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTT 194
                                                                                                                                                                   ·.
                                                                                                       16.5%; Score 34; DB 2; Length 61448; 56.1%; Pred. No. 7.8; ive 0; Mismatches 50; Indels
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64088 195855: contig of 131768 bp in length
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54862 54961: gap of 100 bp
54962 55700: contig of 739 bp in length:
55701 55800: gap of 100 bp
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55701 55800; gap of
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                                                                                                                                    Local Similarity
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Direct Submission
Submitted (27-FBB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Can replaced sanger. ac.uk
On Feb 28, 2002 this sequence version replaced gi:18857781.
Can replaced sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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0
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Human DNA sequence from clone RP5-88207 on chromosome lp33-34.2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGAT 140
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0
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220998 223634: contig of 2637 bp in length 223635 223734: gap of 100 bp 226795 2266794: contig of 3060 bp in length 226795 226694: gap of 100 bp 226895 229736: contig of 2842 bp in length 229737 229837: gap of 101 bp 229838 224836: contig of 24999 bp in length. Location/Qualifiers
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64088. .195855
/note="assembly_fragment:00034.1"
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/note="assembly_fragment:05324"

226895. .229736

200687. .259336

/note="assembly_fragment:05355"

/note="assembly_fragment:05381"

a 50260 c 48899 g 75017 t 80
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213945. .217297
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217398. .220897
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220998. .223634
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                                                                                                                                                                                                                                                        db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                   /chromosome="X"
/clone="RP23-405E21"
/clone_lib="RPCI-23"
1. .63987
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at.
                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC116110 178652 bp DNA linear HTG 24-AUG-2002
Mus musculus clone RP23-19B12, WORKING DRAFT SEQUENCE, 12 ordered
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Tandem repeat. Forced join. Gap size estimated to be approximately 400bp by restriction digest data." 97714. .97772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr1
RPS-88207 is from the library RPCI-5 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.crg/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence from overlapping clone RP11-69J16 (AL359473). Assembly confirmed by restriction digest." 48616 a 38050 c 37699 g 47291 t
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/chromosome="1"
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AC116110.2 GI:22474982
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Matches 89; Conservative
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TITLE

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* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1817 916: gap of 100 bp 170 bp 186: contig of 106 bp in length 1985: contig of 816 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 811 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in length 1985: contig of 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 812 bp in 81
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Quality coverage: 8.4 in Q20 bases; agarose-fp
Quality coverage: 8.3 in Q20 bases; sum-of-contigs
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contig of 112978 bp in length
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7324 13183: contig of 5860 bp in length
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
154138. .175237
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26362. .133596
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/note="assembly_fragment
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/clone="RP23-19B12"
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917. .1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 175241 bases at least Q10 Consensus quality: 176762 bases at least Q20 Consensus quality: 177264 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L22837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert sizė: 176000; agarose-fp
Insert size: 177552; sum-of-contigs
                                      Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-19B12
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JOURNAL
                                      AUTHORS
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REFERENCE
                                                                                                                                              REFERENCE
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COMMENT

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1485 TATGTGGGAAAGTCTG 1500
                                                                                                                          Human DNA
                                                                                                                                                sequence.
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                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                              RESULT 61
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/db_xref="G1:4100899"
/db_xref="G1:4100899"
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LKLERPQCRTDWECFEKQRCCQDAGSKCVNPVPIRKPVWRKPGRCVKTQARCMMLNP
PNVCQRDGQCDGKYKCCEGICGKVCLPPPM"
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (ases 1 to 2435)
Kikuchi,T., Abe,T., Hoshi,S., Matsubara,N., Tominaga,Y., Satoh,K.
                                                                                                                                                                                                                                                                                                    Mus musculus secretory leukoprotease inhibitor gene, complete cds.
AF002719
                                                                                                        Db 102074 TGATTCTCTCTGTTATACTATCAACTTGTGAACTCTAACATTCTGACGTGAAAGCCGAAG 102015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abe, T., Hoshi, S., Matsubara, N., Tominaga, Y., Satoh, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06 MAY-1997) Department of Respiratory Oncology and Molecular Medicine, Institute of Development, Aging and Cancer, Tohoku University, 4-1 Seiryo-machi, Aoba-ku, Sendai, Miyagi-ken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1365 CAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGTATGATGCTTAACC 1424
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                                                                                                                                                                           TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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                        Gaps
                                                                                                                                                   Qy 148 GTAŢÇAAAAAGTGCTGTGAAGGTŢCCTGCGGTATGGCŢŢGŢTTCGTTÇÇACAAŢAAŢ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(101. .205,781. .942,1368. .1517,2080. .2322)
/product="secretory leukoprotease inhibitor"
join(121. .205,781. .942,1368. .1516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structure of the murine secretory leukoprotease inhibitor gene and chromosomal localization of the human and murine
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Pred. No. 11;
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                      52; Indels
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  Pred. No. 8.8;
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/db_xref="taxon:10090"
/chromosome="2"
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52.9%;
  55.6%;
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Kikuchi, T., Abe, T., 1
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Best Local Similarity 52.9
Matches 72; Conservative
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Mus musculus
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                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                88
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                         RESULT 60
AF002719
                        Matches
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Submitted (22-5AN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Um Jan 23, 2002 this sequence version replaced gi:18250572.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annocated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by resolve all sequencing problems; such absentiations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp;, WORMPEP; Information on the WORMPEP databases can be found a with their source databases: Em; EMBL; Sw; Cattabases can be found a with their source databases: Em; EMBL; Sw; Cattabases can be found a with their source databases: Em; EMBL; Sw; Cattabases can be found a with their source databases: Em; EMBL; Sw; Cattabases can be found a with their source databases: Em; Cattabases can be found a with their source databases: Em; Cattabases can be found a with their source databases: Em; Cattabases can be found a with their source databases: Em; Cattabases can be found a with their source databases: Em; Cattabases can be found a with their source databases: Em; Cattabases can be sourced by the cantabase can be sourced by the cattabase can be sourced by the cattabase can be sourced by the cantabase can be sourced by the cattabase can be sourced by the cantabase can be sourced by the cantabase can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-309C8 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP1-198G23 is at 82988 in this sequence. The true right end of clone RP11-378H3 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
PRI 22-JAN-2002
     84987 bp DNA linear PRI 22-JAN-2005 sequence from clone RPI1-309C8 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/ChrX
RP11-309C8 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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15105 c 15585 g 27666 t
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57.7%; Pred. No. 10
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db_xref="taxon:9606"
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                                                                                                                                                         ALG62897
ALG62897.6 GI:18307360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 84987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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## Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humguery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 20, 2001 this sequence version replaced gi:15020991. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either duble-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw;, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP that of the content of t ALS90429 190669 bp DNA linear ROD 17-NOV-2001 Mouse DNA sequence from clone RP23-462016 on chromosome 2, complete http://www.sanger.ac.uk/Projects/C\_elegans/wormpep RP23-462016 is from the RPCI-23 Mouse PAC Library\_constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACG3. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus Db 49853 AACTTACATTTTTGGGATAAATAATAATTGGTCATTTTACATAA 49896 AL590429.9 GI:17017748 (bases 1 to 190669) Direct Submission house mouse. Mus musculus sequence. AI,590429 Kay, M. AL590429/c DEFINITION ORGANISM ACCESSION REFERENCE AUTHORS JOURNAL RESULT 62 KEYWORDS TITLE COMMENT VERSION

```
/note="Tandem repeat. Forced join. Gap size estimated to
be approximately 900bp by restriction digest data."
1 43425 c 42104 g 50027 t
This sequence is the entire insert of clone RP23-462016 The true left end of clone RP23-14014 is at 187423 in this sequence. The true right end of clone RP23-346D16 is at 20063 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 140443. .140460
/note="Single clone region. Sequence from reads from a
short insert library derived from a clone PCR.
Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                             /note="Sequence from uni-directional dGTP big dye terminator reads only"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.3%; Score 33.6; DB 10; Length 190669; Best Local Similarity 52.9%; Pred. No. 10; Matches 72; Conservative 0; Mismatches 64; Indels 0; C
                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
                                                                                                                                                                                                                                       /clone="RP23-462016"
/clone_lib="RPCI-23"
104714_ .104881
                                                                                                                  i. .190669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc feature
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                                                                                                                           source
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ORIGIN
                                                                                            FEATURES
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unknown length

. 0

0; Gaps

52 CTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACC 111

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ACO21992 193302 bp DNA linear HTG 07-JUL-2000
Homo sapiens chromosome X clone RP11-561H2, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA USA ON Apr 21, 2000 this sequence version replaced gi:7024133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamaalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Bases 1 to 193302)
Waterston,R.H.
97004 CAGTGTGGAGGAGGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGTATGATGCTTAACC 96945
                                                                                           96944 CTCCCAATGTCTGCCAGAGGGACGGCAGTGTGACGCCAAATACAAGTGCTGTGAGGGTA 96885
                                            112 CACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is a runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 3.65 in Q20 bases; agarose-fp Quality coverage: 3.58 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           i: contig of 1164 bp in length
i: gap of unknown length
2: contig of 1518 bp in length
2: gap of unknown length
3: contig of 1406 bp in length
3: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 1671 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primer ET; 68% of reads
Chemistry: Dye-terminator Big Dye; 32% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178265 bases at least Q40
Consensus quality: 185356 bases at least Q30
Consensus quality: 185356 bases at least Q30
Insert size: 18500; agarose-fp
Insert size: 18500; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; 68%
Sequencing vector: plasmid; 32%
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 193302)
Waterston, R.H.
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6159:
7486:
                                                                                                                                                                                      Db 96884 TATGTGGGAAAGTCTG 96869
                                                                                                                                                                                                                                                                                                                                                            25 unordered pieces.
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1265
2783
2783
4289
4389
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ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                              RESULT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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g of 5696 bp in length funknown length
                                                                                                                                                                                                                                                                                                               of 13140 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                              118259: contig of 14050 bp in length
118559: gap of unknown length
118555: contig of 20196 bp in length
138655: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                in length
                                                                                                                                                                                                                                                                                                                                        104209: contig of 14515 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                           in length
                                                                                                  length
bp in length
length
bp in length
                                                                                                                                             length
bp in length
                                                                                                                                                                                                                                                            unknown length
of 9131 bp in length
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bp in length
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bp in length
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of 5580 bp in length
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bp in length
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bp in length
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160951: gap of unknown length
193302: contig of 32351 bp in
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/note="assembly_name:Contig28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10566. .12280
/note="assembly_name:Contig29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_name:Contig30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5133. .17864
/note="assembly_name:Contig31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17965. .23051
/note="assembly_name:Contig32"
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37752. .42402
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'note="assembly_name:Contig24"
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note="assembly_name:Contig26"
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/note="assembly_name:Contig25"
4389. .6059
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note="assembly_name:Contig27"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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clone="RP11-561H2"
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This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22 buring sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 131012 icidicirriarricrarriargecegrararirargirearirgarirugeargiraaacea 130953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 11, 1999 this sequence version replaced gi:5002615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 TGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCC 112
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Human DNA sequence from clone RP1-319F24 on chromosome
22q12.3-13.31 Contains a GSS, complete sequence.
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104210. 118259
/note="assembly_name:Contig44"
118360. 138555
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160952. .193302
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61908 a 35369 c 35618 g 57952 t ;
                                       46628. .52207
/note="assembly_name:Contig38"
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/note="assembly_name:Contig39"
58104. .67234
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138656. .160851
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TITLE
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep RP1-319F24 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RPI-319F24 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone RP3-508115 is at 28416 in this sequence. The true right end of clone RP1-199H16 is at 100 in this sequence. Location/Qualifiers
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7794. .8096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L1 repeat: matches 2983. .3047 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L2 repeat: matches 1747. .2746 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .082. .3285
note="MER20 repeat: matches 2. .218 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .863. .6908 Thote="MER74B repeat: matches 1. .46 of consensus"
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/note="AluSx repeat: matches 1. 297 of consensus"
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note="AluSx repeat: matches 1. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "note="Alusx repeat: matches 3. .310 of consensus" 3469. .5542
note="MIR repeat: matches 8. .81 of consensus"
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note="AluSx repeat: matches 1. .206 of consensus"
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note="AluJo repeat: matches 1. .305 of consensus"
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note="MIR repeat: matches 68. .262 of consensus"
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/note="23 copies 2 mer ta 80 conserved"
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note="18 copies 2 mer ag 88 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1. 926. .2825
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note="Single clone region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/map="q12.3-13.31"
/clone="RP1-319F24"
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11525. 11617
'note="AluSp/q repeat: matches 202. 308 of consensus"
1678. 11974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 90. .260 of consensus"
14776. .14976
/note="AluSg/x repeat: matches 85. .291 of consensus"
'note="MLT1J repeat: matches 430. .510 of consensus"
                                                                /note="MLT1J repeat: matches 350. .440 of consensus"
9332. .9625
                                                                                                                                                        1626. .9683
'note="MLT1J repeat: matches 290. .350 of consensus"
                                      /note="AluJb repeat: matches 84. .300 of consensus"
                                                                                                                                                                                                                                                9990. .10296
'note="MLTLJ repeat: matches 11. .290 of consensus"
                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2418, .2548 of consensus" 0656. .10969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "note="MIR repeat: matches 7. .68 of consensus"

15807 .15876

"note="MIR repeat: matches 185. .256 of consensus"

15870 .15956

1000e="L2 repeat: matches 2667. .2748 of consensus"

15877 .16218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L2 repeat: matches 1678. 2473 of consensus"
complement(14319. 14778)
/note="match: GSS: Em:AQ164414"
14607. 14767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 2021. .2667 of consensus"
16812. .17288
//note="L2 repeat: matches 1371. .1777 of consensus"
17899. .17584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /7289. 17584
/note="AluSq repeat: matches 12. 304 of consensus"
17585. 18113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2198. .2414 of consensus"
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1420. .21726
                                                                                                                                                                                                   1684. .9989
"note="AluSx repeat: matches 1. .310 of consensus"
                                                                                                                                'note="AluSx repeat: matches 3. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                             note="AluSq repeat: matches 1. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                        note="AluJb repeat: matches 2. .300 of consensus" .1393. .11517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Alusg repeat: matches 1. .298 of consensus"
2666. .13415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="AluSx repeat: matches 3. .265 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluJo repeat: matches 1. .308 of consensus" 9009. .19579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER34 repeat: matches 5. .543 of consensus"
9628. .19839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Alusg repeat: matches 1. .308 of consensus" 22393. .22509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 623. .1371 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 79. .207 of consensus" [1525. .11617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .8076. .18162
"Note="MR repeat: matches 81. .164 of consensus"
8190. .18491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluY repeat: matches 1. .302 of consensus"
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/note="match: GSS: Em:AQ122011"
14978. .15035
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'note="AluSg/x repeat: matches 174. .295 of consensus"

COMMENT

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Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarate, J., Campopiano, A., Chang, J., Chasgro, B., Cooke, P., Dangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Darellano, K., Darar, V.S., Dodge, S., Faro, S., Gord, S., Goyette, M., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Lamazares, R., Landers, T., Lehoczky, J., Levine, K., Liu, G., MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meltim, J., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McRess, B., Melga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Conne, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuback, R., Schuback, R., Strauers, S., Chuback, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 TIGICCIATTAICTIGATTCGTTGCGCTAIGTTAAACCCACCTAACCGTTGTTTGAAGGA 133
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Homo sapiens chromosome 8 clone RP11-1058E13 map 8, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24594. .24727 |
/note="L2 repeat: matches 2577. .2735 of consensus"
25034. .25299
                                                                                                                                                                                                            note="MER66A repeat: matches 1. .478 of consensus"
                                                                                                                                                                                                                                                     23291. .23377
/note="L2 repeat: matches 2612. .2705 of consensus"
23388. .23490
                                         .189 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                  /note="WIR repeat: matches 86. .201 of consensus"
23491. .23796
/note="AluSx repeat: matches 1. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 14614 TAATGTTTATTGAGTTCTTACTCTGTGCTATGCTGTTTGCTGAGTGCTTGCATGT 14668
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone RP11-1058E13
22613. .22713
/note="MER5A repeat: matches 90.
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Pred. No. 12;
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55.7%;
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Homo sapiens.
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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                               Submitted (08-DBC-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A.& Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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6229; gap of 100 bp
6919: contig of 690 bp in length
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                                                99 17998; gap of 100 bp 18679; contig of 681 bp in length 80 18779; gap of 100 bp 19551; contig of 672 bp in length 19551; gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 b
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chasy, J., Chasy, J., Chang, J., Chang, J., Chang, J., Cooke, P., Cooke, P., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardhan, S., Ginde, S., Govette, M., Graham, L., Garade, Pierreira, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M. McChan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M. McEwan, P., McKernan, K., Medrim, J., Marthews, C., Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnall, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schupback, R., Seaman, S., Strauss, N., Subramanian, A., Trais, N., Traiglio, J., Ver, W. J., Yong, G., Viel, R., Vo, A., Wilson, B., Wand, Zody, M., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wand, Zody, M., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wand, Zody, M., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., And Zody, M., Traiglio, J., Ye, W.J., Young, G., Viel, R., And Zody, M., Cambek, L., Zimmer, A. and Zody, M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56071 TITICCTAATCTCCAGCTGTGTTCTCTAGGTACCACCCTTGTATAATATGATTAAGAGC 56130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 TIGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56131 TAATGTTTATTGAGTTCTTACTCTGTGCTATGCTGTTTGCTGAGTGCTTGCATGT 56185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 CACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGT 188
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20: gap of 100 bp
46985: contig of 665 bp in length
85: gap of 100 bp
47761: contig of 676 bp in length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-187P2
Unpublished
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
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0; Mismatches
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JOURNAL REFERENCE AUTHORS

TITLE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Best Local Similarity
Matches 61; Conserv
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                                                                                                            Surren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Changalor, B., Browm, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Fercerald, M., Fitzhquh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matchen, C., MacCarthy, M., McEwan, P., McKernan, K., Meldrim, J., MacLean, C., Macdonald, P., Major, J., Marquis, N., Marduis, D., Oliver, J., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Norman, C., Norman, C., Norman, C., Norman, C., Norman, C., Sepencer, S., Stolauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolauer, J., Topham, K., Travers, M., Traiglio, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Traiglio, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Traiglio, J., Wyong, C., Zimmer, A. and Zody, M.

Submitted (05-JUN-2002) Whitehead Institute/MIT Center for Genome Submitted (05-JUN-2002) Whitehead Institute/MIT Center for Genome Submitted (05-JUN-2002) Whitehead Institute/MIT Center for Genome Smit, A.F., & Green, P. (1998)
                           Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by the finished sequence as soon as it is available and the accession number will be preserved.

1 31998: contig of 31998 bp in length
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Center Clone name: 187 P. 2

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 220008 bases at least Q40

Consensus quality: 230799 bases at least Q30

Consensus quality: 231399 bases at least Q20

Insert size: 240000; agarose-fp

Insert size: 231693; sum-of-contigs
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Quality coverage: 8.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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35842 38517: contig of 2676 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seg.wi.mit.edu
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                                                                                           (bases 1 to 232793)
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Direct Submission
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TITLE JOURNAL

COMMENT

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AF205374 4090 bp DNA linear ROD 21-DEC-1999
Mus musculus secretory leukocyte protease inhibitor (Slpi) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 167275 AATATGTTGATGGATTTCCTTATATTTAACCATCCCTGCATCCCTGGGATGAAGCCTACT 167216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 ATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 232793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 167215 TGATCACGGATTAACGATGCCTTTGAAGTGTTCTTGGATTTTGGTTTG 167169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Indels
                                                                                           135880 135979: gap of 100 bp 135880 14306: contig of 28327 bp in length 164407 194369: contig of 29963 bp in length 194370 194469: gap of 100 bp 194470 223647: contig of 29178 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 TGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTG 187
101041 101140: gap of 100 bp
101141 116926: contig of 15786 bp in length
116927 117026: gap of 100 bp
117027 115879: config of 18853 bp in length
                                                                                                                                                                                                                                        223648 223747: gap of 100 bp 223748 232793: contig of 9046 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone_end:T7
vector_side:right"
72773 a 45524 c 45372 g 68024 t
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note="assembly_fragment"
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/note="assembly_fragment"
164407. .194369
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/note="assembly_fragment"
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| note="assembly_fragment"
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194470. .223647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="assembly_fragment"
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="RP23-187P2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46270. .101040
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Submitted (10-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Jul 10, 2002 this sequence version replaced gi:21717262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 TATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updaced with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.1%; Score 33.2; DB 2; Length 236121; 59.6%; Pred. No. 13; trive 0; Mismatches 38; Indels 0;
                                                                                                                                                                           Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 0.00 in Q20 bases; agarose-fp Quality coverage: 11.87 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7176: contig of 7176 bp in length
7276: gap of unknown length
18172: contig of 10896 bp in length
18272: gap of unknown length
33690: contig of 15418 bp in length
33790: gap of unknown length
94883: contig of 61093 bp in length
94883: contig of 61093 bp in length
160810: contig of 65827 bp in length
                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 233502 bases at least Q40
Consensus quality: 233911 bases at least Q30
Consensus quality: 234304 bases at least Q20
Insert size: 205000; agarose-fp
Insert size: 205000; agarose-fp
Insert size: 205001 sum-of-contigs
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Location/Qualifiers
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                                                                                                                                                                                                                             /note="assembly_name:Contig7"
46827 c 47077 g 70356 t
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/note="assembly_name:Contig2"
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/note="assembly_name:Contig3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig6"
160911, .236121
                          McPherson, J.D. and Waterston, R.H.
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                                                                                                                                                               ---- Genome Center
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                                               Direct Submission
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Matches 56; Conserva
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94984
160811
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18273
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                          AUTHORS
                                                                  JOURNAL
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                                                                                                                  COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="secretory leukocyte protease inhibitor"
/protein_id="AAPF191941"
/db_xref="G1:666529"
/translation="MKSCGLLPFTVLLALGILAPWTVEGGKNDAIKIGACPAKKPAQC
LKLERPQCRTDWECPGKQRCCQDACGSKCVNPVPIRKPVWRKPGRCVKTQARCMALNP
PNVCQRBQCDGKYKCCEGTGGWCLPPPM"
6 953 c 1069 g 1118 t 6 others
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0
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Mus musculus chromosome UNK clone RP23-384F19, WORKING DRAFT
1 (bases 1 to 4090)
Lei,K.-J., Jin,W.-W. and Wahl,S.M.
Folation and characterization of the gene for secretory leukocyte Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-JUL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 236121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 236121)

McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                        Lei, K.-J., Jin, W.-W. and Wahl, S.M.
Direct Submission
Submitted (16-NOV-1999) Oral Infection and Immunity Branch,
National Institute of Dental & Craniofacial Research, 30 Convert
Dr., MSC4352, Bldg. 30, Rm. B06, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2561 GTGTGGAGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGTATGATGCTTAACCCT 2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2621 CCCAATGTCTGCCAGAGGGACGGCAGTGTGACGCCAATACAAGTGCTGTGAGGGTATA 2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 GIGICTACTAAGCCAGGITCTIGICCTATTAICTTGATTCGTTGCGCTATGITAAACCCA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 CCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="secretory leukocyte protease inhibitor"
join(1266. .1353,1923. .2080,2561. .2710)
/gene="Slpi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.1%; Score 33.2; DB 10; Length 4090; 53.0%; Pred. No. 14; tive 0; Mismatches 63; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(<1266. 1353,1923. .2080,2561. .>2710)
/gene="Slpi"
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 236121)
McPherson, J.D. and Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                             /strain="129/SvJ"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                        <1266. .>2710
/gene="Slpi"
                                                                                                                                                        (bases 1 to 4090)
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                                                                                                                                                                                                                                                                                                                  1. .4090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 TGCGGTATGGCTTG 187
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ORIGIN
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                                        REFERENCE
AUTHORS
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AUTHORS
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JOURNAL
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SOURCE
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VAAATGHTVVLVDOTEDILAKSKKGIEESILKRMAKKKFTENRKAGDEVEKTI.SCL.ST
STAASVVHRSTDLVVBAILVENKLKNRELPQRLDKFRARHTITASANTSSLINTANAT
TRODRFAGGHFFNPVPMKLVPVIKTPMTSQKTFEGLVDFCKTLGKHPVSCKDTPGFI
VNRLLVPYLLEAVRLHERGDASKEDIDTAMKLGAGYPMGPFELLDTYVGLDTTKFILDGFI
VNRLLVPYLLEAVRLHERGDASKEDITAMKLGAGYPMGPFELLDTYVGLDTTKFILDGFI
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O'Brien,L.K., Sims,H.F. and Strauss,A.W.
Direct Submission
Submitted (102-MAY-2001) Pediatrics, Vanderbilt Medical Center, 1161
21st Avenue South, D-2220 MCN, Nashville, TN 37232, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L-3-hydroxyacyl-Coenzyme A dehydrogenase;
NAD-dependent dehydrogenase; specific for medium and short
chain fatty acids; SCHAD; HADH"
                                                                                                                                                                                                ROD 20-MAY-2001
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                                                                                                                                                                        hus musculus medium and short chain L-3-hydroxyacyl-Coenzyme A dehydrogenase (Mschad) gene, exons 2 through 8, and complete cds; AF375597
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
81022 TTTTCACTAGACTCCAAGTCCAGCTCCAATCTCTTCTCCACAGAGTCCTGGGCAATTCTC 81081
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5986. .6112,8631. .8720,10231. .10303,15582. .15698,
16994. .17515)
/gene="Mschad"
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5986. .6112,8631. .8720,10231. .10303,15582. .15698,
16954. .17072)
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O'Brien,L.K., Sims,H.F. and Strauss,A.W.
Mouse medium and short chain L-3-hydroxyacyl-Coenzyme A
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order(AF375596.1:6458. .10094,1. .17515)
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                                                                                                  81082 TIGATICATCACTCTCTGACAAAACAAACAAAC 81115
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/db_xref="GI:14150817"
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/gene="Mschad"
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/gene="Mschad"
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AC119403 40223 bp DNA linear PRI 28-JUN-2002
Homo sapiens chromosome 19 clone LLNLR-265A7, complete sequence.
AC119403
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Submitted (26-APR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 40223)
DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 4022)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9488 GITTIGITITGITITGITITGITITGITITGATATAAGAAGACTCCCTTCCTGACGTGTG 9547
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Finishing Completed at Stanford Human Genome Center
Wuw-shgc.stanford.edu
Wuwlige.stanford.edu
Wuality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.1.
Location/Qualiflers
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/chromosome="19"
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DOE Joint Genome Institute.
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/gene="Mschad"
/number=7
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                    10231. .10303
/gene="Mschad"
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SOURCE
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Homo sapiens chromosome 19 clone LLNLR-300G1, complete sequence.
AC011559
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Dib Joint Genome Institute.
Direct Submission Sequencing Facility, DOE Joint Submitted (07-007-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA
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Submitted (28-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 42665)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                        29885 ACATGCTGGACCAAAACTAGAAGTCATTTAACTTTAAAAAGAACTGCCACACTGTTTT 29944
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    0; Gaps
                                              26 ATATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAAGCCAGGTTCTTGTCCTATTAT 85
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Pred. No. 16;
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
0; Mismatches
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/chromosome="19"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Bequslavkly, L., Bunkgalter, B., Erown, A., Colangelo, M., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kall, C., Lancque, K., Lamazares, R., Lancerky, M., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McBwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McBwan, P., Major, J., Mguyen, C., Nicol, R., Mihova, T., Nurman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Silley, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Travis, N., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Travers, M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Subrission of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the strain of the stra
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Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Si (bases 1 to 213703)

Bulknall Ler, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Brown, A., Camarata, J., Campopiano, A., Chang, JJ., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, JS., Dodge, S., Farreira, P., FitzHugh, W., Gace, D., Galagan, J., Gardyna, S., Gord, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyna, S., Gands, S., Gord, S., Goyette, M., Tilev, L., Johnson, R., Macdonald, P., Milor, J., Marquis, N., Matthews, C., Macdonald, P., Malor, J., Marquis, N., Matthews, C., Macdonald, P., Malor, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, C., Nordan, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Norman, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Saltos, R., Schupback, R., Saman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zammer, A. and Zody, M.

Bybmitted (04-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mus musculus clone RP23-157H14, WORKING DRAFT SEQUENCE, 46 ordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Unpublished
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus.
Mus musculus
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Center: Whitehead Institute/ MIT Center for Genome Research
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On May 4, 2002 this sequence version replaced gi:20389394 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                        Consensus quality: 200834 bases at least Q40 consensus quality: 204678 bases at least Q40 consensus quality: 204678 bases at least Q30 consensus quality: 206239 bases at least Q20 Insert size: 188000; agarose-fp Insert size: 209203; sum-of-contigs Quality coverage: 8.3 in Q20 bases; sum-of-contigs Quality coverage: 7.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                      Center clone name: 157 H 14
------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                                                                                                 652 751: gap of 100 bp 752 1458: contig of 707 bp in length 1459 1558: gap of 100 bp 1559 2267: contig of 709 bp in length
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10478: contig of 667 bp in length
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13536: contig of 651 bp in length
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184611: contig of 17422 bp in length
                                                          17325: contig of 1290 bp in length 17325: gap of 100 bp 19181: contig of 1856 bp in length
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19282 21156: contig of 1875 bp in length
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2271 bp in length
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32803: contig of 2363 bp in length
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49229: contig of 5222 bp in length
49329: gap of 100 bp
52432: contig of 3103 bp in length
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15835: contig of 650 bp in length
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/clone lib="RPCI-23 Female Mouse BAC"
1. .651
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/note="assembly_fragment"
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Bulkaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaiia; Euteleria; Primates; Catarrhini; Hominidae; Homo.

Mammaiia; Euteleria; Primates; Catarrhini; Hominidae; Homo.

Mammaiia; Euteleria; Primates; Catarrhini; Hominidae; Homo.

Manzoks; S.L.; Maratunge, H.C.; Arej.R.; Aptele, M.; Banks, T.; Barbaria, J.; Barbaria, J.; Barbaria, D.; Bancton, J.; Blande, K.; Blankenburg, K.; Bonnin, D.; Banck, J.; Barbaria, J.; Barbaria, J.; Barbaria, J.; Barbaria, J.; Barbaria, J.; Barbaria, J.; Barbaria, J.; Barbaria, J.; Barbaria, J.; Barbaria, C.; Barter, M.; Chod, M.; Chod, M.C.; Chang, J.; Chod, M.C.; Chod, M.D.; Dathorne, S.R.; David, R.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Davisis, C.; Elbaj, C.; Escotto, M.; Parisis, C.; Harria, R.; M.; Dadara, M.; Dang, Y.; Ding, Y.; Dinh, H.; Douthwaite, K.J.; Draper, H.; Dugan-Rocha, S.; Durbin, K.J.; Barnhart, C.; Edgar, D.; Edwards, C.C.; Elbaj, C.; Escotto, M.; Falls, T.; Perragueo, D.; Flagg, M.; Ford, J.; Poster, P.; Frantz, P.; Garbis, A.; Garner, T.; Garza, M.; Gall, R.; Gorrell, J.H.; Guevara, M.; Gunzatne, P.; Hales, S.; Hame, J.; Joackson, E.; Vial, M.; Hawes, A.; Harriandez, J.; Hernandez, O.; Harris, K.; Harr, M.; Havds, P.; Hawes, A.; Harria, K.; Jacobson, B.; Vial, M.; Lewis, L.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J.; Liu, J
                                                                                                                                                                                                                                 AC117425 143620 bp DNA linear PRI 29-JUN-2002 Homo sapiens 3 BAC RPI1-29718 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
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Submitted (31-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                              Db 116581 Griggigigarahritaritranahricacaaaaagagargi 116621
124 GTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGT 164
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Peatures listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the BST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-JUN-2002) Human Genome Sequencing Center, Department
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                                                                                                                          Submitted (28-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                             of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Un 28, 2002 this sequence version replaced gi:21240517.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
Baylor Plaza, Houston, TX 77030, USA
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2698. 2753
/rpt_family="(CA)n"
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/db_xref="taxon:9606"
/chromosome="3"
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3268. .3816
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5222. 5434
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3081. .3117
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2555. .2815
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1532. .2697
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                                   4 (bases 1 to 143620)
Worley, K.C.
Direct Submission
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Murny, D.M., Adama, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Alabbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Baryatt, N.P., Balbarooks, S.L., Barich, M., Brown, M., Baryatt, N.P., Bunch, J., Boncon, J., Binage, K., Blankenburg, K., Bonch, D.C., Cox, C., Coyele, M.D., Dathorne, S.R., David, R., Davis, C., Chowley, J., Christopoulos, C., Cleveland, C.D., Cox, C., Coyele, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D. A., Davis, C., Davy-Carroll, L., Dederich, D. A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y. Duthin, H., Douthwaite, K.J., Drager, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Earnhart, C., Edgar, D., Flagg, M., Ford, J., Foster, P., Franz, P., Franzis, C., Harris, K., Hatt, M., Havlak, P., Haues, S., Hamilton, K., Gorrell, J.H., Guevara, M., Garner, T., Garza, N., Gillen, Kovar, C., Lowis, L.C., Lewis, L.C., Lackson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kallson, E., Huber, J., Liug, L., Kovar, J., Kovar, C., Kractovic, J., Kureshi, A., Landry, N., Lau, B., Lewis, L.C., Lewis, L., Lozado, R.J., Lucier, R., Lunier, R., Lunie, R., Mayen, N., Mascovic, J., Kureshi, A., Landry, N., Lozado, R., Du, X., Lucier, R., Lunier, R., Lunie, R., Mantine, G., Minner, G., Minner, G., Minner, G., Minner, G., Minner, G., Minner, G., Minner, G., Minner, C., Minner, C., Minner, C., Minner, R., Peterer, M., Nayuen, N., Nickerson, E., Navetson, J., Navetson, M., Nayue, R., Peters, M., Peters, M., Peters, M., Peters, M., Peters, L., Pickerson, E., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Navetson, J., Vera, V., Villalon, D., Villan, M., Yaneck, A., Paptor, J., Taaltor, J., Taaltor, J., Taaltor, J., Taaltor, J., Taalto
                                                                                                                                                                                            AC123297 120714 bp DNA linear HTG 18-JUL-2002
Rattus norvegicus clone CH230-351P14, *** SEQUENCING IN PROGRESS
***, 53 unordered pieces.
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Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 120714)
Worley, K.C.
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  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                 AC123297.2 GI:21746249
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Unpublished
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                                            171 TCCT 174
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/rpt family="MIR"
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complement (12811. .13551)
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'2734. .22781
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(8656. .1927
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19823. .19843
/rpt_family="AT_rich"
20062. .2008T_rich"
/rpt_family="(CAAAAA)n"
complement(21139. .21789)
                                                                                                                                                 'rpt_family="MIR"
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/rpt_family="AT_rich"
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                                                                                                                               family="AT_rich"
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5845. .6070
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25587. .25622
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6923. .17892
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24663. .24827
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NOTE: This is a "working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:21240138.
                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.999329 Consensus quality: 86198 bases at least Q40 Consensus quality: 90608 bases at least Q30 Consensus quality: 92445 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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Is Maran, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albarocks, S.L., Amaratungs, H.C., Are, J.R., Ayele, M., Banks, T., Blabbrooks, S.L., Amaratungs, H.C., Are, J.R., Ayele, M., Banks, T., Barbaroks, S.L., Amaratungs, H.C., Are, J.R., Ayele, M., Banks, T., Barbay, C., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Burch, P., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Cor, C., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, C., Chowdhry, I., Dathorne, S.R., David, R., Deladad, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Deabert, D., Deladaro, K.R., Deladado, D., Denn, A.L., Ding, Y., Dhih, H.H., Delaney, K.R., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Hogues, M., Hala, S., Hame, S., Hamlton, K., Garrell, J.H., Guevara, W., Gunarathe, P., Hades, A., Harnandez, O., Hodgson, M., Hogues, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Hollyes, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Hollyes, M., Marcin, J., Li, J., Li, Z., Lichtarge, O., Leal, R., Lander, M., Mayon, M., Mapus, P., Martin, R., Martin, R., Martin, M., Mayon, M., Mapus, P., Martin, R., Martin, M., Mayon, M., Mayon, P., Martin, R., Martin, M., Mayon, M., Mayon, P., Martin, M., Mayon, M., Mayon, P., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters, J., Peters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
AC117109.2 GI:21745874
HTG; HTGS PHASE1.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 14, 2002 this sequence version replaced gi:20069615.
                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                        Chemistry: Dye-Terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 117259 bases at least Q40 Consensus quality: 120122 bases at least Q30 Consensus quality: 122747 bases at least Q20
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1869: gap of unknown length
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4456: contig of 1393 bp in length
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                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------- Project Information
Center project name: GTNB
                                                                                             Center: Baylor College of Medicine
Center code: BCM
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Best Local Similarity 52.6%; Pred. No. 21;
Matches 71; Conservative 0; Mismatches 64; Indels 0;
                 3813 58609: contig of 3579 bp in length 58610: contig of 4008 bp in length 58510: gap of unknown length 58517: gap of unknown length 65317: gap of unknown length 65317: gap of unknown length 65817: gap of unknown length 68861: contig of 5344 bp in length 4431 contig of 5469 bp in length 74530: gap of unknown length 74530: gap of unknown length 74530: gap of unknown length 8112: gap of unknown length 8112: gap of unknown length 8162: contig of 6482 bp in length 8162: gap of unknown length 64872: contig of 6491 bp in length 4872 94971: gap of unknown length 6472: contig of 6810 bp in length 6472: contig of 8491 bp in length 1563: ll1582: contig of 8491 bp in length 1683: ll1582: contig of 8491 bp in length 1683: ll1782: gap of unknown length 1683: ll1782: gap of unknown length 1683: ll2928: contig of 930 bp in length 9259: ll2928: contig of 930 bp in length 9259: ll2928: contig of 13209 bp in length location/Qualifiers
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-242N20"
40398 a 27668 C 27321 g 40112 t 7098 others
  gap of unknown length
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US-08-304-051-11
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US-09-404-879A-198
US-09-434-28B-2
US-08-335-814-8
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US-08-235-814-1
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/ cgn2 6/ptodata1/ina/5B_COMB.seq:*
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/ cgn2 6/ptodata11/ina/PcTUS COMB.seq:*
                         GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                         nucleic search, using frame_plus_p2n model
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US-08-379-437-3
US-08-379-437-5
US-08-379-437-7
US-08-322-742-11
US-07-963-338B-5
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Maximum Match 1008
Listing first 100 summaries
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 2000000000
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Result

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199 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 258
                                                                                                                            1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu 20
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                                                                                                                                                                         41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,437 FILING DATE: 27-MAR.1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
PREDICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP PCT/JP93/01133
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 234085/1992
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ISHIMA, YOSHIAKI
APPLICANT: OKAWA, NORIYUKI
APPLICANT: YOSHIDA, MASAYA
APPLICANT: YOSHIDA, MASAYA
APPLICANT: AMAGAYA, SAKAE
APPLICANT: KAJI, AKIRA
TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
   09-833799-13B (1-57) x US-08-322-742-14 (1-571)
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DESCRIPTION: /desc = "synthetic DNA"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          Sequence 3, Application US/08379437 Patent No. 5734014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION NUMBER: 24,618
TELEBHONE: 703-413-3000
TELEFA: 703-413-2220
TELEX: 24886
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98.25%
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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US-08-379-437-3
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Sequence 4, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
                                     Sequence 2, Ap
Sequence 122,
Sequence 15, A
                       Sequence 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,742
                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08322742
Patent No. 5688641
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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Mismatches:
Indels:
PCT-US91-01726-2
US-09-740-235-36
US-08-470-179-122
US-08-871-827C-15
US-09-290-2028-15
US-09-643-597-347
US-09-61-709-4
US-09-61-709-4
US-08-258-261B-1
                                                                                                                                                                                         US-08-457-342-1
US-08-457-646A-1
US-08-458-076A-1
US-08-457-335A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,823
FILING DATE: September 1,1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28,1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28,1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/048003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1542-5070
TELEPRAX: 0617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                   Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                RESULT 1
US-08-322-742-14
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                                                      Query Match:
DB:
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1 GCACAGGAACCAGTTAAAGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCGATTATCCTG 60
                                                                                                                                                                                                    21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                            1 AlaGluProValLysGlyProValSerThrLysProGlySerCysProIlelleLeu
                                                                                                                                                                                                                                                                                                                                    41 IleLysLysCysCysCluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400 CITY. ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,437
FILING DATE: 27-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP PCT/JP93/01133
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
TILING DATE: 11-AUG-1992
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24 618
REGISTRATION NUMBER: 24 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
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APPLICANT: OKAWA, NORIYUKI
APPLICANT: OKSHIDA, MASAYA
APPLICANT: AWAGAYA, SAKAE
APPLICANT: KAJI, AKIRA
ITILE OF INVENTION: NOVEL ELAFIN DERIVATIVE
WIMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                09-833799-13B (1-57) x US-08-379-437-3 (1-177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                              78-08-379-437-5
; Sequence 5, Application US/08379437
; Patent No. 5734014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-300
TELEX: 703-413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYRE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
99.08%
1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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; LOCATION:
US-08-379-437-5
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  Query Match:
DB:
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21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
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                                                                                                                                                                                                                                                                                                            1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ISHIMA, YOSHIAKI
APPLICANT: ISHIMA, YOSHIAKI
APPLICANT: OKAWA, NORIYUKI
APPLICANT: YOSHIDA, MASAYA
APPLICANT: AMAGAYA, SAKAE
APPLICANT: AMAGAYA, AKIRA
TITLE OF INVENTION: NOVEL ELAFIN DERIVATIVE
NUMBER OF SEQUENCE: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
SITRET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
CITY: ARLINGTON
STATE: VALINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PC-DOS/MS-UOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,437
FILING DATE: 27-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP PCT/JP93/01133
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 234085/1992
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NUMBE: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-220
TELEPHONE: 703-413-220
TELESA: 703-413-220
TELESA: 703-413-220
TELESA: 703-413-220
TELESA: 748855 OPAT UR
SEQUENCE CHARACTERISTICS:
CONTROLLY ASSESTICS:
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Conservative:
Mismatches:
Indels:
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DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7, Application US/08379437; Patent No. 5734014; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
Percent Similarity:
Best Local Similarity:
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, LOCATION:
US-08-379-437-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-379-437-7
                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
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1 AlaGluGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
                                                                                                                                                                                         21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08322742
; Sequence 11, Application US/08322742
; Patent No. 568841
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
COMPUTER: IBM PS/2 Model 502 or 553X
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,742
PILING DATE:
                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
                  Length:
Matches:
                                                                                                                                     09-833799-13B (1-57) x US-08-379-437-7 (1-177)
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                                                                                                      Gaps:
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APPLICATION NUMBER: 07/938,823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,296
FILING DATE: February 28, 1992
APPLICATION NUMBER: 07/552,216
FILING DATE: February 28, 1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                323.00
100.00%
98.25%
98.78%
                  1.41e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322.00
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ropology: linear
                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 F
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 321
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-322-742-11
                                                                                  Query Match:
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APPLICANT: OHTSUKA, EIKO
APPLICANT: MATANAB, ATSUSHI
APPLICANT: WATANABE, KUNIHITO
APPLICANT: SUGA, TETSUYA
APPLICANT: SUGA, TETSUYA
APPLICANT: ARTSUNOO, YOHICHI
APPLICANT: TAKEUCHI, AKIKO
TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
NUMBER OF SEQUENCES: 36
                                                                                                                                                                    144 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTG 203
                                                                                                                                                                                                                                                                               1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                              21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly 40
                                                                                                                                                                                                                                                                                                                                                                                          264 Arcaagaagrecrergaagecrerrecegearesecrerrecerrece 311
                                                                                                                                                                                                                                                                                                                                         41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
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APPLICATION NUMBER: US/07/963,538B
FILING DATE: 20-0CT-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/963,538B
FILING DATE: 20-0CT-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/843,359
FILING DATE: 25-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,483
     000
     Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: COOLEY GODWARD LLP
FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                09-833799-13B (1-57) x US-08-322-742-11 (1-321)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-35553
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62-330219
FILING DATE: 28-DEC-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-212399
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-212398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-963-538B-5
; Sequence 5, Application US/07963538B
; Patent No. 5851983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SUGIYAMA, TAKASHI
APPLICANT: KAMIMURA, TAKASHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MASUDA, KENICHI
APPLICANT: OKADA, MASAHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-1992
Best Local Similarity: 100.00%
                           98.478
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                              Query Match:
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NEELEY PH.D., RICHARD L.

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61 GGTCAGTĠTCTGATĠĊTĠAAĊĊĠĊĊĠAAĊTTCTĠTGAAATGĠAĊGGTCAGTĠTAAACGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GluProvalLysGlyProvalSerThr-----LysProGlySerCysProllelleLeu 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 IleArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 IleLysLysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Eisenberg, Stephen
APPLICANT: Wahl, Sharon M.
APPLICANT: Wahl, Sharon M.
APPLICANT: Thompson, Robert C.
APPLICANT: Dripps, David J.
TITLE OF INVENTION: IMHIBITION OF RETROVIRUS INFECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARES PATENT FOLGS/MS-DOS
SOFTWARES PATENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,503A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,040
FILING DATE: 09-MAR.1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,369
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-833799-13B (1-57) x US-07-963-538B-5 (1-194)
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                                 TEJN-005/02US
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ZIP: 2006-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08483503A Patent No. 6017880 GENERAL INFORMATION:
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: TEJN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5070
TELEFAX: 415-857-0663
TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                         2.14e-10
143.00
55.36%
48.21%
43.73%
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                                                                                                                                                                                                                                                             linear
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           4 GATCCTGTTGACACCCCAACAACAAGAAGGAAGCCTGGGAAGTGCCCAGTGACTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
TILLE REFERENCE: 210.21.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEC ID NOS: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 IlelyslysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
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Matches:
Conservative:
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Matches:
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Mismatches:
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               04189.0084-02000
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REGISTRATION NUMBER: 32,013
            REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                            TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  6.32e-10
139.00
53.57%
46.43%
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105.00
57.14%
51.43%
32.11%
                                                                                                                 LENGTH: 180 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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DB:
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313 AAACCACCGGGAGGTCAAGTCTCCACGAAGCCACCGGCTGTGACCAGGGAAGGCTTAGGT 372
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                                                                                                                              GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Watson, James G
APPLICANT: Watson, James G
TITLE OF INVENTION: Polynucleotides and methods for their use.
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REPRENENT: 1000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 724
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Patent No. 6243419

GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compounds isolated from stromal cells
TITLE OF INVENTION: and methods for their use
FILE REFERENCE: 11000.1037c1
TTGAAGTGTTGCATGGGCATGTGTGGGAAATCCTGCGTTTCCCCT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 recegenaregarereganearescricerecacaccean 519
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Matches:
Conservative:
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CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PASTSEQ for Windows Version 3.0
                                                                                       Sequence 23, Application US/09724864 Patent No. 6380362
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43.24%
33.78%
29.97%
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; ORGANISM: Mouse
US-09-383-586-29
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                                                               US-09-724-864-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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DB:
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TITLE OF INVENTION: NUCLEIC SEQUENCE OF THE GENE ASSOCIATED WITH TITLE OF INVENTION: X CHROMOSOME LINKED KALLMANN SYNDROME, CORRESPONDING TITLE OF INVENTION: PEPTIDE SEQUENCES, DIAGNOSTIC APPLICATIONS.

NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                               80 AAACCTGGAGCTTGTCCC--------AAGCCTTCACCAGAA 112
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                                                                                                                                                                                                                                                        ---AsnArgCysLeuLysAspThrAspCysProGlylleLysLys 43
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,430
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                     Conservative:
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                 Length:
Matches:
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Matches:
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                                                                                        Indels:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
foetal brain cells
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08211430
; Patent No. 5763166
; GENERAL INFORMATION:
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                 0.00109
                                94.50
41.51%
35.85%
28.90%
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EDNESS: double
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                                                  Percent Similarity:
Best Local Similarity:
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ORGANISM: HOM
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US-08-211-430-1
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                   Pred. No.:
                                      Score:
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145 GAATGTGAA---TTCCAAGAAAGGGATGTGTGTACAAAGGACAGACAATGCCAGGACAAC 201
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                              TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PSO03P1.05
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER PILING DATE: 1998-03-12
EARLIER FILING DATE: 1998-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER PELICATION NUMBER: 60/040,710
EARLIER PELICATION NUMBER: 60/040,710
EARLIER PELICATION NUMBER: 60/048,100
EARLIER PILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-05-30
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EARLIER PILING DATE: 1997-05-30
EARLIER PILING DATE: 1997-06-65
EARLIER PILING DATE: 1997-06-65
EARLIER FILING DATE: 1997-06-65
EARLIER FILING DATE: 1997-06-66
EARLIER FILING DATE: 1997-10-19
643 TCGAATGGGTGTGGACACCTGTCAAGTACCCAAG 678
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TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: PZ003P1.US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
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                                                                                                US-09-152-060-34
; Sequence 34, Application US/09152060
; Patent No. 6448230
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44.23%
40.38%
25.99%
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SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                                                                                                                                              GENERAL INFORMATION:
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LENGTH: 753
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TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLECTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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Mismatches:
Indels:
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OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
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APPLICATION NUMBER: PCT/US98/04858
             EARLIER FILING DATE: 1998-03-12
EARLIER PELING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER APPLICATION NUMBER: 60/060,710
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-03-14
EARLIER FILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
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EARLIER PILING DATE: 1997-05-30
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-01-06-06
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
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SEQ ID NO 50
LENGTH: 783
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44.23%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity:
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ZIP: 77002
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262 CAGGCCACACGCTGCCAGTCTGACTCTGAGTGCCCACGACACAGACGCTGCTGTTACAAC 321
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Patent No. 5958735
GENERAL INFORMATION:
APPLICANT: ROWNEY, DAVID R.
TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
TITLE OF INVENTION: FACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jenkens & Gilchrist
STREET: 1100 Louisiana, Suite 1800
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Mismatches:
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APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
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                                                             APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: TURIEY, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 34012.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
                                                                                                                                                                    34012.6
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APPLICATION NUMBER: 60/008,348
FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1042 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
      06-DEC-1996
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30.43%
24.92%
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FILING DATE: 06-DEC-1-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
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ZIP: 77002
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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US-08-761-248B-1
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262 CAGGCCACACGCGCAGTCTGACTCTGAGTGCCCACGACACAGACGCTGCTGTTACAAC 321
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; Patent No. 5958735
; GENERAL INFORMATION:
    APPLICANT: ROWLEY, DAVID R.
    TITLE OF INVENTION: UROGENITAL SINUS DERIVED GROWTH
    TITLE OF INVENTION: PACTOR NUCLEOTIDE AND AMINO ACID SEQUENCES
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14
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11
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Mismatches:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,248B
FILING DATE: 06-DEC-1996
CLASSIFICATION: 435
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1100 Louisiana, Suite 1800
                    35,723
ER: 34012.6
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FILING DATE: 07-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 ccacgacgcraccccccccccccrcr-
NAME: Turley, Charles P
REGISTRATION NUMBER: 35,723
REFERENCE/DOCKET NUMBER: 340
TELECOMMUNICATION:
TELECOMMUNICATION: (713)9513310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)9513310
TELEFAX: (713)9513314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35,723
                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1071 base pairs
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REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                     0.172
81.50
43.48%
30.43%
24.92%
                                                                         TELEFAX: (713)95133J4
                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 6
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                usa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                US-08-761-248B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
US-08-761-248B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                      TELEX:
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398 ------CGCTGTCAGGCGGACTCCGAGTGCCCGCGGCACCGGCGCTGCTACAAC 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 ProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOUDERINE, Louis-Marie
APPLICANT: HOUDERINE, Louis-Marie
APPLICANT: DEVINOY, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folly & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: USA
ZID: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEB PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,146
FILING DATE: 10-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-162-146-2; Sequence 2, Application US/08162146; Patent No. 5965788; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
                INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 GGATGCGCCTACGCCTGC 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 SerCysGlyMetAlaCys 53
                                                                                                                                                                                                                                                                  79.50
43.48%
30.43%
24.31%
                                                                                                                                                      MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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TELEX
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2938 ICCCAGITGIGIGAGGAGCIGAGCGACIGIGCCAACGACATCGAGIGCAGGGGGGACAAG 2997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOUDEINE, Louis-Marie
APPLICANT: HOUDEINE, Louis-Marie
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                            join(1868..1949, 2462..2587, 2888..3046, 3416
..3429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2998 AAGTGCTTCAGCCGCTGCGCCATGCGCTATCTGGAACCC 3039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 LysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/314,127
                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                              09-833799-13B (1-57) x US-08-162-146-2 (1-4157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-7UN-1991
ATTORNE; MEGNER, Harold C.
REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09314127
Patent No. 6268545
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                     LENGTH: 4157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                  3.5
77.50
46.30%
37.04%
23.70%
SEQUENCE CHARACTERISTICS:
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                   Alignment Scores:
                                                                                   TOPOLOGY:
                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                            ; LOCATION:
; LOCATION:
US-08-162-146-2
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TELEX: 9
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904136

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2884 CCAGICCCTACCCCCAAGGCTGGCCGCTGCCCC----TGGGTGCAGGCGCCAATGCTG 2937
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Patent No. 5633277

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an TITLE OF INVENTION: Inhibitor of Tryptase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Miles Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ProValSerThr---LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 Asn------ProProAsnArgCysLeuLysAspThrAspCysProGlyIleLys 42
                                                                                                                                                                   join(1868..1949, 2462..2587, 2888..3046, 3416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2998 AAGTGCTGCTTCAGCCGCTGCGCCATGCGCTATCTGGAACCC 3039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 LysCysCysGluGlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                     09-833799-13B (1-57) x US-09-314-127-2 (1-4157)
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SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,051
FILING DATE: 12-Sept-1994
CLASSIPICATION: 5:4
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFRENCE/DOCKET NUMBER: MWH
TELECOMMUNICATION INFORMATION:
TELEFAX: (203) 937-2795
TELEX: 221949 MILES UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
             SEQUENCE CHARACTERISTICS:
LENGTH: 4157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: System
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400 Morgan Lane
                                                                                                                                                                                                                                                                                                                                                37.04%
23.70%
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: West Haven
STATE: Connecticut
                                                                                                                                                                                            ..3429)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 bases
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                        ; LOCATION:
; LOCATION:
US-09-314-127-2
                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                   NAME/KEY:
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                                                                                                                             FEATURE
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; NAME/KEY: Primer for Polymerase Chain Reaction used to make mutein; NAME/KEY: of human SLPI.
US-08-304-051-11
                                                                                                                                  \ensuremath{\mathsf{NAME}}\xspace({\mathsf{KEY}}\xspace) . Primer for Polymerase Chain Reaction used to make mutein \ensuremath{\mathsf{NAME}}\xspace({\mathsf{KEY}}\xspace) . of human SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria, Katherine A. TITLE OF INVENTION: Secretory Leukocyte Protease Inhibitor as an TITLE OF INVENTION: Inhibitor of Tryptase
                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsn 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AAGCCTGGGAAGTGCCCAGTGACTTATGGCCAATGTAGGATGCTTAACCCCCCCAAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.1
                                                                                                                                                                                                                                               80
17
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                                               - Other nucleic Acid: synthetic
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Mismatches:
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                                                                                                                                                                                                                                                                    Matches:
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                                                                                                                                                                                                                                                                                                                                   indels:
                                                                                                                                                                                                                                                                                                                                                                                                   09-833799-13B (1-57) x US-08-304-051-7 (1-80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION 577: No. 5633227e
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322
TELECOWNUICATION INFORMATION:
TELEPHONE: (203) 937-2712
TELEFAX: (203) 937-275
TELEFAX: 221949 MILES UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/304,051
FILING DATE: 12-Sept-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08304051; Patent No. 5633227; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: System 7.1 SOFTWARE: Word Perfect 3.0a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
                                                                                                                                                                                                                                                                 75.00
73.68%
63.16%
22.94%
                                                                                                                                                                                                                                             0.0354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miles Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
      TOPOLOGY

MOLECULE TYPE:

MOLECULE TYPE: - Ot
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                      ANTI-SENSE: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: 1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
MOLECULE TYPE:
                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-304-051-11
                                                                                                                                                                             US-08-304-051-7
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                                                                                                             FEATURE:
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FEATURE
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| Sequence 7, Application PC/TUS9511445
| Sequence 7, Application PC/TUS9511445
| GENERAL INFORMATION: APPLICANT: Maller, Daniel K.; Brownell, Elise; Delaria, APPLICANT: Matherine A. |
| TITLE OF INVENTION: Secretory Leukocyte Protease | TITLE OF INVENTION: Inhibitor as an Inhibitor of Tryptase | TITLE OF INVENTION: Inhibitor as an Inhibitor of Tryptase | NUMBER OF SEQUENCES: 21 | CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Bayer Corporation | STREET: 400 Morgan Lane | CITY West Haven |
| STRIET: Connecticut | COUNTRY: USA | COUNTRY: USA | COUNTRY: USA | COUNTRY: USA | COUNTRY: USA | COUNTRY: CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1,300 Kb storage CMPUTER: Apple Macintcoh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word Perfect 3.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11445
FILING DATE: 11 September 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/304,051
FILING DATE: 12 SEPTEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: William F. Gray
REGISTRATION NUMBER: 31018
REFERENCE/DOCKET NUMBER: MWH 322P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 bases
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                        Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
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                                                                                                                      Indels:
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                                                                                                                                                                                           09-833799-13B (1-57) x US-08-304-051-11 (1-80)
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                                                                                                                                                 Gaps:
                                                 75.00
73.68%
63.16%
22.94%
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75.00
73.68%
63.16%
22.94%
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STRANDEDNESS: single
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                                                                  Percent Similarity:
Best Local Similarity:
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Alignment Scores:
Pred. No.:
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                                                                                                                      Query Match:
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12 LysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsn 30
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12 LysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnProProAsn 30
                                          21 AAGCCTGGGAAGTGCCCAGTGACTTATGGCCAATGTAGGTTAACCCTCCCCCAAT 77
                                                                                                                                   PCT-US95-11445-11
Sequence 11, Application PC/TUS9511445
Sequence 11, Application PC/TUS9511445
GENERAL INFORMATION:
APPLICANT: Muller, Daniel K.; Brownell, Elise; Delaria,
APPLICANT: Katherine A.
TITLE OF INVENTION: Secretory Leukocyte Protease
TITLE OF INVENTION: Inhibitor as an Inhibitor of Tryptase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \label{eq:NAME/KEY: Primer for Polymerase Chain Reaction used to NAME/KEY: make mutein of human SLPI.
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Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette, 3.50 inch, 1,:
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11445
FILING DATE: 11 September 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/304,051
FILING DATE: 12 SEPTEMBER 1994
ATTORNEY AGENT INPORMATION:
NAWE: William F. Gray
REGISTRATION NUMBER: 31018
REFREENCE/POCKET NUMBER: 31018
REFRENCE/POCKET NUMBER: 31018
REFREENCE/POCKET NUMBER: 31018
REGISTRATION NUMBER: 31018
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REGISTRATION NUMBER: 310
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US-09-404-879A-198/c
; Sequence 198, Application US/09404879A
; Patent No. 6468946
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STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
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EDNESS: single
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Query Match:
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06516
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282 ccagriccaggradacagccagriccriddccagargaargccgccgcaarggcrigigg 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08335865J
Patent No. 6107472
GENERAL INFORMATION:
APPLICANT: Stacker, Steven A.; Hovens, Christopher M.,
APPLICANT: WILKS, Andrew F.
TITLE OF INVENTION: RECEPTOR-TYPE TYROSINE KINASE-LIKE MOLBCULES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rulbright & Jaworski L.L.P.
STREET: 666 Pifth Ave
               APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210.11.46202
CURRENT APPLICATION NUMBER: US/09/404,879A
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FRAKSEQ FOR WINDOWS Version 3.0
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MEDIUM TYPE: Diskette, 3.5 inch, 720 KB storage COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
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Matches:
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OPERATING SYSTEM: PC-DOS
SOFTWARE: ASCII/Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/335,865J
FILING DATE: 19-January-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU93/00210
FILLING DATE: 10-May-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PL2358
                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1).....(403)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-198
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37.50%
21.10%
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NAME/KEY: misc feature
LOCATION: (1)...(403)
                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapien
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STREET: 660 ...
CITY: New York
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Best Local Similarity:
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                 TYPE: DNA
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1828 CCAGCAGCTGGTCCAGTGCCTCACAGAGTTCCACGCTGCCCTGGGAGCCTACGTCTGACT 1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Betlach C., Melanie
APPLICANT: Betlach C., Melanie
APPLICANT: Betlach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
TITLE OF INVENTION: CONSTRUCTS THEREFOR
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT FILING DATE: 1999-11-05
PRIOR PILING DATE: 1998-11-05
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16
6
22
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Conservative:
Mismatches:
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Mismatches:
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                                                                           LUD-5277
                                     NAME: Hanson, No. 6107472man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces narbonensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-434-288-2; Sequence 2, Application US/09434288; Patent No. 6303767
                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEPAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1948 GCGCAGTGCCTGCAGGGG 1965
FILING DATE: 11-May-1992
ATTORNEY/AGENT INFORMATION:
                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver, 2.1
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34.78%
21.10%
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68.00
44.44%
33.33%
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69.00
                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                  linear
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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5757 TCTTGACCTGGAAGTCATTACGACCTAGATACTCGACCTCCCCGCTGCTTCCAGGAATCC 5698
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                                                                                                                                                                                                                       Veenstra, Annemarie E.
Martin, Juan F.
Garcia, Bruno D.
                                                                                                                                                                Sequence 1, Application US/08222617A
Patent No. 5882879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394
66.50
35.44%
21.52%
20.34%
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264..11600
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: USA
                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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DB:
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5877 CAACCAGGAATTTCTGGGCCCCTTCTCTGGAATCCTTGGCAATCACCAGACTGTTTGA 5818
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5817 TTCCGTGATAAGACGATAGGATGGCCTCAATCTCGCCTACTTCGATGCGCAGTCCGCGAA 5758
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
CORRESPONDENCE: 27
CORRESPONDENCE ADDRESS:
                                                    846 GTCCCCGTGCCGTGCGCCTCGACGACATCGACCTCGCCCGGCGTGAGCCGGGCGTCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GinGluProValLysGlyProValSerThrLysProGlySerCysProIlelle----- 19
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                 906 AGGCCCGCCGGATGACGCCTGCTGCGACGGCCCGTTCGGA 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
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Indels:
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04-APR-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 US-08-222-617A-26/c
; Sequence 26, Application US/08222617A
; Patent No. 5882879
                                                                                                                                                                                                                                                            Veenstra, Annemarie E.
                                                                                                                                                                                                                                                                             Martin, Juan F.
Garcia, Bruno D.
Gutterrez, Santiago
Barredo, Jose L.
Von Doehren, Hans
Palissa, Harriet
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REFERENCE/DOCKET NUMBER: 9
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 11444 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 11444 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.50
35.44%
21.52%
20.34%
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-APR
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Garcia, Bruno D.
APPLICANT: Garcia, Santiago
APPLICANT: Gutierrez, Santiago
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Palissa, Harriet
APPLICANT: Palissa, Harriet
APPLICANT: Won Liempt, Henk
APPLICANT: Montenegro, Budardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF EXCURNICES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GlnGluProValLysGlyProValSerThrLysProGlySerCysProIlelle---- 19
                                             5697 AGCGTACCAGGTCACCGGTCTTGTACAAACGGGAGTTACGACCTTCTCGCTTATCTT 5641
37 AspCysProGlyIleLysLysCysCysGluGlySerCysGlyMetAlaCysPheVal 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALT: 00000

CAPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/22,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 12364 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
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OTHER INFORMATION: /product= "ACV Synthetase"
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US-08-306-691B-50
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TITLE OF INVENTION: ELASTASE INHIBITORY POLYPEPTIDE AND
TITLE OF INVENTION: PROCESS FOR PRODUCTION THEREOF BY RECOMBINANT GENE
TITLE OF INVENTION: TECHNOLOGY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
5877 CAACCAGGAATTTCTGGGCCCCTTCTCTGCAATCCTTGGCAATCACCACAGACTGTTTGA 5818
                                                             5757 TCTTGACCTGGAAGTCATTACGACCTAGATACTCGACCTCCCCGCTGCTTCCAGGAATCC 5698
                                         -----LeulleArgCysAlaMetLeuAsn 27
                                                                                                                           ---ProAsnArgCysLeuLysAspThr 36
                                                                                                                                                                                                                                     37 AspCysProGlyIleLysLysCysCysGluGlySerCysGlyMetAlaCysPheVal 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/963,538B
FILING DATE: 20-OCT-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: COOLEY GODWARD LLP
FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30,092
FR: TEJN-005/02US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/843,359
FILING DATE: 25-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/408,483
FILING APPLICATION DATA:
APPLICATION NUMBER: JP 4-212399
FILING DATE: 17-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-212399
FILING DATE: 17-JUL-1992
FILING DATE: 17-JUL-1992
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APPLICATION NUMBER: JP 3-35553
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62-330219
FILING DATE: 28-DEC-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/07963538B Patent No. 5851983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NEELEY PH.D., RICHARD L. REGISTRATION NUMBER: 30,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OHTSUKA, BIKO
IMAIZUMI, ATSUSHI
WATANABE, KUNIHITO
SUGA, TETSUYA
MATSUMOTO, YOHICHI
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                                                                                                                                                                                                                                                                                                                                                                                                   SUGIYAMA, TAKASHI
KAMIMURA, TAKASHI
                                                                                                                                                                                                                                                                                                                                                                                                                                             MASUDA, KENICHI
OKADA, MASAHIRO
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SUGIYAL
APPLICANT: KAMIMUI
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APPLICANT:
APPLICANT:
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                                                                                                                           28 Pro--
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APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Seidel, Gonda, Lavorgna & Monaco, P.C.
                                                                                                                                                                                                                                                                                                                                                                                    25 MetLeuAsnProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCys
                                                                                                                                                                                                                                                                                                                                                                                                         JARGETING COO JARGESE: JARGETING COO STREET: Two Penn Center, Suite 1800 CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S. ZTD.
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Mismatches:
Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                09-833799-13B (1-57) x US-07-963-538B-34 (1-68)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50, Application US/08306691B; Patent No. 5734039; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    September 15, 1994
                                                                                     TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFRENCE/DOCKET NUMBER: 8321
TELEPCOMMUNICATION INFORMATION:
TELEPRAX: (215) 568-5349
TELERX: (215) 568-5549
ILLEX: NO. 57340396
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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               TELEX: 380816 COOLEY PA INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1364 base pairs
                                                                                                                                                                                                                                                     57.14%
57.14%
19.88%
                                                                                                                                                                                                                    0.548
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                        68 base pairs
415-857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: double
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Query Match:
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US-08-306-691B-50/c
                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                                                                                                     Alignment Scores:
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 TELEFAX:
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                                                                        LENGTH:
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RESULT 31
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Sequence 65, Application PC/TUS9306251

GENERAL INFORMATION:

APPLICANT: Wickstrom, Eric and Rife, Jason P.

TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 Garden City Plaza

CITY: Garden City Plaza
                                                                                                                                                                                                                                      800 ACGAGAACTGGAAGGTGCCCT-----TGTCCTTGT-----CCACCCACC 762
                                                                                                                                                                                                                                                                                                                761 AGATGC------TGTCCTTCATGTCGCCGCTGCGGAGCAGGTCCAACAGGA 717
                                                                                                                                                                                            11 ThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsn 30
                                                                                                                                                                                                                                                                             31 ArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGly
                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                               716 ACTGGTACAGGCGGATCTTCTTCTTGCTGCCTGTCTCCCCAG 675
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
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Matches:
Conservative:
Mismatches:
                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                       09-833799-13B (1-57) x US-08-306-691B-50 (1-1364)
                  Length:
Matches:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: DiGGIGLO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEPHONE: 516-742-4366
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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64.50
37.04%
31.48%
                  36.4
64.50
37.04%
31.48%
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EDNESS: double
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                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Alignment Scores:
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COUNTRY:
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DB:
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09-833799-13B (1-57) x PCT-US93-06251-65 (1-1364)

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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequenc
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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                                            800 ACGAGAACTGGAAGGTGCCCT-----TGTCCTTGT-----CCACCCACC 762
                                                                                                                                      761 AGATGC------TGTCCTTCATGTCGCCGCTGCGGAGCAGGTCCAACAGGA 717
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11 ThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsn 30
                                                                                            31 ArgCysLeuLysAspThrAspCysProGlylleLysLysCysCysGluGlySerCysGly
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16
10
29
3
                                                                                                                                                                                                                                     716 ACTGGTACAGGCGGATCTTCTTGCTGCCTGTCTCCCCAG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                      -------MetAlaCysPheValProGln 57
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Conservative:
Mismatches:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             Sequence 184, Application US/08961527; Patent No. 6420135; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1590 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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64.50
45.61$
28.07$
19.72$
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Best Local Similarity:
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STRANDEDNESS:
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nucleic acid
EDNESS: single
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STREET: 45
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US-08-459-009-1
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                                   667 GTTGAAAACACCTGCCGGAATCCCTGCTTCTAAATGCTTTAGCCAACAA 617
41 IleLysLysCysGluGlySerCysGlyMetAlaCysPheValProGln 57
                                                                                                                                                                     APPLICANT: OPPERMANN, HERMANN
APPLICANT: OPPERMANN, HERMANN
APPLICANT: KUBERASAMFATH, THANGAVEL
APPLICANT: SMART, JOHN E
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, ADDRESSEE: INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /product= "DROSOPHILA MORPHOGEN OTHER INFORMATION: RECEPTOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                CALL: 01/48
CAMPUTER TADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,533A
FILING DATE: 16-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AlaGlnGluProValLysGlyProValSerThrLysProGly----
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Mismatches:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)-435-9001
TELEPAX: (508)-435-0992
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                              US-08-357-533A-1/c
; Sequence 1, Application US/08357533A
; Patent No. 5831050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                        ': 45 SOUTH STREET HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379..1929
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                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        01748
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1192 AATATTCCG---GCTTGTCCATGTGCTTCTCAACGCCCAGGAATTCGAGGATGTTCGGAT 1136
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                                                                                                                                                                                                                                                                                                                          APPLICANT: SWART, JOHN E.
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 379..1929
OTHER INFORMATION: /product= "DROSOPHILA MORPHOGEN OTHER INFORMATION: RECEPTOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
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REIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,533
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: JIN, DONALD F
APPLICANT: OPPERMANN, HERMANN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: SMART, JOHN E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   US-08-459-009-1/c
; Sequence 1, Application US/08459009
; Patent No. 5861479
                                                                                            1135 GGCGCATGCGCGCCAGCTTGT 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: CR
                                              47 GlySerCysGlyMetAlaCys 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (508)-435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEE: INC: 45 SOUTH STREET HOPKINTON
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44.78%
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APPLICANT: Broughton, Mary C.

APPLICANT: Broughton, Mary C.

APPLICANT: Crawford, Kathryn P.

APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J.

APPLICANT: Treadway, Patti J.

APPLICANT: Treadway, Patti J.

APPLICANT: Treadway, Patti J.

APPLICANT: Treadway, Patti J.

APPLICANT: Waldron, Clive

TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

TITLE OF INVENTION: Broduction

NUMBER OF SEQUENCES: 39

CORRESPENDENCE ADDRESS:

ADDRESSEE: Dow AgroSciences LLC Patent Department

STREET: 9330 Zionsville Road

CITY: Indianapolis

CONTRY: USA

ZIP.
                                              1312 GCAGATGTGCCATTGGCCATGGACTCAGCGATGCGGCACAACTCTGGCCATGAGA 1253
                                                                                                                                                                                                                                                                                 1192 AATATTCCG---GCTTGTCCATGTGCTTCTCAACGCCCAGGAATTCGAGGATGTTCGGAT 1136
                                                                                                                                              27 AsiproproAsnArgCysLeulysAspThrAspCysProGlylleLysLysCysCysGlu
                                                                                                           15 SerCysProlle------ileLeulleArgCysAla----
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,987A
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REFERENCE/DOCKET NUMBER: 50,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEPHONE: (317)337-4816
TELEPHORE: (317)337-4816
TELEPHORE: (317)337-4816
TELEPHORE: (317)337-4816
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TELEPHORE: (317)37-4816
1 AlaGlnGluProValLysGlyProValSerThrLysProGly----
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Conservative:
Mismatches:
Indels:
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64.00
41.94%
32.26%
19.57%
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Best Local Similarity:
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-036-987A-1/c
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                 1252 redidirecearitreaggragregeriagrearceirarieciegraggraggrancagec 1193
                                                                                                                               1192 AATATTCCG---GCTTGTCCATGTGCTTCTCAACGCCCAGGAATTCGAGGATGTTCGGAT 1136
                                                                        27 AsiProProAsnArgCysLeuLysAspThrAspCysProGly11eLysLysCysClu
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: OPPERMANN HERMANN
APPLICANT: OPPERMANN HERMANN
APPLICANT: SMART: JIN.
APPLICANT: SMART: THANGAVEL
APPLICANT: SMART: JOHN E
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
ADDRESSEE: INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /product= "DROSOPHILA MORPHOGEN
OTHER INFORMATION: RECEPTOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,951
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,533
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRP-073FW
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                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08459951
Patent No. 6093547
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) -435-9001
TELEPK: (508) -435-9001
TELEFK: (508) -435-9001
TELEFK: (508) -435-0001
TELEFK: (508) -435-001
TELEFK: (508) -435-001
TELEFK: (508) -435-001
SEQUENCE CHARACTERISTICS: LENGTH: 2625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                         1135 GGGGATGCGGGCAGCTTGT 1115
                                                                                                                                                                                    47 GlySerCysGlyMetAlaCys 53
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MEDIUM TYPE: Floppy disk
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LOCATION: 379..1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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Pred. No.:
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                                                                                                                                                        8 ProValSerThr-----LysProGlySerCysProllelleLeulleArg---Cys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            websulf 36
US-09-370-700-1/c

i Sequence 1, Application US/09370700

j Patent No. 6274350

i GENERAL INFORMATION:

j APPLICANT: Baltz, Richard H

APPLICANT: Broughton, Mary C

j APPLICANT: Treadway, Patti J

APPLICANT: Treadway, Patti J

APPLICANT: Triner, Jan R

j APPLICANT: Triner, Jan R

TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

FILE REFRERENCE: 50489 DIV1

CURRENT FILING DATE: 1999-08-09

CURRENT FILING DATE: 1999-08-09

SOFTWARE: PATCHING DATE: 1998-03-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SERVILER PATCHING DATE: 100-00-09

SERVILER PILING DATE: 100-00-09

SOFTWARE: PatentIn Ver. 2.0
8 ProValSerThr-----LysProGlySerCysProllelleLeulleArg---Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-833799-13B (1-57) x US-09-370-700-1 (1-80161)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Saccharopolyspora spinosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08619198; Patent No. 5885831
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64.00
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32.268
19.578
                                                                                24 AlaMetLeuAsnProProAsn
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3919 AGGTGTTACCTCCTCCTCCGCCGCGCGCGCGTGCTCATCAGAGCCACCATGGACAGGGAGG 3860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA DESCRIPTION: tim cDNA sequence wherein R at position 1335
GENERAL INFORMATION:
APPLICANT: Young, Michael W.
APPLICANT: Sehgal, Amite
APPLICANT: Osshall, Leslie B.
APPLICANT: Price, Jeffrey L.
APPLICANT: Myers, Michael
TITLE OF INVENTION: WICLEAR LOCALIZATION FACTOR ASSOCIATED
TITLES OF INVENTION: WITH CIRCADIAN RHYTHMS
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAsp--
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                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                        411 Hackensack Avenue
                                                                                                                                                                                                                  Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4170 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.50
41.86%
32.56%
19.42%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3799 TTAGCATGT 3791
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                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                    07601
                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-619-198-4
                                                                                                                                                                                                                                          STREET:
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RESULT 38

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4338 AGACGGIGCCCCCGCAACCAGAACTGCTGTTCTCGTTGTGGCTTCCCATGAAGGTGT 4279
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                                                                                APPLICANT: Young, Michael W.
APPLICANT: Sehgal, Amita
APPLICANT: Vosball, Leslie B.
APPLICANT: Price, Jeffrey L.
APPLICANT: Myers, Michael
TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REPERENEC/POCKET NUMBER: 600-1-128A CP1
TELECOMMUNICATION INFORMATION:
TELEPAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5192 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
             Sequence 8, Application US/08619198
Patent No. 5885831
GENERAL INFORMATION:
APPLICANT: Young, Michael W.
APPLICANT: Sehgal, Amita
APPLICANT: Vosshall, Leslie B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-619-198-1/c; Sequence 1, Application US/08619198; Patent No. 5885831
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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41.86%
32.56%
19.42%
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                   New Jersey
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                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                            07601
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US-08-619-198-8/c
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4396 Addretraccrecrecrecededecededefectearcagageaceaearagacaagagaga 4337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA DESCRIPTION: tim cDNA sequence wherein R at position 1575
                   APPLICANT: Sengal, Amita
APPLICANT: Vosshall, Leslie B.
PELICANT: Price, Jeffrey L.
APPLICANT: Myers, Michael
TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ArgCysAlaMetLeuAsnProProAsnArgCysLeuLysAspThrAsp----
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ZIP: 057601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-128A CP1
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEFAX: 201 343-1684
TELEFAX: 201 343-1684
TELEFAX: 213521
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 131521
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 131951
TYPE: MOLGIC acid
STRANDEDNESS: double
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-833799-13B (1-57) x US-08-619-198-1 (1-5198)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster
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; Sequence 28, Application US/09028934
; Patent No. 6117670
                                                                                                                                                                                                               E: Klauber & Jackson
411 Hackensack Avenue
Young, Michael W.
                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                              CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4276 TTAGCATGT 4268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
Pred. No.:
                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                        STREET:
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APPLICANT: Hammer, Philip E.
APPLICANT: van Dee, Karl-Heinz
APPLICANT: Kirner, Sabine
APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrrolnitrin Biosynthesis Genes and Uses
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                   SEE: No. 6117670artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
ATTORNEY/ABRT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: CGC1506/CIP7
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LOCATION: 657..2267
OTHER INFORMATION: /product= "PrnA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 5145..6266
OTHER INFORMATION: /product= "PrnD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 2270..3355
OTHER INFORMATION: /product= "PrnB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /product= "PrnC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
Ligon, James M.
Hill, Dwight S.
Lam, Steven T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 8931 base pairs
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 5145..6266
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LOCATION: 3421.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                  APPLICANT:
APPLICANT:
APPLICANT:
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-----TGT 1380
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                                                                                                                                                                                                                    24 AlaMetLeuAsnProProAsnArgCysLeuLysAspThrAspCys------38
                                                                                                                     4 ProVallysGlyProValSerThrLysProGlySerCysProllelleLeuIleArgCys 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morin, Gregg B.
Harley, Calliam H.
Andrews, William H.
VENTION: Human Telomerase Catalytic Subunit
                                                                                                                                                                   1339 cccrgaaagagcccrrcarcaacargrccaacraccrgc-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARES PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A FILING DATE: US/08/974,549A FILING DATE: US/08/977 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643 FILING DATE: US-08/844,419 FILING DATE: US-08/844,419 FILING DATE: US-08/844,419 FILING DATE: US-08/846,017 FILING DATE: US-08/846,017 FILING DATE: US-08/846,017 FILING DATE: US-08/851,843 APPLICATION NUMBER: US-08/851,843 APPLICATION NUMBER: US-08/851,843 APPLICATION NUMBER: US-08/851,843 APPLICATION NUMBER: US-08/851,843 APPLICATION NUMBER: US-08/851,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                  09-833799-13B (1-57) x US-09-028-934-28 (1-8931)
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PRIOR PELICATION DATA:
APPLICATION NUMBER: US 08/912,951
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APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08974549A
Patent No. 6166178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1501 TCGGCAGCGGCTACGTGT 1518
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              San Francisco
California
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APPLICANT: Cech,
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APPLICANT:
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APPLICANT:
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Query Match:
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Page 21

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1317 CAGCAGCCGGTG-------TCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGG 1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "nucleic acid sequence with an
open reading frame encoding a delta-182
variant polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 56..2479
OTHER INFORMATION: /product= "delta-182 variant
OTHER INFORMATION: polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
RIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE RANGED TO TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 DASE PAIRS
TYPE: NUCleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 ArgCysAlaMetLeuAsnProProAsnArg-----
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Sequence 224, Application US/08851843A
Sequence 224, Application US/08851843A
PERICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Raren B.
APPLICANT: Chapman, Raren B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
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38.24%
33.82%
19.11%
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LOCATION: 1.3855
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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1317 CAGCAGCCGGTG-------TCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGG 1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
                   NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
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                                                                                           STREET: Two Embarcadero Center, 8th Floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
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TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
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CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        UMBER: US/08/851,843A
06-MAY-1997
                                                                                                                                                             COUNTRY: United States of America
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38.24%
33.82%
19.11%
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STRANDEDNESS: single
                                                                                                               CITY: San Francisco
STATE: California
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MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56.3454
OTHER INFORMATION: /
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OTHER INFORMATION:
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Best Local Similarity:
Query Match:
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----AGGIGIACGGCTICGIGCGGCCT 1457
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Patent No. 616678

GENERAL INFORMATION:
APPLICANT: Cach, Thomas R.
APPLICANT: Ingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Applicant, Raren B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
CORRESPONDENCE ADDRESS: 727
ADDRESSEE: Townsend and Townsend and Crew LLP
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MUDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER TRADABLE FORM:
MUDIUM TYPE: The Compatible
COMPUTER TABLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FRIUNG APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
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REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELERPHONE: (415) 576-0200
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APPLICATION UNDERR: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
ATPORREY/AGENT INRORMATION:
APPLICATION NUMBER: WO PCT/US97/17885
ATTORNEY/AGENT INRORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
1407 TGCTCCGCCAGCACAGCAGCCCCTGGC----
                                                                                                                      1458 GCCTGCCCGGCTGCTGCCCCAG 1481
                                                              52 AlaCys-----PheValProGln 57
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TELEFAX: (
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1407 Idercegecageacaecaeceeridae-----aggrandaecricereegeer 1457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GlnGluProValLysGlyProValSerThrLysProGlySerCysProileIleLeuIle 21
                                                                                                                                                                                                                                        /note= "human telomerase reverse transcriptase (hTRT) catalytic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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Mismatches:
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TITLE OF INVENTION: No. 6261836el Telomerase
TIMBER OF SUCUENCES: 225
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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Matches:
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                                                                                                                                                                                                                 /product= "hTRT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 224, Application US/08854050; Patent No. 6261836; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
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                                                                                                                                                                                         LOCATION: 56..3454
LOCATION: 66..3454
OTHER INFORMATION: /note= "hur
OTHER INFORMATION: transcripte
OTHER INFORMATION: component"
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chapman, Karen
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
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38.24%
33.82%
19.11%
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                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                           NAME/KEY: CDS
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OTHER INF
US-08-974-549A-1
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                                                                                                                                                     FEATURE
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Best Local Similarity:
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| 1317 | CAGCAGCCGGTG------TCTGTGCCCGGGAAGCCCCAGGGCTCTGTGG 1361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
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Mismatches:
Indels:
Gaps:
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            FILING DATE: 0.50 08/851,843

CLASSIFICATION NUMBER: 0.50 08/851,843

CLASSIFICATION 536

PRIOR APPLICATION NUMBER: 0.50 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION 15.36

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0.50 / 24,419

FILING DATE: 18-APR-1997

CLASSIFICATION 536

PRIOR APPLICATION 536

PRIOR APPLICATION 536

PRIOR APPLICATION 536

ATTORNEY/AGENT INFORMATION: 0.50 / 22,419

REGISTRATION NUMBER: 0.50 / 4.29

REGISTRATION NUMBER: 0.50 / 4.29

REFERENCE/DOCKET NUMBER: 0.50 / 4.29

REFERENCE/DOCKET NUMBER: 0.50 / 4.29

REFERENCE/DOCKET NUMBER: 0.50 / 4.29
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Matches:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
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Patent No. 6309867;
GENERAL INFORMATION:
Linguer, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1407 TGCTCCGCCAGCACAGCCCCCCTGGC----
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                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHRARACTERISTICS:
LENGTH: 4015 base pairs
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38.24%
33.82%
19.11%
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STRANDEDNESS: single
TOPOLOGY: linear
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OTHER INFORMATION: /
OTHER INFORMATION: /
OTHER INFORMATION: c
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Best Local Similarity:
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| 1317 | CAGCAGCCGGTG------TCTGTGCCCGGGAAGCCCCAGGGCTCTGTGG 1361
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                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                           Crew LLP
                                       Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
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                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "human telomerase reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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| 1317 CAGCAGCCGGTG------TCTGTGCCCGGGAAGCCCCAGGGCTCTGTGG 1361
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32 CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet 51
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APPLICANT: Mornin, Greeg B.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
FILE REPERENCE: 015389-0031003
CURRENT APPLICATION NUMBER: US/09/128,354
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 08/851,843
EARLIER FILING DATE: 1997-05-06
EARLIER FILING DATE: 1997-05-09
EARLIER FILING DATE: 1997-05-09
EARLIER FILING DATE: 1997-05-09
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Mismatches:
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CURRENT FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                             Sequence 3, Application US/09572423B Patent No. 6331399 GENERAL INFORMATION:
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Patent No. 6337200
GENERAL INFORMATION:
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                                                                                             52 AlaCys-----PheValProGln 57
                                                                                                                                                                                                                                                                                           APPLICANT: Brett P. Monia APPLICANT: William A. Gaarde APPLICANT: Edward Wancewicz TITLE OF INVENTION: ISPH-0462 FILE REFERENCE:
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38.24%
33.82%
19.11%
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TOCATION: (56)...(3454)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                                                                                       RESULT 46
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1317 CAGCAGCCGGTG------TCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGG 1361
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APPLICANT: Gaeta, Federico C.A.
APPLICANT: Gaeta Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
FILE REPERENCE: 015389-003500PC
CURRENT APPLICATION NUMBER: US/09/675,321
CURRENT PILING DATE: 2000-09-28
PRIOR PLING DATE: 1998-03-31
PRIOR FILING DATE: 1998-03-31
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet
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Matches:
Conservative:
Mismatches:
                                                                                 EARLIER FILING DATE: 1997-08-14
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-01
EARLIER FILING DATE: 1997-10-01
EARLIER APPLICATION NUMBER: WO PCT/US97/17618
EARLIER APPLICATION NUMBER: WO PCT/US97/17685
EARLIER FILING DATE: 1997-11-19
EARLIER APPLICATION NUMBER: US 08/974,549
EARLIER APPLICATION NUMBER: US 08/974,584
EARLIER APPLICATION NUMBER: US 08/974,584
EARLIER FILING DATE: 1997-11-19
EARLIER FILING DATE: 1997-11-19
EARLIER FILING DATE: 1997-11-19
EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 21
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                                            EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US 08/915,503
                   EARLIER APPLICATION NUMBER: US 08/912,951
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; Patent No. 6440735
; GENERAL INFORMATION:
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EARLIER FILING DATE: 1997-08-14
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38.24%
33.82%
19.11%
                                                                                                                                                                                                                                                                                                                                                                              : PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: I
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                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.:
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LENGTH: 4015

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1362 CGG--------CCCCCGAGGAGGAGACACACAGACCCCCGTCGCTGGTGCAGC 1406
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APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Kren B.
APPLICANT: Chapman, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Andrews, William B.
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APPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet
                                                                              NAME/KEY: CDS
LOCATION: (56)..(3454)
COTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
NS-09-675-321-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PETENT Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATA:
APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846 A17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ArgCysAlaMetLeuAsnProProAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1407 TGCTCCGCCAGCACAGCAGCCCCTGGC---
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1458 GCCTGCGCCGGCTGGCCCCCAG 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AlaCys-----PheValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09052919
Patent No. 6444650
                                                                                                                                                                                                                                                                                                                                                                           62.50
38.24%
33.82%
19.11%
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COMPUTER READABLE FORM:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San
STATE: Ca
COUNTRY:
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                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                        Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                    Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeuIle 21
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LOCATION: 56..3454
OTHER INORMATION: /product= "human telomerase reverse OTHER INFORMATION: transcriptase (hTRT)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 19-NOV-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-007-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-007-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-007-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-007-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-007-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-007-1997
APPLICATION NUMBER: APPLICATION NUMBER: 42,058
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.50
38.24%
33.82%
19.11%
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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1458 GCCIGCGCCGGCTGGTGCCCCCAG 1481

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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Galvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION WIMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
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PRIOR DATE: 06-MAY-1997

PRIOR DATE: 06-MAY-1997

PRIOR DATE: 09-MAY-1997

PRIOR DATE: 09-MAY-1997

PRIOR APPLICATION DATA: 09-MAY-1997

PRIOR APPLICATION DATA: 09-MAY-1997

PRIOR DATE: 14-AUG-1997

PRIOR DATE: 14-AUG-1997

PRIOR DATE: 14-AUG-1997

PRIOR DATE: 14-AUG-1997

PRIOR DATE: 14-AUG-1997

PRIOR DATE: 14-AUG-1997

PRIOR DATE: 14-AUG-1997

PRIOR DATE: 10-CU-1997

PRIOR DATE: 10-CU-1997

PRIOR APPLICATION DATA: 08/915,503

PRIOR APPLICATION DATA: 08-MAG-1997

PRIOR APPLICATION DATA: 09-MAG-1997

PRIOR DATE: 01-CU-1997

PRIOR DATE: 01-CU-1997

PRIOR DATE: 01-CU-1997

PRIOR DATE: 01-CU-1997

PRIOR DATE: 01-CU-1997

PRIOR DATE: 01-CU-1997

PRIOR DATE: 01-CU-1997

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PRIOR DATE: 01-CU-1997

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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
BILING DATE: 01-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-ARR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
                                                            Sequence 343, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                              US-08-974-549A-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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RESULT 50
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1362 CGG-------CCCCCCGAGGAGGACACACAGACCCCCGTCGCCTGGTGCAGC 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AGGTGTACGCCTTCGTGCGGGCCT 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                        ------TCTGTGCCCGGGAGAGCCCCCAGGGCTCTGTGG 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 CysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySerCysGlyMet 51
                                                                                                                                                                                                                                                                                                                                                                                                 2 GlnGluProValLysGlyProValSerThrLysProGlySerCysProIleIleLeuIle 21
                                                                                                    LOCATION: 56..3454
CTHER INFORMATION: /note= "refined sequence of hTRT cDNA"
US-08-974-549A-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
STREFF
STREFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRICH APPLICATION BATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                                                                        09-833799-13B (1-57) x US-08-974-549A-343 (1-4037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 ArgCysAlaMetLeuAsnProProAsnArg------
                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                             Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1458 GCCTGCCCGGCTGGTGCCCCCAG 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08974549A Patent No. 6166178 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 AlaCys-----PheValProGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
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38.24%
33.82%
19.11%
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                     TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
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1317 CAGCAGCCGGTG---
                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                  NAME/KEY: CDS
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                                                                                                                                                                                         Alignment Scores:
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US-08-974-549A-6
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 1..4335
OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATORNEX/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 36,429

REGISTRATION NUMBER: 35,429

TELEPHONE: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH 415) SAG-0300

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH 415) SAG-0300
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; OTHER INFORMATION: /note= "intron 2"
US-08-974-549A-6
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OTHER INFORMATION: /note= "intron 1"
                                                                                      PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAX-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
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38.24%
33.82%
19.11%
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STRANDEDNESS: single
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Best Local Similarity:
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3861 CAGCAGCCGGTG-
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3647 TCCCCTAAGCCAGGGTCACCACCGCTC-----TGTGCCTGCCTCAGTGGTTTT 3694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 LeulysAsp-----ThrAspCysProGlyIleLysLysCysCysGluGlySerCys 49
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                                                                                        US-08-939-366-27
Sequence 27, Application US/08939366
Sequence 27, Application US/08939366
GENERAL INFORMATION:
APPLICANT: Wagner, Thomas E.
APPLICANT: Xie, Yuesheng
TITLE OF INVENTION: Compositions and Methods for the Use of TITLE OF INVENTION: Ribozymes to Determine Gene Function NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE PATENTIAN STATES OF SOFTWARE PATENTIAN STATES OF SOFTWARE PATENTIAN DATA:

APPLICATION NUMBER: US/08/939,366
FILING DATE: 29-SEP-1997
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REGISTRATION NUMBER: 32,001-02749
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER: RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
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4002 GCCTGCGCCGGCTGCCCCCAG 4025
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6677 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GlyMetAlaCysPheValPro 56
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40.30%
29.85%
19.11%
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Query Match:
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3647 rcccraagccaggrancaccgcrc----rgraccrccrcagrarrr 3694
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                                                             APPLICANT: Kitelewski, Jan
APPLICANT: Wytendaele, Hendrik
TITLE OF INVENTION: ANGOMETIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
FILE REPERENCE: 53863-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/467,997
CURRENT APPLICATION NUMBER: US/09/467,997
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsn---- 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESS: Edmonds STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,159
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
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APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Julian H.
APPLICANT: Myat, Anna M.
APPLICANT: Fleming, Robert J.
APPLICANT: Arrawnis-Trakonas, Spyridon
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 6, Application US/09467997
Patent No. 6379925
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08400159
Patent No. 5869282
GENERAL INFORMATION:
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APPLICANT: Mann, Robert S.
APPLICANT: Gray, Grace E.
                                                                                                                                                                                                                                                                                                                                                                                                                              62.50
40.30%
29.85%
19.11%
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New York
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                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: mouse
US-09-467-997-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                                                                                                                                                                                                  SEQ ID NO 6
LENGTH: 6677
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                           No.:
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-----TCGCTCCGTCCGACTCCCCCCCTGC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ISh-Horowicz, David
APPLICANT: Henrique, Domingos M.P.
APPLICANT: Lewis, Unlian H.
APPLICANT: Fleming, Robert J.
APPLICANT: Fleming, Robert J.
APPLICANT: Aravanis-Tsakonas, Spyridon
APPLICANT: Mann, Robert S.
APPLICANT: Mann, Robert S.
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,729A FILING DATE: 06-MAR-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 AGCAGCGACCCTCGTTGTCCGCCCGTGATCGTTGC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 LeulysAspThrAspCysProGlyIleLysLysCys 44
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Matches:
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STREET: 1155 Avenue of the Americas
                                                                                                        7326-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                    ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-
TELECHOMMURICATION INFORMATION:
TELEPHONE: (212) 790-9091
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08611729A Patent No. 6004924
                                                                                                                                                                TELERAX: (212) 869-9741/88
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                        LENGTH: 708 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.4
61.50
43.75%
37.50%
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                                                                                                                                                                                                                                                                                                                          unknown
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COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
FILING DATE: 07 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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US-08-400-159-3
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; Sequence 2. Application US/08886152
; Patent No. 5890273
; Patent No. 5890273
; APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: ARAL, HIROYUKI
TITLE OF INVENTION: PLATELET ACTIVATING FACTOR
TITLE OF INVENTION: PLATELET ACTIVATING FACTOR
TITLE OF INVENTION: ACETYLHYDROLASE, AND GENE THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/886,152 FILING DATE: 30-JUN-1997 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-041-0
                                                    7326-037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION UNDER: 18 872 - REGISTRATION UNDER: 18 873 - TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPAX: (212) 86-9741/8864 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 708 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.4
61.50
43.75%
37.50%
18.81%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-611-729A-3
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823 ccaaatgaatgrcccattacagccacacgccrcacgrcaatgccgccctrcaaggrcarc 764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1758 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: ARAI, HIROYUKI
APPLICANT: INOUE, KEIZO
ITILE OF INVENTION: PLATELET ACTIVATING FACTOR
ITILE OF INVENTION: ACETYLHYDROLASE, AND GENE THEREOF
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
SOFTWARING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,222
FILING APPLICATION NUMBER: US/09/196,222
FILING DATE: 30-JUN-1997
APPLICATION NUMBER: UP 8-188369
FILING DATE: 28-JUN-1997
APPLICATION NUMBER: JP 8-188369
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
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Mismatches:
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; Sequence 2. Application US/09196222
; Patent No. 6323017
; GENERAL INFORMATION:
                                                                                                                                                                                             TOPOLOGY: linear
MOLECUL TYPE: CDNA
OCHICHLAL OUNCE:
ORGANISM: BOVINE (Bos taurus)
TELECOMMUNICATION INFORMATION:
                                                               INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1665 base pairs TYPE: nucleic acid STRANDEDNESS: single
                          TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.50
42.50%
32.50%
18.81%
                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 111..1286
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                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                  TELEFAX:
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REFERENCE/DOCKET NUMBER: 2292-041-0

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Sequence 5, Application US/08264534

Patent No. 5648464

GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5648464ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITTY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     823 CCAAATGAATGTCCCATTACAGCCACACGGCTCACGTCAATGCCGCCCTTCAAGGTCATC 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763 AGATCCAATCCGCCAGGCAAGATGTTGAGA---ACGGCCTGCCCAGCAGTGACCTCTTGT 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 -----AsnProProAsnArgCysLeuLysAspThrAspCysProGly11eLysLysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 ProGlySerCysProllelleLeulleArgCysAlaMetLeu---
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
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Matches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,189
FILING DATE: 03-MAX-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE DOCKET NUMBER: 7326-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/264,534
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                 ORGANISM: BOVINE (Bos taurus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INPERATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                ; LOCATION: 111..1286
US-09-196-222-2
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: U.S.A.
                                                                                                                                                                                  linear
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                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
Pred. No.:
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                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
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Sequence 1, Application US/08081590A
Patent No. 5786158
RENERAL INFORMATION:
APPLICANT: Arravanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 AGCAGCGÁCCTCGTTGTCCCGCCCGTGATCGTTGC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITX: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7326-015
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REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET UNBER: 73.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212 869864/9741
TELEEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
LENGTH: 2892 base pairs
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                                                                                                                                                                                                                                        61.50
43.75%
37.50%
18.81%
                       TYPE: nucleic acid
STRANDEDNESS: double
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EDNESS: double
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                                                           TOPOLOGY: unknown MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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: U.S.A.
                                                                                                                                                                                                                                                                                     Best Local Similarity:
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; LOCATION: 142.
US-08-083-590A-1
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                Percent Similarity:
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US-08-083-590A-1/C
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ZIP: 10036
                                                                                                                                                                                                       Alignment Scores:
                                                                                                                      NAME/KEY:
                                                                                                                                           LOCATION:
                                                                                                                                                              US-08-264-534-5
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%308-465-500-5/c

| Sequence 5, Application US/08465500
| Sequence 5, Application US/08465500
| Patent No. 5789195
| GENERAL INFORMATION:
| APPLICANT: Artavanis-Tsakonas, Spyridon
| APPLICANT: Muskavitch, Marc A.T.
| APPLICANT: Rebay, Ilaria
| APPLICANT: Rebay, Ilaria
| APPLICANT: Blaumueller, Cristine M. APPLICANT: Shepard, Scott B. TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOMAINS
| TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON
| WUMBER OF SEQUENCES: 34
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          -----recricercearcecececeire 278
                                                                                                                                                                                                                                              13 ProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsnArgCys 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,500

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INPORMATION:

NAME: Misrock, S. Leblie

REFERENCE/DOCKET NUMBER: 7326-034

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2892 base pairs

TYPE: UCLEIC acid

TYPE: UCLEIC acid

TYPE: MICLEIC acid

TYPE: MICLEIC acid
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Matches:
Conservative:
Mismatches:
                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                          33 LeulysAspThrAspCysProGlyIleLysLysCys 44
                                                                                                                                                                                              09-833799-13B (1-57) x US-08-083-590A-1 (1-2892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
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43.75%
37.50%
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US-08-465-500-5
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Best Local Similarity:
                                                                       Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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                                                                                                                       Query Match:
                           Pred. No.:
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APPLICANT: Arravanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5849869ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                       -----TCGCTCCGTCCACTCCCCCCCTGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 ProGlySerCysProllelleLeulleArgCysAlaMetLeuAsnProProAsnArgCys 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/346,126 FILING DATE: CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/791,923 FILING DATE: 14-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                277 AGCAGCGÁCCCTCGTTGTCCCGCCCGTGATCGTTGC 242
                                                                                                                                                                                                    33 LeuLysAspThrAspCysProGlyIleLysLysCys 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
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                                                                09-833799-13B (1-57) x US-08-465-500-5 (1-2892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: PROMPTER: PC POSS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIUKNAL MARE: MARTOCK, S. LESIGE
REGISTRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 7326-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869864/9741
TELEFAX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2892 base pairs
                                                                                                                                                                                                                                                                                                                     US-08-346-126-5/c
; Sequence 5. Application US/08346126
; Patent No. 5849869
; GENERAL INFORMATION:
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18.81%
18.81%
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                            316 CCAGGCACTTGCCCG----
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LOCATION: 142..2640
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Best Local Similarity:
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Pred. No.:
Query Match:
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STRANDEDNESS:
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    US-08-532-384-1/c
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                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
APPLICANT: Artavanis-Tsakonas, Spyridon et al.
TITLE OF INVENTION: Human No. 5856441ch And Delta, Binding Domains
TITLE OF INVENTION: In Toporythmic Proteins, And Methods Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
    ----TCGCTCCGTCCGACTCCCCGCTGC 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                           277 AGCAGCGACCTCGTTGTCCCGCCCGTGATCGTTGC 242
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                                        33 LeuLysAspThrAspCysProGlylleLysLysCys 44
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                                                                                                                                                                                                                                                                                                                            SSEE: Pennie & Edmonds
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879,038
FILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             Sequence 5, Application US/08346128
Patent No. 5856441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REPERDICE/DOCKET NUMBER: 7326-
TELEPHONE: 212 790-9090
TELERAX: 212 869864/9741
TELEX 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGRAL 2892 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.50
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EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
316 CCAGGCACTTGCCCG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U. ZIP: 10036
                                                                                                                                     US-08-346-128-5/c
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                                                                                                                                                                                                                                                                                                                                                STREET:
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No.:
                                                                                                                      RESULT 62
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GENERAL INFORMATION:
APPLICANT: Attavanis-Tsakonas, S. et al.
APPLICANT: Attavanis-Tsakonas, S. et al.
TILLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
TITLE OF INVENTION: Nucleic Acids
TITLE OF SEQUENCES. 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 CCAGGCACTTGCCCG-----TCGCTCCGTCCGACTCCCGCTGC 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 AGCAGCGACCTCGTTGTCCCGCCCGTGATCGTTGC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-833799-13B (1-57) x US-08-532-384-1 (1-2892)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Muskavitch, Marc A.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7326-015
                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/083,590
FILING DATE: 25-JUN-1993
ATTONNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
Sequence 1, Application US/08532384; Patent No. 6083904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/08893828; Patent No. 6090922; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 733
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2892 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 142..2640
US-08-532-384-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                               New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity:
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09-833799-13b.rni

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APPLICANT: Fehon, Richard G.
APPLICANT: Rebay, Ilaria
APPLICANT: Blaumueller, Cristine M.
APPLICANT: Shepard, Scott B.
TITLE OF INVENTION: HUMAN NOTCH AND DELTA, BINDING DOWAINS
TITLE OF INVENTION: IN TOPORYTHMIC PROTEINS, AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08747887

Sequence 4, Application US/08747887

Patent No. 5853734

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Russo, James J.

APPLICANT: Redelman, Isidore S.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: Glycoprotein L And Glycoprotein M From Kaposi's TITLE OF INVENTION: Same And Uses Thereof

TITLE OF INVENTION: Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TegeréceréceAereceéérée 278
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                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,828
FILING DATE: 11-UUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 LeuLysAspThrAspCysProGlyIleLysLysCys 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-833799-13B (1-57) x US-08-893-828-5 (1-2892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNAL MARIE MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-050
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2892 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 CCAGGCACTTGCCCG----
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LOCATION: 142..2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                             USA
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US-08-747-887-4
                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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21 IleArgCysAlaMetLeuAsnProPro---AsnArg-CysLeuLysAspThrAspCysPr 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4. Application US/08728323A
Sequence 4. Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Encoding Same And Uses Thereof TITLE OF INVENTION: Encoding Same And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 oGiyileLysLysCysCysGluGlySerCysGlyMetAlaCysPheVal 55
                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,887 FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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475 GCACGGGTCCCAGGGCCGGTCCGGTGGCATACAGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                               CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Wihlte, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cooper & Dunham LLP
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
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ADDRESSEE:

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1 AlaGlnGluProValLysGlyProValSerThrLysProGlySerCysProllelleLeu 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Word, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 AGGCGGGAATACCCCTCTGCACGCTGCTGTGGACGTGGATGTATGCTC 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 odlylleLysLysCysCysGluGlySerCysGlyMetAlaCysPheVal 55
                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park
1185 Avenue of the Americas
                                                                                                                                                                                                        APPLICATION NUMBER: US/08/728,323A
                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 149, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.2
61.00
45.61%
31.58%
18.65%
                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 631 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             212-391-0525
                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                 : New York
RY: U.S.A.
10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
Query Match:
                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-998-416-149/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-728-323A-4
                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
STREET:
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275 GGACCCTGCCACCACCACGTGCTCCTGCTCGTTGTTGCTCCGCCTGCTGCTGCTG 216
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Sequence 191, Application US/09056556

Fatent No. 63504656

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PR.
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMINICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-833799-13B (1-57) x US-08-998-416-149 (1-653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.64%
50.00%
18.65%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAG1057RP
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 AACCCA 210
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                                         27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: W. COUNTRY:
                                                                                                                                                                                                                                                                                                                            NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
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TREA

PatentIn Release #1.0, Version #1.30

SOFTWARE:

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449 CGCCTTTGCCGCCGACGCGGTGGTGGCGAAACGGGCTGAGTCGGCGGGT 508
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275 AAACCCGCCCAGGGCCGCTGGGCTCATGGCAGAGAATTAGAAAACCCGGGATAT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----Progly1leLysLysCysCysGluGlySer 48
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasır A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Common Commo
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-833799-13B (1-57) x US-09-056-556-191 (1-1055)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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                         APPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998 CLASSIFICATION:
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Patent No. 6458366
                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-6930
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 1055 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
US-09-056-556-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.4
61.00
32.10%
24.69%
18.65%
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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STATE: Washing
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Pred. No.:
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389 GAGTGTGGATGTTGAGACCCTGGCCTGGÄÄGGGGÄCÄACGTGCTTTTGCCTCTTGGTC 448
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275 AAACCCGCCGCCAGGGCCGCTGGACGGCCATGGCAATTAGAAAACCCGGGGATAT 334
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335 TGTCCGCGGATTGTCATACGATGCTGAGTGCTTGGT-----GGTTCGTGTTTAGCCATT 388
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Sequence 172/2
Sequence 172/2
Sequence 172/2
Sequence 172/3
Patent No. 6410718
SERENTI INFORMATION:
APPLICANT: Blokeberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content; TITLE OF INVENTION: Modification of Plant Lignin Content; TILE REFERENCE: 11000.1003c40
CURRENT APPLICATION NUMBER: US 08/975,316
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1999-11-21
PRIOR FILING DATE: 1999-11-21
PRIOR PRILICATION NUMBER: US 09/13,000
PRIOR PLING DATE: 1999-10-09
PRIOR PLING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
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MEDIUM TYPE: Floppy disk
COMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 1055 base pairs
TYPE: nucleic acid
STRANDENDES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
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                                                                                                                               APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
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61.00
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Best Local Similarity:
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US-09-615-192A-172/c
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TOPOLOGY:
US-09-072-596-186
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211 CCTGGTAGCTGCCCATTGACGGTGATTAT-TGTATTCTCCTTGCATAGCCTGGTAACTGT 153
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                                                                                                                                                                                                                                                                          33 LeuLysAspThrAspCysProGlylleLysLysCys-----CysGluGlySer 48
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnology TITLE OF INVENTION: SWAD-INTERACTING POLYPEPTIDES AND THEIR USE CURRENT PAPLICATION NUMBER: US/09/449,285A CURRENT FILING DATE: 1999-11-24 PRIOR FILING DATE: 1999-11-24 PRIOR FILING DATE: 1998-11-24 PRIOR FILING DATE: 1998-10:28 PRIOR FILING DATE: 1990-16-52 NUMBER: 97201645.5 NUMBER OF SEQ ID NOS: 27 SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                152 CTTCGCTTCAATGATGAAGGTATAATTGACGATTGCTGCATTTGTGATGGCAGC 99
                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
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                                                                                                                                                           Indels:
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Matches:
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                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09449285A; Patent No. 6313280; GENERAL INFORMATION:
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60.00
57.89%
44.74%
18.35%
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60.00
39.06%
29.69%
18.35%
                         TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 GCGGAGACCCCA 241
                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                     US-09-615-192A-172
                                                                                Alignment Scores:
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Best Local Similari
               LENGTH: 518
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; SEQ ID NO 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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LENGTH: 850
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                                                                                             Pred. No.:
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852 GCGCCTGAAAAAGCACTCAATGTGTCAGACAAGAGGTTAAGGAGACAAATAAAGGTTACT 793
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                                                             APPLICANT: Black, Michael
APPLICANT: Black, Michael
APPLICANT: Modgson, John
APPLICANT: Knowles, David
APPLICANT: Knowles, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
CORRESONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 05-MAY-1997
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-833799-13B (1-57) x US-08-858-207A-161 (1-1089)
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US-08-858-207A-161/c
Sequence 161, Application US/08858207A
Patent No. 6348328
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P50475
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY AGENT INPORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
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US-09-282-147-37/c
; Sequence 37, Application US/09282147
; Patent No. 6274147
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P5C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 -----LysAspThrAspCysPro 39
                                                                                                                                                                                                                                                                                                                          IBM Compatible
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                                                                                                                                                                                                         STREET: 70% smc-
                                                                                                                                                                                                                                                                                                              Diskette
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60.00
43.75%
27.08%
18.35%
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                                                                                                                                                                                                                                                                          ZIP: 19406-0939
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                           COUNTRY:
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US-09-543-084A-29/c
; Sequence 29, Application US/09543084A
; Sequence 29, Application US/09543084A
; Patent No. 6361988
; GENERAL INFORMATION:
; APPLICANT: Erances H. Arnold
APPLICANT: All Animin Shao
; APPLICANT: Lorraine J. Giver
TILLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
; TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
; TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
; TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
; TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
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                              APPLICANT: YAO, KUN
TITLE OF INVENTION. METHOD FOR GENERATING NONPATHOGENIC, INFECTIOUS
TITLE OF INVENTION. PANCREATIC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA
TITLE OF INVENTION: PANCRENITC NECROSIS VIRUS (IPNV) FROM SYNTHETIC RNA
TITLE OF INVENTION: PANCRENITS
FILE REFERENCE: 8288-9023
FILE REFERENCE: 8288-9023
CURRENT APPLICATION WUMBER: US/09/282,147
CURRENT FILING DATE: 1998-03-31
EARLIER APPLICATION WUMBER: US/60/080,278
EARLIER PAPLICATION WUMBER: PCT/US97/12955
EARLIER FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ProValSerThrLysProGlySerCysProllelleLeulleArgCysAlaMetLeuAsn 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 ProProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCys-----
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-833799-13B (1-57) x US-09-282-147-37 (1-2783)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,084A
FILING DATE: April 4, 2000
CLASSIFICATION: 435
PRIOR ADDITETION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
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APPLICATION NUMBER: 09/381,935
APPLICATION NUMBER: 60/041,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1256 AGATCATCACTAGGTCCTCGTTGT 1233
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APPLICANT: VAKHARIA, Vikram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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APPLICANT: Frances H. Arnold
APPLICANT: Frances H. Arnold
APPLICANT: Anixin Shao
APPLICANT: Huimin Zhao
APPLICANT: Horraine J. Giver
TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
TITLE OF INVENTION: Sequences Using Defined or Random Primer Sequences
CORRESPONDENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1164 ACGICGIAGCGGCCGGCACCIIGAGGIGCAICCGGIAGAAGCGIGCGGCGCCCTGCCAC 1105
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-833799-13B (1-57) x US-09-543-084A-29 (1-3222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows 98 SOFTWARE: Word 97 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/543,084A FILING DATE: April 4, 2000 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 GlySerCysGlyMetAlaCysPheValPro 56
                                                                                                                                                                                        330187-89
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PILING DATE: MACHINE, 178, 1997
APPLICATION NUMBER: 60/045,211
FILING DATE: April 30, 1997
APPLICATION NUMBER: 60/046,256
FILING DATE: May 12, 1997
APPLICATION NUMBER: 60/905,359
FILING DATE: August 4, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 330187-8
TELECOMMUNICATION INFORMATION:
TELEPHOME: (310) 788-5000
TELEPHOME: (310) 788-5000
TELEPHOME: (310) 788-5100
INFORMATION POR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-543-084A-26/c
Sequence 26, Application US/09543084A
Patent No. 6361988
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: polynucleotide
                                                                                                                                                                                                                                                                                                                  3222 nucleotides
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MEDIUM TYPE: Floppy
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EDNESS: single
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Best Local Similarity:
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2038 ACGTCGTAGCGGCCCGGCACCTTGAGGTGCATCCGGTAGAAGCGTGCGGCGCCCTGCCAC 1979
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Matches:
Conservative:
Mismatches:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/381,935
APPLICATION NUMBER: 60/041,666
APPLICATION NUMBER: 60/041,666
APPLICATION NUMBER: 60/045,211
FILING DATE: May 12, 1997
FILING DATE: May 12, 1997
FILING DATE: May 12, 1997
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FILING DATE: May 12, 1997
FILING DATE: May 12, 1997
FILING NUMBER: 39,421
FREGISTRATION NUMBER: 330187-89
FELEPHONE: (310) 788-5000
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Job time : 101 secs
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Perfect score:

Sequence:

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Run on:

Scoring table:

Minimum DB Maximum DB

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BE772602
BE715602
BE715626
BE715626
BE772160
BF838555
BE772166
AI285400
                                       BE715603
BE772155
BE772171
BE182879
BE772169
AA583997
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AI393896
AI989737
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BE772137
AA586974
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BF825204
AW860590
AA586983
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BE772154
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BF836224
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BF824934
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BE182652 K23-HT064
BG987761 CM3-HT119
BE182993 CM4-HT065
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                         February 15, 2003, 21:53:32; Search time 1184 Seconds (without alignments) 2817.796 Million cell updates/sec
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                                                                                                                                                                                                                                                                   Description
                                                  1 AATTCGAGCTCGGTACCATA......GTTTCGTTCCACAATAATAG
                                                                               32308132
   5.1.4 p5 4578
Compugen Ltd.
                                                                      16154066 segs, 8097743376 residues
                                                                             Total number of hits satisfying chosen parameters:
   GenCore version
Copyright (c) 1993 - 2003
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                  nucleic search, using sw model
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AW001880
BE182652
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                                                          IDENTITY NUC
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Match
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61.3
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423 bp mRNA linear EST 21-DEC-1999 similar to gb:S58717 rnal ELAFIN PRECURSOR (HUMAN); contains element AI830872
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tunor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to con R adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of
profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under tow stringency conditions."

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
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81.6%; Pred. No. 8.8e-30;
tive 0; Mismatches 33; Indels
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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WRNA linear EST 09-MAR-2000
WR1d06.x1 Soares thymus NHFTh Homo sapiens cDNA clone
IMAGE:2513867 3' similar to gb.558717 rnal ELAFIN PRECURSOR (HUMAN
);contains element MER28 repetitive element; , mRNA sequence.
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NCI-CRAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 552 Std Error: 0.00 Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                            361 AAGCGCAAGGACCAGTCAAAGGTCCCAATAAAGCCTGGCTCCTGCCCCATTATCT 302
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                                                                                                                        Score 126.2; DB 9; Length 423;
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/clone="IMAGE:2513867"
/clone lib="Soares_thymus_NHFTh"
/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
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Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 81.6%;
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib=#HT0649"

/clove stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 219)

1 (bases 1 to 219)

1 (bases 2 to 219)

1 (bases 3 to 219)

1 (bases 3 to 219)

1 (bases 3 to 210)

1 (bases 4 to 210)

1 (cataia Carcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Rogai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0649-090 500-011-N05k13-2000.05-09&t4=1) Seq primer: puc 18 forward High quality sequence start: 22 High quality sequence stop: 219.
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sax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                          88 IGAITCGITGCGCTAIGITAAACCCACCIAACCGITGITIGAAGGACACIGAITGICCAG 147
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 340)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Gardian,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                 BG987761 13-JUN-2001 CM3-HT1190-110101-624-h04 HT1190 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=CM3&t2=CM3-HT1190-
110101-624-h04&t3=2001-01-11&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 340.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                         142 GAATCAAGAAGIGCTGTGAAAGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGAAG 200
148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
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Pred. No. 2.8e-29;
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/clone_lib="HT1190"
/dev_stage="Adult"
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Matches 145; Conservative (
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sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.hrscripts/gethtml2.pl?tl=&t2=CM4.HT0653-180 400-146-all&t3=2000-04-18&t4=1) Seq primer: puc 18 forward High quality sequence start: 21 High quality sequence start: 21 High quality sequence stop: 342.
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//dev_sTage="Adult"
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//doce="Corgan: head neck; Vector: puc18; Site_1: Smal;
//doce="Corgan: head neck; Vector: puc18; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application of 16,7716 - Ludwig Institute for Cancer Research)
//docetries into the puc18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Coste, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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CM4-HT0653-180400-146-all HT0653 Homo sapiens CDNA, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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120 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCCAGTGAGAG 62
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/clone_lib="HT0653"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 359)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunctein,A., deoliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922

Rax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0652-150 Seq primer: puc 18 forward
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            CM4-HT0652-150400-143-a07 HT0652 Homo sapiens cDNA, mRNA seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/dev_stage="Adult"
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                                              BE181546 34-270300-308-f02 HT0634 Homo sapiens cDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t2=CMO-HT0634-270300-308-f02&t3=2000-03-27&t4=1)
                                                                                                                                                                                                                                                                  1 (bases 1 to 344)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from (ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20202663
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Pred. No. 2.8e-29;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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High quality sequence stop: 344.
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/clone_lib="HT0634"
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60.5%; Score 124.6; DB 10; Length 359; 81.0%; Pred. No. 2.8e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmal2.pl?tl=&t2=CM4-FT0104-230
600-215-c09&t3=2000-06-23&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 360.
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                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 361)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="FT0104"
/dev_stage="Adult"
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/clone_in= n.v...
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: head neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                                Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Coofman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 370)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 364)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                          Shorgun sequencing of the human transcriptome with ORF expressed
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Best Local Similarity 81.0%; Pred. No. 2.8e-29;
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High quality sequence start: 20
High quality sequence stop: 364.
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Query Match
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 Seq primer: puc 18 forward
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 370)
                                                                                                                                                                                                                                                                                                  Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                       Shorgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 370.
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/clone_lib="HT0744"
/dev_stage="Adult"
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Laboratory of Cancer Genetics
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Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 600-201-h09&t3=2000-06-16&t4=1) Seq primer: puc 18 forward High quality sequence start: 13 High quality sequence stop: 370.
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/clone_lib="HT0744"

/clone_lib="HT0744"

/clone_lib="HT0744"

/note="Organ: head neck; Vector: pucl8; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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1 (Dases I to 370)

1 bias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Prunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 2.8e-29;
0; Mismatches 34; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
Emall: asimpson@ludwig.org.br
This sequence was derived from
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Ludwig Institute for Cancer Research
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 371)

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Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carrahlo, A.F., Matshtuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                 Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM4-FT0104-230600-215-c08&t3=2000-06-23&t4=1)
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                                                                                                                                                                                               Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
sequencing of the human transcriptome with ORF expressed
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                        sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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High quality sequence start: 8
High quality sequence stop: 370.
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                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%;
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                                                                                                                                                                             Tel: +55-11-2704922
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/clone_lib="HT0990"
//dev stage="Adult"
/ndev stage="Adult"
/note="Organ: head neck; Vector: puc18; Site_1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                                                       Fax: +55-11-270701
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-HT0990-
251100-263-g08&t3=2000-11-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stops: 367.
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                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 2.8e-29;
0; Mismatches 34;
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Laboratory of Cancer Genetics
Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.0%;
Matches 145; Conservative C
                                                                                                                                                                               Tel: +55-11-2704922
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qt69f06.x1 NCI CGAP Eso2 Homo sapiens cDNA clone IMAGE:1960547 3' similar to gb:558717_rna1 ELAFIN PRECURSOR (HUMAN);contains element THR repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone_lib="FF00104"

/dov $Eage="Adult"

/note="Organ: prostate tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip
Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                             Fax: +55-11-2707001
Email: asimpsom@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
Seq primer: puc 18 forward
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 375)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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60.5%; Score 124.6; DB 12; Length 371;

Best Local Similarity 81.0%; Pred. No. 2.8e-29;

Matches 145; Conservative 0; Mismatches 34; Indels 0;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                            High quality sequence start: 8
High quality sequence stop: 371.
Location/Qualifiers
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                                                                                    Tel: +55-11-2704922
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/derhtml2.pl?tl=&t2=CM4-HT0744-160 Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                  /note="Organ: esophagus; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo ald. Average insert size 1.1 kb. Life Technologies catalog #: 11502-010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE715603 379 bp mRNA linear EST 12-SEP-2000 CM4-HT0744-160600-201-a07 HT0744 Homo sapiens cDNA, mRNA sequence.
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1 (bases I to 37)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costas, F.F., Barbustein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Buchter, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 292
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Pred. No. 2.8e-29;
0; Mismatches 34; Indels 0;
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20202663
                                                                                                                                                                                                                                                                                                                                                                           1 others
                                                                                                   /organism="Homo sapiens"
/db xref="taxon.9606"
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Seq primer: -40UP from Gibco
High quality sequence stop: 356.
Location/Qualifiers
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High quality sequence stop: 379.
Location/Qualifiers
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BE715603.1 GI:10103868
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Best Local Similarity 81.0%;
Matches 145; Conservative
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Fax: +55-11-2707001
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source

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db_xref="taxon:9606"
/clone lib="HT0744"
/dv_erage="Adult"
/dv_erage="Adult"
/note="Organ: head neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t2=CM4-FT0104-230
600-215-b05&t3=2000-06-23&t4=1)
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1 (bases 1 to 30)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matewikuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 AagdgddaAgagddaAaAgdrddaGrcdaCradcraAgddragdcrigcdgddarrardr 203
                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
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95 c 112 g 86 t
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/db xref="taxon:9606"
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High quality sequence stop: 365.
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/clone\_lib="FT0104"

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/note="Organ: prostate tumor; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This enty can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=CM4-FT0104-230
600-215-g07kt3=2000-06-23&t4=1)
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/db_xref="taxon:9606"
/db_clone_lib="FT0104"
/dev_stage="Adult"
/note="Organ: prostate tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 380)
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 380
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stage="Adult"
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Best Local Similarity 81.0%;
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/db_xref="taxon:9606"
/clone_lib="FT0104"
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High quality sequence start: 45
High quality sequence stop: 386.
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Laboratory of Cancer Genetics
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Best Local Similarity 81.07
Matches 145; Conservative
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CM4-HT0652-150400-143-g08 HT0652 Homo sapiens cDNA, mRNA sequence.
BE182879
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Bukaryota, Matazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Butheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 386)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, W. Ur, Zago, M.A., Bordin, S., Costa, F.F.
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Simpson, A.J.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This ent be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0652-150
400-143-908&t3=2000-04-15&t4=1)
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 2.9e-29;
                                                                                    low stringency conditions."
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/db_xref="taxon:9606"
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/dev_stage="Adult"
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/clone_ince_incorrections.
/dev_stage="Adult"
/note="Organ: prostate_tumor; Vector: pucl8; Site_1: Smal;
/note="Organ: prostate_tumor; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
roject. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
600-215-F02&t3=2000-06-23&t4=1)
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                       34; Indels
Score 124.6; DB 10 Pred. No. 2.9e-29;
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Tel: +55-11-2704922
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Simpson,A.J.
                                                                                                                                                                                                                                                                                         Homo sapiens
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BE772168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:

Www-bio.llhl.gov/bbrp/image/image.html
Insert Length: 480 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                   EST 26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                     nn65a01.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088712 3' similar to gb:S58717_rnal ELAFIN PRECURSOR (HUMAN);, mRNA sequence. AAS83397
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 388)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                               257 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCCCCGTTATCT 198
                                                                                                                                                                   88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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                   DB 12; Length 386;
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Score 124.6; DB 12; ----
Pred. No. 2.9e-29; Indels
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/clone="IMAGE:108712"

/clone lib="NCI_CGAP_Lar1"

/tissue_type="larynx"

/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.9e-29;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               388 bp
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                 60.5%;
81.0%;
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                                                   Matches 145; Conservative
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Matches 145; Conservative
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/clone_inc="rice.v."
/dev_stage="Adult"
/note="Organ: prostate tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230 600-215-d07&t3=c00-06-23&t4=1)
Seq primer: puc 18 forward
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(bases 1 to 389)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Soldmai,G.H., Carvalho,A.F., Matsukuma,A., Baid,G.S., Singson,D.H., Goldmai,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Singson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                      EST 20-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
305 TGAICCGGTGCGCCAIGTTGAAICCCCCTAACCGCTGCTTGAAAGAIACTGACTGCCCAG 246
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Pred. No. 2.9e-29;
0; Mismatches 34; Indels 0;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 389
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/clone_lib="FT0104"
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Email: cgapbs-remail.nlw.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

CDNA Library Arrayed by: Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 802 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 381.
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41393896

4205e09.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107912 3'

4205e09.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107912 3'

520 similar to gb:558717 rnal ELAFIN PRECURSOR (HUMAN); contains element

THR repetitive element;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 390)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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234 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTTCGTTCCCCCAGTGAGA 292
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Matches 145; Conservative
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Unpublished (1997)
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                human.
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willed. XI Soares Dieckgraefe colon NHCD Homo sapiens cDNA clone IMAGE:2520710 3' Similar to gb:S587Ī7_rnal ELAFIN PRECURSOR (HUMAN A1989737.1 GI:S836618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Soares Dieckgraefe colon NHCD"
/tissue type="colonic mucosa from 3 patients with Crohn's
disease"
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(Dases 1 to 390)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:2520710"
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Page 14

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/dev grage="Adult"
/note="Organ: head neck; Vector: puc18; Site_1: Smal;
Site_2: Smal, A minl: library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
a 115 c 96 g 93 t
                                       Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coste,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001

Bmail: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
600-201-dl0&t3=2000-06-16&t4=1)
Seq primer: puc 18 forward

High quality sequence start: 4

High quality sequence story: 395.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 397)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone lib="HT0744"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simpson A.J.G.
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    1 (bases 1 to 395)
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                                                                                                                                                                                                                                                   Simpson, A.J.
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/db xref="taxon:9606"

/clon=lib="HT0744"

/dev stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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mail: satingson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
futp://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
600-201-c07&t1=2000-06-16&t4=1)
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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0; Mismatches 34
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High quality sequence stop: 390.
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/dev_stage="Adult"
/note="Organ: prostate tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230
600-215-a12&t3=2000-06-23&t4=1)
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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60.5%; Score 124.6; DB 12; Length 397;
cal Similarity 81.0%; Pred. No. 2.9e-29;
145; Conservative 0; Mismatches 34; Indels 0;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence stop: 397.
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                                                                                        Simpson, A.J.
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CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 523 Std Error: 0.00
Seq primer: -40ml3 #wd. ET from Amersham.
Location/Qualifiers
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CM4-HT0744-160600-201-b10 HT0744 Homo sapiens cDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 9; Length 399;
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20202663
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                                        Contact: Robert Strausberg, Ph.D.
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Brazil

Tumor Gene Index

AUTHORS TITLE

Page 16

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This sequence was derived from the FAPESP/LICR Human Cancer Genome
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Insert Length: 644 Std Error: 0.00
Seg primer: -400P from Gibco.
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Contact: Robert Strausberg, Ph.D.
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High quality sequence start: 12
High quality sequence stop: 403.
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/db xref="taxon:9606"
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                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
600-201-blo&t3=2000-06-16&t4=1)
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bb/lbevy 110-8ET 12-SEP-2000 403 bp mRNA linear EST 12-SEP-2000 4M4 HT0744-160600-201-c04 HT0744 Homo sapiens cDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 400;
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Pred. No. 2.9e-29;
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High quality sequence stop: 400.
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                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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81.0%;
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Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
98 c 113 g 96 t
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Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 600-201-c04&t3=2000-06-16&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 40. NOT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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NCI CGAP Sub1 library is a subtracted library derived from En. BI constitutes a mixture of 21
normalized or subtracted NCI CGAP libraries: NCI CGAP PC2, NCI CGAP PC3, NCI CGAP PC10,
NCI CGAP PC10; NCI CGAP PC3, NCI CGAP PC10,
NCI CGAP PC10; NCI CGAP PC3, NCI CGAP PC10,
NCI CGAP PC10; NCI CGAP PC11, NCI CGAP LDM2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs remail.nih.gov
The sequence contained an oilgo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

www-bio.llni.gov/bbrp/image/image.html
POLYA=Yes.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 406)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW137392
UI-H-BII-acs-b-12-0-UI.sl NCI CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2715238 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                     34; Indels
                                                                                                                                                                                                                                                                                                                                                      Score 124.6; DB 5
Pred. No. 2.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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/clone="IMAGE:2439338"
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NCI CGAP Br2, NCI CGAP CO8, NCI CGAP CLL1, NCI CGAP Lei2, NCI CGAP Enr23, NCI CGAP Lus,
NCI CGAP Enr23, NCI CGAP Lus,
NCI CGAP Lus,
NCI CGAP Lus,
NCI CGAP Lus,
NCI CGAP Lus,
NCI CGAP Enr25.
NCI CGAP Enr25.
NCI CGAP Mare ere pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI CGAP Kid3 pool 1 LLAM 334-337, 3682-3683,
3796-3903 (IMAGE CloneIDS 1323911, 1456008-1456775,
1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 3338-3342,
3722-3725, 3776-3778 (IMAGE CloneIDS 1323912-1325831,
1471368-1472993, 1492104-1493255); NCI CGAP Lus pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDS 127096-1477991,
152094-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE CloneIDS 127096-128631,
1469064-1470983, 1475592-1476743); NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 18706-18706,
3716-3720, 3733-3735 (IMAGE CloneIDS 127096-128631,
11AM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 6, 791-2806,
NCI CGAP CO10 pool 1 LLAM 2644-2653, 2811-2872 (IMAGE CloneIDS 1057096-12863),
NCI CGAP CO10 pool 1 LLAM 2644-2653, 2811-2872 (IMAGE CloneIDS 1057096-1806),
NCI CGAP CO10 pool 1 LLAM 2644-145351); Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research 6, 731-806.
TAG IIB=NCI CGAP CO10
TAG IISB-NCI CGAP CO10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ыв/15604 160600-201-a08 HT0744 Homo sapiens cDNA, mRNA sequence.
ВБ715604
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 600-201-a08&t3=2000-06-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence start: 21
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: head neck, Vector: puc18, Site 1: Smal, Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/limage/limage.html
Insert Length: 615 Std Error: 0.00
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NCI-CAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Best Local Similarity 81.0%; Pred. No. 2.9e-29;
Matches 145; Conservative 0; Mismatches 34;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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/clone_lib="HT0744"
/dev_stage="Adult"
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Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 c
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ORIGIN
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AA586943/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                           FEATURES
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Nan Hu, M.D., Ph.D., Mark Roth, M.D., Phillip

Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clond distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AM082097

xb60d08.xl NCI_CGAP_ESO2 Homo sapiens cDNA clone IMAGE:2580687 3'
similar to gb:858717 rnal ELAFIN PRECURSOR (HUMAN); contains element
MER28 MER28 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                           /note="Organ: larynx; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dr. Larynx. 5' adaptor sequence: 5' GAATTCGGCACGAG
3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTTT 3'
Average insert size: 0.9 kb."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 422)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                                                                                                                                                           db_xref="taxon:966"

/clone="IMAGE:1089096"

/clone_lib="NCI_CGAP_Larl"

/tissue_type="larynx"

/lab_hogt="SOLR (kanamycin resistant)"
Seg primer: -40m13 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: polyT not found
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/db_xref="taxon:9606"
/clone="IMAGE:2580687"
/clone_lib="NCI_CGAP_Eso2"
                                                                                                                                             /organism="Homo sapiens"
                                  High quality sequence stop: 335.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -40UP from Gibco
High quality sequence stop: 407.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone lib="FF0104"
/dcv_sfage="Adult"
/note="Organ: prostate tumor; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B"
/note="Organ: esophagus; Vector: pCMV-SPORT6; Site_1: Sall
isite_2: NotI; Cloned unidirectionally. Primer: Öligo
dT. Average insert size 1.1 kb. Life Technologies catalog
#: 11502-010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ык/72154 428 bp mRNA linear EST 20-SEP-2000
СМ4-FT0104-230600-215-b04 FT0104 Homo sapiens cDNA, mRNA sequence.
BE772154
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-FT0104-230 600-215-b04&t3=2000-06-33&t=1)
Seq primer: puc 18 forward
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1 (bases 1 to 428)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, C.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, P., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                      373 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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                                                                                                                                                                                                                                                      60.5%; Score 124.6; DB 10; Length 422; 81.0%; Pred. No. 3e-29;
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                                                                                                                                                                                                                                                                                                            0; Mismatches
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High quality sequence stop: 428.
Location/Qualifiers
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Laboratory of Cancer Genetics
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                                                                                                                                                                                                                                                                                  Best Local Similarity 81.0%;
Matches 145; Conservative
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BE772154/c
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ACCESSION
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COMMENT
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qt66a10.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960218 3' similar to gb:S58717_rnal ELAFIN PRECURSOR (HUMAN);contains element THR repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taste Producement: Nam. Hu, M.D., Ph.D., Mark Roth, M.D., Phillip Taylor, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html
Insert Lenght for G.E. Consortium/LNL at:
Insert Lenght for Gibco
High quality sequence stop: 428.
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profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 429)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                     88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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/clone="IMAGE:196021B
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/tissue_type="squamous cell carcinoma"
/lab_host="DH108"
                                                                                                                                                   Score 124.6; DB 12;
Pred. No. 3e-29;
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                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                 60.5%;
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Unpublished (1997)
                                                                                                                                                                                                    Matches 145; Conservative
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/db xref="taxon:9606"

/clonellb="HT1016"

/dev stage="Adult"

/dev stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: Smal;

Site_2: Smal; A mini-library was made by cloning products

Site_2: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA maplification were performed under

low stringency conditions."

99 a 120 c 118 g 100 t
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Jasa Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F. Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                          BF836224 173 100-474-h01 HT1016 Homo sapiens CDNA, mRNA sequence.
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Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Project. This entry on be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016-171100-474-h01&t3=2000-11-17&t4=1)

Seg primer: puc 18 forward

High quality sequence stop: 437.

Location/Qualitiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
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                                            352 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 293
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Property of the factor of the fallowing URL Project. This entry can be seen in the following URL (http://www.ludwirg.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160 600-201-a04&t3=2000-06-16&t4=1) Seq primer: puc 18 forward High quality sequence start: 24 High quality sequence stop: 437.
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//dev stage="Organ: head_neck; Vector: puc18; Site_1: Smal;
//oce="Organ: head_neck; Vector: puc18; Site_1: Smal;
//oce 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 438)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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88 IGATTCGTTGCGCTAFGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: head neck, Vector: puc18, Site 1: Smal, Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Parent application No. 196,716 - Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                              Ubases 1 to 441)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

Pris sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry on be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-HT0969-

181100-509-b06&t3=2000-11-18&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 8

High quality sequence stop: 441.

Location/Qualifiers
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0
                                                                                                                                                                                                  BF836743 1100-509-b06 HT0969 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 205
88 IGATICGIIGCGCIAIGIIAAACCCACCIAACCGIIGIIIIGAAGGACACIGAIIGICCAG 147
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                                                               209 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGGATGGCCTGTTTCGTTCCCCAGTGAGAG 151
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                                          148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 3e-29;
0; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0969"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
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ORIGIN
                                                                                                                                                                                                                       DEFINITION
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VERSION
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 598 Std Error: 0.00
                                                                                                                                                                                                         tq66g09.xl NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2213824 3' similar to gb:S58717_rnal BLAFIN PRECURSOR (HUMAN);contains element THR repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //dev stage="adult"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pT713b-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not orgoidT) primer. Double-stranded cDNA was ligated to coligo(dT) primer. Double-stranded cDNA was ligated to cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 448)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="NCI_CGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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266 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGGATGGCCTGTTTCGTTCCCCCAGTGAGAG 324
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llarity 81.0%; Pred. No. 3e-29;
Conservative 0; Mismatches 34; Indels 0
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/db_xref="taxon:9606"
/clone="IMAGE:2213824"
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AI582329.1 GI:4568226
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Unpublished (1997)
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                                             KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: M. Bento Soares, Ph.D.
CNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCL-CGAP clone distribution information can be
Wow-bio.lln.gov/bbrp/inage/image.html
Insert Length: 554 Std Brror: 0.00
Seq primer: -40UP from Gibco.
                                                                                       EST 14-APR-1999
                                                                                                         tk11c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2150704 3' similar to gb:558717_rnal ELAFIN PRECURSOR (HUMAN); contains element
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
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Pred. No. 3e-29;
0; Mismatches 34; Indels 0;
                                                                                         linear
                                                                                                                                    THR repetitive element ;, mRNA sequence. AI459240
                                                                                         mRNA
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2150704"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                  453 bp
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81.0%;
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Unpublished (1997)
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VERSION
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                                           RESULT 43
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BF824934 101100-500-b06 HN0039 Homo sapiens CDNA, mRNA sequence.

BF824934

LOCUS' DEFINITION

BF824934

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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: head normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HN0039-I01100-500-b06&t2=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 465.
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                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                            \operatorname{Simpson}, A.J. Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCATTATCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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137 c 117 g 113 t
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/db_xref="taxon:9606"
/clone_lib="HN0039"
/dev_stage="Adult"
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BF824934.1 GI:12167001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +55-11-2707001
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BF824932
BF824932.1 GI:12166998
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81.0%;
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                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
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/dev_stage="Adult"
/dev_stage="Adult"
/note="Vorgan: head normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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                                                              1 (bases 1 to 467)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +55-11-2707001
famil: satingson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=IL0&t2=IL0-HN0039-
131100-501-d07&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
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                                                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                    sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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137 g 99 t
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/db_xref="taxon:9606"
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ORGANISM
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BF837734/c
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/db xref="taxon:9606"
/clone_lib="HT1016"
/clone_lib="HT1016"
/note="Organ: head_neck; Vector: puc18; Site_l: Smal;
/note="Organ: head_neck; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016 Seq primer: puc 18 forward
High quality sequence stop: 468
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        Briones, M.R.,
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Erunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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LLO-HN0039-101100-500-a12 HN0039 Homo sapiens cDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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Pred. No. 3.1e-29;
0; Mismatches 34
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Query Match
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                                                                                                                                                                                                                                                     Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
This sequence was derived from the Fallowing URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HN0039-
101100-500-al2&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev stage="Adult"
/note="Organ: head_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector: Reverse transcription of
tissue mRNA and cDNA amplification were performed under
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Nditonal Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                         Shotgun sequencing of the human transcriptome with ORF expressed
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M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Pred. No. 3.1e-29;
0; Mismatches 34; Indels 0;
                                                                                  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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139 c 121 q 114 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="HN0039"
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                                                                                                                                Contact: Simpson A.J.G.
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Best Local Similarity 81.0%;
Matches 145; Conservative (
                                                                                                                                                                                                                                            Tel: +55-11-2704922
                                                           sequence tags
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                      Simpson, A.J.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/dbc="Taxon:9606"
/clone="Insel" 1899400"
/clone lib="NOI CGAP Larl"
/tissue_type="larynx"
/tab host="SOLM (kanamycin resistant)"
/note="Organ: larynx; Vector: Bluescript SK-; Site_1:
EcoHI, Stre_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Larynx. 5' adaptor sequence: 5' GAATTCGGCACGAG
3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'
Average insert size: 0.9 kb."
                          Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Preparation: Stratagene, Inc.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 647 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 430.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%; Score 124.6; DB 9; Length 480; 81.0%; Pred. No. 3.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 145; Conservative
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human.
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 51
BQ941085
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KEYWORDS
                                  FEATURES
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                                                                                                                                                                                                                         /note="Organ: colon, Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco R1; Plasmid DNA from the normalized library OTL CGAP Colo was prepared, and ss circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clone1Ds 1057416-1061255, and 1144584-1144351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Paroject. This entry can be seen in the following URL (http://www.ludwigg.org.br/scripts/gethtm12.pl?tl=QV3&t2=QV3-HT1016-221100-480-908&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 498)

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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.5%; Score 124.6; DB 12; Length 490; 81.0%; Pred. No. 3.1e-29; Live 0; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                              db_xref="taxon:9606"
|clone="IMAGE:3314575"
|clone=lib="NCI_CGAP_Co16"
|fissue=type="colon_tumor, RER+"
|lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 t
                                                                              /organism="Homo sapiens"
High quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF837735.1 GI:12189957
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 c
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ORIGIN
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BF837735
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MEDLINE
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KEYWORDS
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/db_xref="taxon:9606"
/clone_lib="HT1016"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_l: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH MGC_18"
/tissue_type="large_cell carcinoma"
/tissue_type="large_cell carcinoma"
/tisb host="DH10B (phage-resistant)
/note="Organ: lung (phage-resistant)
ECRI; cDNA made by oligo-dT priming. Directionally cloned into EcORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 21-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522 bp mRNA linear EST 21-AUG-200;
Solveourr_8794612 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6374832
BQ941085
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2554 row: h column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCATTATCT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 IGATICGITGCGCIAIGITAAACCCACCIAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 3.1e-29;
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146 c 128 q 120 t
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Tissue Procurement: DCTD/DTP/Gazdar
                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6374832"
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Location/Qualifiers
High quality sequence stop: 498
                               Location/Qualifiers
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81.0%;
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                                                  .498
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/organism="Homo sapiens"

/db xref="taxon:9606"
/clone="InAGE:4637906"
/clone="InAGE:4637906"
/clone="InAGE:4637906"
/clone="InAGE:4637906"
/clone="InAGE:40906"
/clone="InAGE:40906"
/clone="Organ: lung: Vector: poCFE7; Site 1: XhoI; Site 2: Anote="Organ: lung: Vector: poCFE7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
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0
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Londact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 564.
laboratory of Gerald M. Rubin (University of California,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library. NIH MGC Library. 125 c 121 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DC45U4/2 11near EST 27-MAR-
602519610F1 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:4637906 5'
MRNA sequence.
                                                                                                                                                                                                                                                                                                                                             88 IGATICGIIGCGCIAIGIIAAACCCACCIAACCGIIGIIIIGAAGGACACIGAIIGICCAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                             28 ATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAG 332
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                                                                                                                                                                                              60.5%; Score 124.6; DB 14; Length 522;
                                                                                                                                                                                                                                                     34; Indels
                                                                                                                                                                                                                           Pred. No. 3.2e-29;
                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                     Matches 145; Conservative
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                                                                                                               BASE COUNT
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AUTHORS
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Gaps

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34; Indels

0; Mismatches

Matches 145; Conservative

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbry/mage/image.html
Insert Length: 609 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                     418 bp mRNA linear EST 30-MAR-1999 tg23g03.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109652 3' similar to gb:S58717 rna1 ELAFIN PRECURSOR (HUMAN);contains element HGR repetitive element ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 GCGCAAGAGCCAGTCAAAGGTCCAGTCTCACTAAGCCTGGCTCCTGCCCCATTATCTTG 290
                                                                                         TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                          186 Aagcgcaagagccagrcaaaggrccagrcrccacraagccrggcrccrgcccarrarcr 245
                                                                                                                                        87
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                                                                                                                                                                                        148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                                                                                                                                                                                        306 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGA 364
28 ATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCCAGGTTCTTGTCCTATTATCT
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/clone=!IMAGE:2109662"
/clone=lib="NCI CGAP CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 418;
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81.4%; Pred. No. 4e-29;
tive 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Unpublished (1997)
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ORIGIN
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llhi.gov/bbrp/fmage/fmage.html
Insert Length: 551 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                      444 bp mRNA linear EST 21-DEC-1999 similar to gb:S58717_rnal ELAFIN PRECURSOR (HUMAN);contains element THR repetitive element; mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .444
/orgatism="Homo sapiens"
/orgatism="Eaxon:9606"
/clone="IMAGE:2408140"
/clone lib="NCI_CGAP_L019"
/rissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCANTAAGCCTGGCTCCTGCCCCATTATCT 303
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90 ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT 149
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                                                                                                           150 ATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
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/lab_host="DH10B (phage-resistant)"
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Unpublished (1997)
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AI858070/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                         AI807596 527 bp mRNA linear EST 18-DEC-1999 we43c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2343860 3' similar to gb:558717_rnal ELAFIN PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: lung, Vector: pT7T3D-Pac (Pharmacia) with modified polylinker; Plasmid DNA from the normalized library NCI CGAP LuS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rearccegrececcarerreaarcccccraaccecrrcraaagaracreacrecocae 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
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148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                 242 GPATCAAGAAGTGCTGTGAAAGGTCTTTGGGGATGGCCTGTTTCGTTCCCCAGTGAGAG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Indels
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/clone="IMAGE:2343860"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
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Mammalia; Eutheria;
1 (bases 1 to 527)
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AI807596/c
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High quality sequence start: 17
High quality sequence stop: 289.
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                                                                                                                                         BE181373.1 GI:8660549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
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                                                                                                                                                                                                                     Homo sapiens
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VERSION
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                             RESULT 57
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                                                                                                                                                                 KEYWORDS
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/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
/note="Organ: head_neck; Vector: Patent application No. 196; 716 - Ludwig Institute for Cancer Research)
/note="Didwig Institute for Cancer Research"
/note="Organ: head_neck; Vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                            BE711100 263 bp mRNA linear EST 12-SEP-2000 RC3-HT0649-270700-012-£03 HT0649 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                  1 (bases 1 to 263)
Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, F.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +55-11-2707001
mail: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0649-270
700-012-f03&t.b=2000-07-27&t4=1)
Seq primer: puc 18 forward
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                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 TCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAG 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCAGGT 71
                                                                                                                                                                                                                                 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                     Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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71 c 74 g 56 t
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High quality sequence stop: 263.
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/clone_lib="HT0649"
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BE711100.1 GI:10099365
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ORIGIN
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                                                                                        ACCESSION
VERSION
RESULT 56
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                                                                                                                                      KEYWORDS
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/organism="Homo sapiens"
/db xref="texon:9606"
/clone lib="Hof03"
/dev_stage="Adult"
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/note="Corgan: head; Vector: pucl8; Site 1: SmaI;
/note="Corgan: head; Network necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking necking
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This enty can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CMO-HT0633-240 300-304-g12&t3=2000-03-24&t4=1)
       22-JUN-2000
EST 22-JUN-2000
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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beleli373
CMO-HID633-240300-304-gl2 HT0633 Homo sapiens CDNA,
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| Corganism="Homo sapiens" |
| Ab xref="=taxon:966" |
| Clone lib="HT0641" |
| dev stage="Adult" |
| Incte="lorgan: head neck; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products Site_2: Smal; A mini-library was made by cloning products Gerived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) |
| Drofiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1-HT0641-280 Seq primer: puc 18 forward.
  EST 22-JUN-2000
                                                                                                                                                                                                                                                Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, C.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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CM4-HT0744-160600-201-f01 HT0744 Homo sapiens cDNA, mRNA sequence.
BE715619
BE181959 312 bp mRNA linear EST 22-JUN-200
CM1-HT0641-280400-206-d02 HT0641 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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High quality sequence stop: 312.
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                                                                          BE181959.1 GI:8661135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                           (bases 1 to 312)
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DEFINITION ACCESSION

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/organism="Homo sapiens"

/db xref="taxon:9606"
/clone lib="HT0744"
/dev stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
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/note="Organ: head_neck; Vector: Puc18; Site_1: SmaI;
/note="Organ: head_neck; Vector: Parent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
Enail: asimpsonoludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-HT0744-160
600-201-f01&t3=2000-06-16&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 342.
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                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 342)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C. V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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80.4%; Pred. No. 9e-29;
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Laboratory of Cancer Genetics
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09-833799-13a.rst

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organism="Homo sapiens"
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/clone lib="HT1016"
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Dias Neto, E., Garcio
(bases 1 to 374)
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//dev stage="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li bases 1 to 345,
Dias Neto,E., Garcia Correa,R., Verjovski. Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Rrunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM4-UT0043-090
g00-309-Dl0&t3=2000-09-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
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BF836201
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
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/clone_lib="UT0043"
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                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-270700
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/dev stage="Adult"
/note="Organ: head neck, Vector: puc18, Site_1: Smal;
/note="Organ: head neck, Vector: puc18, Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016-
171100-474-c05&t3=2000-11-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 11
High quality sequence start: 11
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 Aagcgcaagagccagrcaaaggrccagrcrcacraaaggccragcrcgccccarrarcr 226
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                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 9.3e-29;
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/db_xref="taxon:9606"

/dclone lib="MT0316"

/dev_srage="Adult"

/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORSSTES POR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mink and cDNA amplification were performed under low
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Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
mail: asimpsonoludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
This entry can be seen in the following URL
This introper of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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106 c 108 g E
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AI924155.1 GI:5660119
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstein,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., M.J., Soares,F., Brentani,R., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and coloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                           CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.igov/bbrp/image.imm/
Insert Length: 511 Std Brror: 0.00
Seq primer: -40UP from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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/clone="IMAGB:245022"
/clone_lib="NCI_GGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
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Contact: Robert Strausberg, Ph.D.
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Unpublished (1997)

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pooled lung tunnor tissue, and was then primed with a lot I oligo (dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and Coloned into the Not I and Eco RI sites of the modified pTTT vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo. "
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     Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from
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QV3-HT1016-151100-463-c10 HT1016 Homo sapiens cDNA, mRNA sequence.
BF835679
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:2408998"
/clone lib="NGCECGAP_Lu19"
/tissue_type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
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                            found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 531 Std Error: 0.00
Seg primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0116-0201-464-F04&t2=2001-02-02&t4=1)
Seg primer: puc 18 forward
High quality sequence scop: 353.
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                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 242
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/clone_lib="UT0116"
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Matches 144; Conservative
                                                                                                                                                              Tel: +55-11-2704922
                                                                                                                                                                                           Fax: +55-11-2707001
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AUTHORS
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Pred. No. 9.9e-29;
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Laboratory of Cancer Genetics
                                                                                                                                    Location/Qualifiers
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80.4%;
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                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="HT0106"
/dev stage="halut"
/dev stage="halut"
/note="Organ: head_neck; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
derived from (PSESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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1 (bases 1 to 453)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, C.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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                Email: asimpson@ludwig.org.bx
This sequence was derived from the FAPESP/LICR Human Cancer Genome rooject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV3&t2=QV3-HT1016-151100-463-c10&t3=2000-11-15&t4=1)
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LLO-CT0008-140599-007 CT0008 Homo sapiens cDNA, mRNA sequence
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Pred. No. 9.9e-29;
0; Mismatches 35;
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Ludwig Institute for Cancer Research
                                                                                                                                                          High quality sequence start: 8
High quality sequence stop: 447.
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Email: asimpson@ludwig.org.br
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                                                                                                                                         Seq primer: puc 18 forward
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AW845140.1 GI:7940657
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80.4%;
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Fax: +55-11-2707001
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Tel: +55-11-2704922
Fax: +55-11-2707001
Exat: +55-11-2707001
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=ILO-CT0008-140 599-001&t3=1999-05-14&t4=1)
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"

db_xref="axon:9606"

/db_ne_lib="cr10008"

/dov_stage="Adult"

/dov_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196

/76 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=ILO-CT0008-140 599-007&t2=1599-05-14&t4=1) Seq primer: puc 18 forwards Seq primer: puc 18 forwards 139 High quality sequence start: 39 High quality sequence stop: 454.
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                             /organism="Homo sapiens"

db_xref="taxon:9606"
/dlone_lib="cr0008"
/dov stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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ILO-HN0039-101100-500-a05 HN0039 Homo sapiens CDNA, mRNA sequence.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome robject. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HN0039-101100-500-a05&t3=2000-11-10&t4=1)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 9.9e-29;
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                     High quality sequence stop: 455.
Location/Qualifiers
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Location/Qualifiers
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Seq primer: puc 18 forward
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Indee "Organ: head normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Seq primer: puc 18 forward 466.
High quality sequence stop: 466.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 466)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/clone_lib="HN0039"
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/clone lib="HN0039"
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                     /dev stage="Adult"
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/dev stage="Adult"
/note="Organ: head_normal; Vector: puc18; Site_1: Smal;
/note="Organ: head_normal; Vector: puc18; Site_1: Smal;
/note="Organ: head_normal; Vector: puc18; Site_1: Smal;
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=LL0&t2=LL0-HN0039-
101100-500-005&t3=2000-11-10&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 467.
/note="Organ: head_normal; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 (bases 1 to 467)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/db_xref="taxon:9606"
/clone_lib="HN0039"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.4%;
Matches 144; Conservative
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Fax: +55-11-2707001
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/dev_stage="Addit"
/note="Organ: head_normal; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
pofiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions."
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1 (Bases I to 487).

1 (Bases I to 487).

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carralho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., M.J., Soares,F., Goliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." 137~c~117~g~114~t
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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High quality sequence stop: 487.
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               77.88;
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Unpublished (1997)
                      Best Local Similarity 77.83
Matches 147; Conservative
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//dev stage="Adult"
//dev stage="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A min.-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
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1 (Bases 1 to 344)

Diass 1 to 344)

Nagai, M.A., da accia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV0-CT0383-030 300-139-d12&t3=2000-03-03&t4=1)
Seq primer: puc 18 forward
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                      88 IGATICGIIGCGCIAIGIIAAACCCACCIAACCGIIGIIIIGAAGGACACIGAIIGICCAG 147
                                                                                                                                                                                                                                                                      Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                 DB 12; Length 487;
                                                                                                          35; Indels
                                                               Score 123; DB 17
Pred. No. 1e-28;
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="CT0383"
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High quality sequence stop: 344.
Location/Qualifiers
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                                                             59.7%;
80.4%;
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  O
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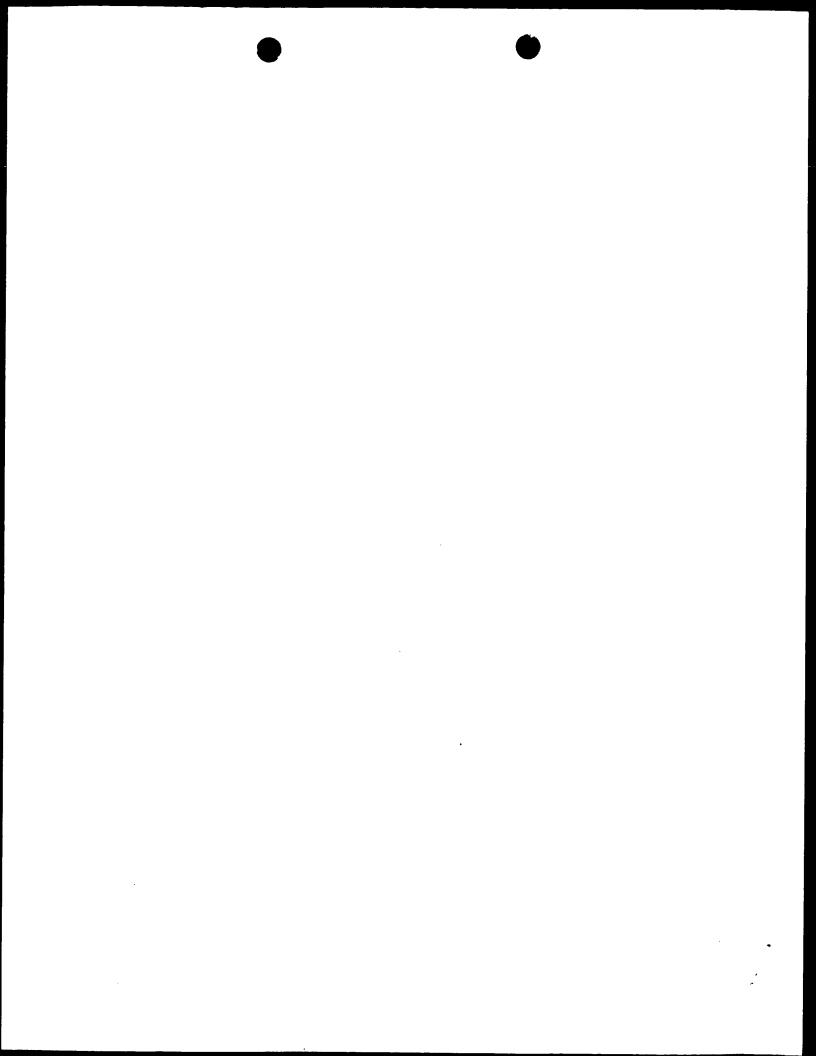
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Email: cgapbs-r@mail.nih.gov
Tissue Produrement: L. Jeffrey Medeiros, M.D., Michael R.
Tissue Produrement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M. A.G.E. Consortium/LLNL at:
Mww-bio.llni.gov/bbrp/image/image.html
Insert Length: 642 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                               193 GACTGCCCAGGAATCAAGAAGAGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCC 252
                                                                                                                                                                                                                                                                                                                                                          138 GATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCA 197
                                                                                                                                                                                                                                         78 CCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACT 137
                                                                                                                                                                                                                                                                                                   133 CCCATTATCTTGATCCGGTGCGCCATGTTGAATCCCCCTAACCGCTGCTTGAAAGATACT 192
                                                                                                                                                                              73 ATAAAGTCTAAAGCGCAAGAGCCAGTCTAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGC 132
                                                                Gaps
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59.1%; Score 121.8; DB 10; Length 344; 77.8%; Pred. No. 2.2e-28; ive 0; Mismatches 42; Indels 0;
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 241.
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/organism="Homo sapiens"
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09-833799-13a.rst

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/note="Organ: bladder_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsu,Muna,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOlivaira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-KT0004-
241100-001-004&t3=2000-11-24&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 419.
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PM1-KT0004-241100-001-c04 KT0004 Homo sapiens cDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATICGTIGCGCTATGTIAAACCCACCTAACCGTIGTITGAAGGACACTGATTGTCCAG 147
386 AAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCCCCATTATCTTGATCC 327
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                                                                                GTTGCGCTATGTTAAACCCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCA 153
                                                                                                                                    326 gerececarerrearceceraaceerreareaanearacrearacrearecendenes
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                                                                                                                                                                                                                           266 AGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGG 214
                                                                                                                                                                                              154 AAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="KT0004"
/dev_stage="Adult"
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148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                                                                 167 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAG 109
                                                                                                                                                                                  Search completed: February 15, 2003, 23:10:13 Job time : 1193 secs
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Sequence 1393, Ap Sequence 1393, Ap Sequence 1126, Ap Sequence 1798, Ap Sequence 2134, Ap Sequence 3, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 155, Appli Sequence 2155, Appli Sequence 2155, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Sequence 255, Appli Se
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(without alignments)
1565.980 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                             206
1 AATTCGAGCTCGGTACCATA......GTTTCGTTCCACAATAATAG 206
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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US-09-815-242-8956

US-09-925-637-9

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Maximum Match 100%
Listing first 100 summaries
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0 00 000	Sequence 279, App. Sequence 279, App. Sequence 612, App. Sequence 7107, Ap. Sequence 72, App. Sequence 355, App. Sequence 1, Appl.	Sequence seq	Sequence Seq	Sequence 7281, Ap Sequence 2180, Ap Sequence 2180, Ap Sequence 55, Appl Sequence 574, Appl Sequence 6, Appli Sequence 175, App Sequence 175, App
US-09-852-659A-1 US-09-852-797-34 US-09-853-161-34 US-09-852-659A-3 US-09-852-797-50 US-09-852-659A-50 US-09-815-265-65 US-09-815-24-66 US-09-815-24-66 US-09-815-24-66 US-10-277-884-59 US-10-114-893-118	US-09-775-93846-31 US-09-962-436-279 US-09-070-927A-611 US-09-915-242-710 US-09-070-927A-72 US-09-070-927A-72 US-09-764-869-355 US-10-105-936-1	US-09-338-842A-487 US-09-822-849A-29- US-09-35-64-11 US-09-790-988-1 US-09-790-988-1 US-09-78-842A-403- US-09-78-842A-403- US-09-78-86-05-410- US-09-86-05-410- US-09-86-05-410- US-09-800-729-67- US-09-938-540-1 US-09-938-540-1 US-09-938-540-1 US-09-938-540-1 US-09-938-540-1 US-09-938-540-1 US-09-938-540-1 US-09-925-300-693-1 US-09-822-866-104-09-333-1 US-09-822-866-104-09-333-1 US-09-802-20-35-30-1 US-09-802-20-80-129-68-10-10-10-10-10-10-10-10-10-10-10-10-10-		US-09-786-692-73 US-09-786-692-73 US-09-927-939-55 US-09-974-298-14 US-10-044-090-5 US-10-044-090-5 US-10-174-590-17 US-10-174-590-17 US-10-175-737-17 US-10-175-737-17 US-10-175-737-17 US-10-175-737-17 US-10-175-737-17 US-10-175-737-17 US-10-175-75-17 US-10-176-482-17 US-10-176-913-17 US-10-176-913-17 US-10-176-913-17 US-10-176-913-17 US-10-176-913-17 US-10-176-913-17 US-10-176-913-17 US-10-176-913-17 US-10-176-913-17 US-10-180-552-17 US-10-180-552-17 US-10-178-913-17
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                        Sequence
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Su, Jiangohun
APPLICANT: Su, Jiangohun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REPERENCE: 210121.54761.
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER: OF SEQ ID NOS: 1896
SOFTWARE: FRACESQ for Windows Version 4.0
SEQ ID NO 1393
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
US-10-174-579-175
US-10-174-582-175
US-10-174-588-175
US-10-175-739-175
US-10-175-740-175
US-10-175-743-175
US-10-176-488-175
US-10-176-488-175
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                                                                                                                                                                                                                                                                                          Sequence 1393, Application US/09920300A Patent No. US20020136728A1 GENERAL INFORMATION:
APPLICANT: King, Gordon E. APPLICANT: Meagher, Madeleine Joy
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LOCATION: 27, 56, 343
COTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapiens
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US-10-033-528-1393/c
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION:
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; Patent No. US20020115057A1
                                                                                                                                                      NAME/KEY: misc_feature

// COCATION: 27, 56, 343

US-10-033-528-1393
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OTHER INFORMATION: n=a,t,g or c
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ORGANISM: Homo sapiens
                                      TYPE: DNA
ORGANISM: Homo sapiens
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US-09-954-456-1126
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LENGTH: 480
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28 ATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCT 87

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312 ATTTGGCTTAGACCCTGCACCTGCAGAACCTACAAAACCAGTAACGCCTGGTGTATTTCT 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 TITITITAACGGIIGITITIAGCITIACCAICITIAACITIGAGITICITICITICICGGIAT 133
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                                                                                                                        APPLICANT: Oblean, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Traniel, Daniel
APPLICANT: Traniel, John D.
APPLICANT: Tammoto, Robert T.
APPLICANT: Yammoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILLE REPERENCE: ELITRA.011A
CURRENT APPLICANTON NUMBER: US/09/815,242
CURRENT FILLNG DATE: 2001-03-21
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yeshort T.
APPLICANT: Xu, H. Noobert T.
APPLICANT: Yu, H. Applicantion of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98;
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Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLICATION NUMBER: 60/253,625
PRIOR PLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRAELSEQ FOR WINDOWS Version 4.0
   Sequence 4199, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 8354, Application US/09815242; Patent No. US20020061569A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus aureus
US-09-815-242-4199
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Best Local Similarity 48.1%;
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Zyskind, Judith W.
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US-09-815-242-8354/c
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APPLICANT: Young, Paul

TITLE OF INVENTION: Sees
FILE REFERENCE: 689290-76

CURRENT APPLICATION WHERE: US/09/954,456

CURRENT APPLICATION NUMBER: US/60/233,617

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR FILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-26

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PRIOR PRIOR PLING DATE: 2000-09-27

PRIOR PRIOR PRIOR PLING DATE: 2000-09-27

PRIOR PRIOR PRIOR PLING NUMBER: US/60/235,840
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1552 AAGCGCAAGAGCCAGTCAAAAGTCCAGTTAAGCCTGGCTCGCCCATTATCT 1611
                                                                                                                                                   1552 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 1611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1672 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCGGTGA 1727
                                                                                                                                                                                                                                                                                      1672 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGA 1727
                                                                                                                                                                                                                             148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1798, Application US/09954456 Patent No. US20020115057A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc feature
; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-1798
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 2309
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Length 546;

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, LOCATION: 460..1290
US-09-731-872-213
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US-09-800-528-14/c
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LENGTH: 36159
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US-10-135-687-3/C
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Sequence 213, Application US/09731872

Sequence 213, Application US/09731872

SEQUENCE CONTROL SEQUENCE SEQUENCE

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REPERENCE: 78.U35.REG

CURRENT APPLICATION NUMBER: US 60/169,629

FRIOR APPLICATION NUMBER: US 60/169,629

FRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR FILING DATE: 2000-03-06

MUMBER OF SEQ ID NOS: 482

SOGTWARE: Patent.pm

SEQ ID NO 213

LENGTH: 1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 TAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 Aitrigectiagacectecaecticagaaectacaaaaecaaaaecgiaaaeccigorgiatrict 253
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Pred. No. 0.12;
0; Mismatches 98; Indels 0.
                    TITLE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOSFWARE: PEALSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Staphylococcus aureus
       OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.6%;
48.1%;
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Matches 91; Conservative
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ORGANISM; Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i LOCATION: (1)...(549)
US-09-815-242-8354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GGCTTGTTT 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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Sequence 3, Application US/10135687

Sequence 3, Application US/10135687

Sequence 3, Application US/10135687

Sequence 3, Application US/20020123120A1

GENERAL INFORMATION:
THEREAL INFORMATION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: UMBER: US/10/135,687

CURRENT APPLICATION NUMBER: US/10/135,687

CURRENT FILING DATE: 2002-05-01

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 4

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FREESE FREESE FOR Windows Version 4.0
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Ouery Match
Best Local Similarity 50.3%; Pred. No. 0.98;
Matches 74; Conservative 0; Mismatches 73; Indels 0;
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APPLICANT: Taylor, Mark Andrew
APPLICANT: Brennan, Rex Michael
TITLE OF INVENTION: BLACKCURRANT PROMOTERS AND GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 AACTGGATTTCTAGATAGAAGCTGGAT 291
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US-10-135-687-3
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Best Local Similarity 49.1%
Matches 80, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.3%; Score 29.4; DB 10; Length 5150; 55.3%; Pred. No. 3.4; tive 0; Mismatches 46; Indels 0;
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APPLICANT: Johlsen, Karl L.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Cart, Grant J.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITAN. 011A

CURRENT APPLICATION NUMBER: 00/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR PELLING DATE: 2000-11-22

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PRIOR PELLING DATE: 2000-11-22
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FILE REFERENCE: C70237D1
CURRENT APPLICATION NUMBER: US/09/800,528
CURRENT FILING DATE: 2001-03-07
FRIOR APPLICATION NUMBER: 09/68,140
PRIOR APPLICATION NUMBER: PCT/EP/9604807
PRIOR APPLICATION NUMBER: PCT/EP/9604807
PRIOR APPLICATION NUMBER: B95-11-04
PRIOR FILING DATE: 1996-11-04
PRIOR FILING DATE: 1995-11-03
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14
LENGTHES: 5150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8688, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Best Local Similarity 55.33
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Ribes nigrum
US-09-800-528-14
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; LOCATION: (1)...
US-09-815-242-8688
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                                                                                                                                                62 TAAGCCAGGTTCTTGTCTTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCG 121
                                                           0; Gaps
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                                                                                                           2 ATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTAC 61
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14.1%; Score 29; DB 10; Length 549; 51.1%; Pred. No. 1.6; tive 0; Mismatches 65; Indels
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION:
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: 02/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRASKEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8956, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Staphylococcus aureus
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith 1
                                                        68; Conservative
                                                                                                                                                                                                                                                                                                                            122 TTGTTTGAAGGAC 134
                                                                                                                                                                                                                                                                                                                                                                                  192 TTTTTAACAGTC 180
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; LOCATION: (1)...(549)
US-09-815-242-8956
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Best Local Similarity
                         Best Local Similarity
Matches 68; Conserv
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US-09-815-242-8956/c
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  Query Match
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OTHER INFORMATION: MAP TO AC008014.5
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                                                                                                                                                                                                                                                                                                                     RESULT 14
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                                                                                                                                                                                             TITLE OF INVESTIGES.

FILE REPERENCE: PB60
CURRENT APPLICATION: Staphylococcus aureus Polymucleotides and Polypeptides
FILE REPERENCE: PB60
CURRENT APPLICATION NUMBER: US/09/925,637
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-31
PRIOR PILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1997-01-03
PRIOR PILING DATE: 1997-01-03
PRIOR FILING DATE: 1997-01-06
NUMBER: US 60/009,861
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
COFFURED PATER: 1996-01-06
NUMBER OF SEQ ID NOS: 74
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; Sequence 6, Application US/09835232
; Sequence 6, Application US/09835232
; Patent No. US2002008489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
APPLICANT: Leder, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: PORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-13
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENTH: 180216
; LENTH: 180216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 14.1%; Score 29; DB 10; Length 549; l Similarity 51.1%; Pred. No. 1.6; 68; Conservative 0; Mismatches 65; Indels
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LOCATION: (1)...(180216)
OTHER INFORMATION: n = A,T,C or G
                                                                                                             Sequence 9, Application US/09925637, Patent No. US20020103338A1, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Homo sapiens
US-09-925-637-9
192 TTTTTTAACAGTC 180
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Best Local Similarity
                                                                                RESULT 12
US-09-925-637-9/c
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APPLICANT: Chen, wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                0
                                                                                                                                                                                                                                                           Db 169405 İCİTTİCAĞTGATĞAATİTTCTTAAİİTTİCİİTTCAİCTİAĞAATİTİTİTİTİTÇTCAĞÇİ 169464
                                                                                                                                                                                 57 renaraspecasenterrerratrarerreariestrasecraterrasacceaeer 116
                                                                                                                       0; Gaps
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                                      117 AACCGTTGTTTGAAGGACACTGATTGTCCAAGAAAAAAGTGCTGTGAAGGTT 171
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                                                                         Query Match
Best Local Similarity 53.0%
Matches 61; Conservative
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LENGTH: 464
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US-09-835-232-6
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"...ong, Gordon G.

APPLICANT: Clark, Hilary
APPLICANT: Rechtel, Kim
APPLICANT: Genetics Institute, Inc.
ITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
PRIOR PLILNG DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 19
LENGTH: 1656
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                       Ouery Match 13.8%; Score 28.4; DB 10; Length 464; Best Local Similarity 54.9%; Pred. No. 2.4; Matches 56; Conservative 0; Mismatches 46; Indels 0
HER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
HER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
HER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
HER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
HER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
HER INFORMATION: EXPRESSED IN BA174, SIGNAL = 1.6
HER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
HER INFORMATION: EXPRESSED IN HELION, SIGNAL = 1.8
HER INFORMATION: EXPRESSED IN HELION, SIGNAL = 1.5
HER INFORMATION: EXPRESSED IN HELION, SIGNAL = 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
APPLICANT: Evans, Cheryl
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Best Local Similarity
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Sequence 3, Application US/09816095
Fatent No. US2020137164A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THREEOF
FILE REFERENCE: CLO01147
CURRENT APPLICATION NUMBER: US/09/816,095
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 3
FALLS APPLICATION OF SEQ ID NOS: 5
SEQ ID NO. 3
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                                                                               APPLICANT: Cao, Li
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 1458 0.04/200130.449
CURRENT APPLICATION NUMBER: US/09/765,205
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/09/212,440
PRIOR FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FASESEQ for Windows Version 3.0
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Sequence 25, Application US/09765205
Patent No. US20020034800A1
GENERAL INFORMATION:
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; LOCATION: (1)...(99916)
; CTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: human
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US-09-816-095-3
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RESULT 18

US-09-765-205-25/c

RESULT 16

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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
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Patent No. US20020032918A1
GENERAL INFORMATION:
APPLICANT: Lorbiecker, Rene
TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
TITLE OF INVENTION: CONDITIONS
FILE REPERENCE: 2283/201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.5%; Pred. No. 6.8;
Matches 52; Conservative 0; Mismatches 40; Indels
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OTHER INFORMATION: Incyte ID No. US20020137081A1 1989707CB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 CCTGCGGTATGGCTTGTTTCGTTCCACAATAA 203
                        ; Sequence 335, Application US/10044090
; Patent No. US20020137081A1
; GENERAL INFORMATION:
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Matches 76; Conservative
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; LOCATION: (139)..(735)
US-09-785-738A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Rice
US-10-044-090-335/c
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LENGTH: 2125
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123 IGITIGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
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                                                                                    APPLICANT: AND CONTRACTOR. 28 Human Secreted Proteins TITLE OF INVENTION: 28 Human Secreted Proteins FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
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Sequence 34, Application US/09852797;
Patent No. US20020172994A1
GENERAL INFORMATION:
TITLE OF INVENTION: 28 Human Secreted Proteins;
FILE REFERENCE: PZ003F2
CURRENT APPLICATION NUMBER: US/09/852,797;
CURRENT FILING DATE: 2001-05-11
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PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR PLILING DATE: 1998-09-11
PRIOR PLILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-03-12
             , Sequence 121, Application US/09852659A
, Patent No. US20020077287A1
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Best Local Similarity 57.8%
Matches 48; Conservative
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                                                                      GENERAL INFORMATION:
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US-09-852-659A-121
US-09-852-659A-121
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13.1%;
57.8%;
         NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
LENGTH: 753
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 48; Conserva
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US-09-852-659A-34
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Patent No. US20020076756A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ603P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
PRIOR PILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR PILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1999-03-14
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PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/640,762
PRIOR FILING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR PELING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
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NUMBER: 05/0503
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R FILING DATE: 1997-09-05
R APPLICATION NUMBER: 60/048,970
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/068,368
R FILING DATE: 1997-12-19
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, ORGANISM: Homo sapiens
US-09-852-797-34
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Best Local Similarity
Matches 48; Conserva
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US-09-853-161-34
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Length 753;
Score 27; DB 10; Length 75:
Pred. No. 9.3;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRNERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILTE OF INVENTION: 28 Human Secreted Proteins
FILTE OF INVENTION: 28 Human Secreted Proteins
FILE OF INVENTION NUMBER: US/09/852,659A
CURRENT APPLICATION NUMBER: 00/10-65-13
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR APPLICATION NUMBER: 00/40,762
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR APPLICATION NUMBER: 60/040,703
PRIOR APPLICATION NUMBER: 60/040,703
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR PILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR PLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR PLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR PLING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR APPLICATION NUMBER: 60/069,368
PRIOR PLING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/069,368
PRIOR PLING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/069,368
PRIOR PLING DATE: 1997-06-06
PRIOR PRIOR PLING DATE: 1997-06-06
PRIOR PLING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/069,368
PRIOR PLING DATE: 1997-06-06
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PRIOR PLING DATE: 1997-06-06
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FILING DATE: 1997-09-05
APPLICATION UNMBER: 60/048,970
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/068,368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-09-853-161-50
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                                                                                                                                                                                                                                        TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/852,797
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 00/265,583
PRIOR APPLICATION NUMBER: 00/152,060
PRIOR PILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 00/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR PELLING DATE: 1998-09-11
PRIOR PELLING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-14
PRIOR PELLING DATE: 1997-03-03-04
PRIOR FILING DATE: 1997-05-30
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Fatent No. US20020076756A1
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE OF INVENTION: 28 Human Secreted Proteins
TITLE REFERENCE: P2003P3
CURRENT APPLICATION NUMBER: US/09/853,161
CURRENT FILING DATE: 2001-05-11
FRIOR APPLICATION NUMBER: 60/265,583
FRIOR FILING DATE: 1908-09-11
FRIOR APPLICATION NUMBER: 09/152,060
FRIOR FILING DATE: 1998-09-11
FRIOR APPLICATION NUMBER: PCT/US98/04858
                                                                                                                                                    Sequence 50, Application US/09852797
Patent No. US20020172994A1
GENERAL INFORMATION:
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232 AAATGTTTAGATCTCAAACAAGA 254
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 50
LENGTH: 783
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ORGANISM: Homo sapiens
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US-09-853-161-50
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123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGGTATG 182
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US-09-862-659A-50

sequence 50, Application US/09852659A
sequence 50, Application US/09852659A
sequence 50, Application US/09852659A
sequence 50, Application US/09852659A
can be sequence 50, Application 50
respectively 100. US20020077287A1
TITLE CONTENT ROSEN et al.
TITLE REFRENCE: PS003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR PELING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-14
PRIOR FILING DATE: 1997-03-03-04
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR APPLICATION NUMBER: 60/040,70
PRIOR APPLICATION NUMBER: 60/040,357
PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-30
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PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR PILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
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                                                                                                                                                                                                                                                                                                                                                                                           172 TGTACAAAGGACAGACAATGCCAGGACAACAAGAAGTGTTGTGTTTCAGCTGCGGGAAA 231
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                                                                                                                                                                                                                                                                                                      Gaps
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Best Local Similarity 57.8%; Pred. No. 13;
Matches 48; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                         Query Match 13.1%; Score 27; DB 10; Length 783; Best Local Similarity 57.8%; Pred. No. 9.5; Matches 48; Conservative 0; Mismatches 35; Indels
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APPLICANT: Obleach, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Transcript, John D.
APPLICANT: Transcript, John D.
APPLICANT: Transcript, John D.
APPLICANT: Transcript, John D.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Xu, H. Howari
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Deckaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: DATE: 2000-03-21
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22-16
NUMBER OF SEQ ID NOS: 14110
SOFTHARES FALSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6640, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 GCTTGTTTCGTTCCACATAATA 205
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PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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US-09-815-242-6640/c
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LENGTH: 783
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FILING DATE: 1998-12-15
APPLICATION NUMBER: 60/113296
FILING DATE: 1998-12-22
APPLICATION NUMBER: 60/113605
FILING DATE: 1998-12-23 FILING DATE: 1998-11-17 APPLICATION NUMBER: 60/108801 FILING DATE: 1998-11-17 APPLICATION NUMBER: 60/108849 FILING DATE: 1998-11-18 FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/101477
FILING DATE: 1998-09-23
APPLICATION NUMBER: 60/101738 FILING DATE: 1998-09-24 APPLICATION UNDBER: 60/101741 FILING DATE: 1998-09-24 APPLICATION NUMBER: 60/101786 FILING DATE: 1998-10-28 APPLICATION NUMBER: 60/106248 FILING DATE: 1998-10-29 APPLICATION NUMBER: 60/106464 APPLICATION NUMBER: 60/112422 APPLICATION NUMBER: 60/101916 FILING DATE: 1998-09-24 APPLICATION NUMBER: 60/106178 APPLICATION NUMBER: 60/106905 FILING DATE: 1998-11-03 APPLICATION NUMBER: 60/108787 FILING DATE: 1998-09-15 APPLICATION NUMBER: 60/100390 FILING DATE: 1998-09-15 APPLICATION NUMBER: 60/100627 FILING DATE: 1998-09-16 APPLICATION NUMBER: 60/100848 FILING DATE: 1998-09-18 APPLICATION NUMBER: 60/100919 APPLICATION NUMBER: 60/101922 APPLICATION NUMBER: 60/095318 FILING DATE: 1998-08-04 APPLICATION NUMBER: 60/095916 FILING DATE: 1998-08-10 APPLICATION NUMBER: 60/099812 APPLICATION NUMBER: 60/099816 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/100385 APPLICATION NUMBER: 60/097986 FILING DATE: 1998-08-26 FILING DATE: 1998-08-31 APPLICATION NUMBER: 60/099596 APPLICATION NUMBER: 60/099598 FILING DATE: 1998-09-09 APPLICATION NUMBER: 60/099803 APPLICATION NUMBER: 60/099811 FILING DATE: 1998-09-10 APPLICATION NUMBER: 60/100038 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/095302 APPLICATION NUMBER: 60/098544 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/096146 APPLICATION NUMBER: 60/096791 FILING DATE: 1998-09-24 1998-10-30 FILING DATE: 1998-09-25 LING DATE: 1998-09-10 LING DATE: 1998-09-10 FILING DATE: 1998-08-04 ILING DATE: 1998-09-09 ILING DATE: 1998-09-11 FILING DATE: 1998-08-11 LING DATE: 1998-08-17 FILING DATE: PRIOR

2993 dadaididititacccchcragaracaratritgccacrggriagitciccarcraacrca 3052 2933 AATAATTICAAGTIGAAGIGITITTTAAAAACACTTIGITTIGTAAIGTITTIGAAITCTCTI 2992 97 GCGCTATGTTAAACCCAACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAA 156 37 AACCAGITAAAAGGICCIGIGICTACIAAGCCAGGITCTIGICCIAITAICITGAITCGIT 96 · 0 DB 9; Length 3976; 62; Indels 13.0%; Score 26.8; D 50.8%; Pred. No. 24; Live 0; Mismatches APPLICATION NUMBER: 60/169495 FILING DATE: 1999-12-07 APPLICATION NUMBER: 60/169835 FILING DATE: 1999-08-17 APPLICATION NUMBER: 60/149638 APPLICATION NUMBER: 60/151733 APPLICATION NUMBER: 60/164418 APPLICATION NUMBER: 60/169445 FILING DATE: 1999-04-28 APPLICATION NUMBER: 60/134287 FILING DATE: 1999-05-14 FILING DATE: 1999-07-20 APPLICATION NUMBER: 60/145698 FILING DATE: 1999-07-26 APPLICATION NUMBER: 60/146222 APPLICATION NUMBER: 60/146963 APPLICATION NUMBER: 60/149320 APPLICATION NUMBER: 60/166361 APPLICATION NUMBER: 60/115565 FILING DATE: 1999-01-12 APPLICATION NUMBER: 60/115733 APPLICATION NUMBER: 60/126773 FILING DATE: 1999-03-29 APPLICATION NUMBER: 60/127887 FILING DATE: 1999-04-05 APPLICATION NUMBER: 60/130232 APPLICATION NUMBER: 60/131022 FILING DATE: 1999-04-26 APPLICATION NUMBER: 60/131291 FILING DATE: 1999-04-27 APPLICATION NUMBER: 60/131445 APPLICATION NUMBER: 60/140650 FILING DATE: 1999-06-22 APPLICATION NUMBER: 60/140723 APPLICATION NUMBER: 60/141037 APPLICATION NUMBER: 60/144758 APPLICATION NUMBER: 60/123618 FILING DATE: 1999-03-10 APPLICATION NUMBER: 60/125259 FILING DATE: 1999-03-19 APPLICATION NUMBER: 60/125775 FILING DATE: 1999-03-23 APPLICATION NUMBER: 60/131270 FILING DATE: 1998-12-23 APPLICATION NUMBER: 60/115558 FILING DATE: 1999-01-12 APPLICATION NUMBER: 60/119549 FILING DATE: 1999-07-28 FILING DATE: 1999-12-07 1999-06-22 1999-06-22 1999-08-03 FILING DATE: 1999-06-23 FILING DATE: 1999-04-21 FILING DATE: 1999-04-27 1999-08-3 FILING DATE: 1999-01-12 1999-08-1 Query Match Best Local Similarity 50.8 Matches 64; Conservative FILING DATE: 1999-02-FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: PRIOR q ò ò

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Gaps

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TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturing of INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signaturing OF INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE REPERENCE: 689290-75
CURRENT APPLICATION NUMBER: US/69/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                        2495 GCCCAAGTTGCAATGTWTWCGGCAARAWCAATTAAGCSMAWTTCCCTACCTYTTTGCTTC 2436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6952 CATGAACCATTTCCTGGACATTGGGCCTATATTGCAGGGTTTGATGATGATATGGTGGAAATT 7011
                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                    DB 10; Length 5686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7012 crigerrereradaaceaagarrierriadagererenga 7061
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                                                                                                                                                                                                                                                                                                                                       43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2435 ATTTTTTTYGATAAACTTTAAGCAAACGATCCMYTWTTT 2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTT 127
                                                                                                                        FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(5686)

OTHER INFORMATION: N refers to any nucleotide.
US-09-775-938A-31
                                                                                                                                                                                                                                                                                  ; Score 26.8; DB
; Pred. No. 29;
6; Mismatches
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Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 279, Application US/09962436 Patent No. US20020081301A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               13.0%;
50.0%;
                                                                                                ORGANISM: Endobugula sertula
                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 32
US-09-070-927A-612/c
SEQ ID NO 31
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                                                                           TYPE: DNA
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FILE REPERENCE: 1133.010019.

CURRENT APPLICATION NUMBER: US/09/775,938A

CURRENT FILING DATE: 2000-08-04

PRIOR PILING DATE: 2000-08-04

PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSED for Windows Version 4.0
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APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Lavallie, Edward R.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
APPLICANT: Wenberg, David
APPLICANT: Preacy, Mauric
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKecugh
APPLICANT: Carlin-Duckett, McKecugh
APPLICANT: Carlin-Duckett, McKecugh
APPLICANT: Carlin-Duckett, McKecugh
APPLICANT: Carlin-Duckett, McKecugh
APPLICANT: Carlin-Duckett, McKecugh
APPLICANT: Ganetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: 09/413,232
EARLIER PLING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3530 GAGATGTGTTTACCCCACTAGATACATATTTGCCACTGGTTAGTTCTCCATCTAAGCTCA 3589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 GCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 AACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 13.0%; Score 26.8; DB 9; Length 4 ll Similarity 50.8%; Pred. No. 26; 64; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31, Application US/09775938A Patent No. US20020081665A1 GENERAL INFORMATION:
                                                                                                                                                                                                                    Sequence 118, Application US/10114893
Publication No. US20020193567A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                              3053 AGAGGT 3058
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                                             157 AGTGCT 162
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534 AAATACCGCTAATAACAATCCCTGGATATGGTCGTGGAATATTTTTAGCTGCTGCTTCAA 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 687;
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APPLICANT: Obligation, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tammoto, Robert T.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Tenchification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REFERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
FILE REPERENCE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Indels
                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION UNBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474 CTACTICITICCTITICCACCAKACAAGAAGATICGINCC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.9%; Score 26.6; DB Best Local Similarity 54.1%; Pred. No. 12; Matches 53; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 612:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7107, Application US/09815242; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 687 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 612:
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
                                                                             COMPUTER READABLE FORM:
STATE: Maryland
                                                   ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-815-242-7107/c
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Sequence 72, Application US/09070927A
Sequence 72, Application US/09070927A
Sequence 72, Application US/09070927A
Sequence 72, Application 1
Sequence 72, Application 1
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1376 CATTGCCGCTAAAACCCTTTTTTCGACCCATTACCACGAATTGACGCGGTTGGCTGATTC 1435
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Best Local Similarity 58.0%; Pred. No. 20;
Matches 47; Conservative 0; Mismatches 34; Indels 0;
                                                                                                                                                                                                                                                                                                                                                        Query Match
12.9%; Score 26.6; DB 10; Length 891;
Best Local Similarity 78.0%; Pred. No. 14;
Matches 32; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 AAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 AATTGTGCAGTGAAGGTTTTTGCTGTTTTGCTTGTTTCGGT 376
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SUMBER OF SEQ ID NOS: 14110
SEQ ID NO 7107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6054
LENGTH: 1857
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                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 TCTTGATTCGTTGCGCTATGT 105
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                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(891)
US-09-815-242-7107
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US-09-070-927A-72
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                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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OTHER INFORMATION: n equals a,t,g, or c
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-070-927A-68
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Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5100 TTGGAATCTGAAAGTTTTGAAATTTCTTTATCAAATTTTGGTGTAAAGTTGC 5159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5040 Tridargaradadecarcirtiridacageaticgearadeagecearicticages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 TGTGTCTACTAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 ACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.4%; Pred. No. 68;
Matches 65; Conservative 0; Mismatches 64; Indels 0;
                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/046,031
FILING DATE: 1997-05-6
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTONEY.AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
TELECOMMUNICATION NUMBER: 90.0566,009
TELEPERSKCE/DOCKET NUMBER: PB369
TELEPRANCE 100-8512
                                          ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 24004 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                         STATE: Maryland
COUNTRY: USA
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                                                                                                                                                    20850
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US-09-070-927A-68
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6974 ATATIGCTGAAAAGCCTTGATATTGTCATTTGGGTACTAATTGCTGTTTCTGGTTCTTTAG 7033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-764-869-355/c

Sequence 155, Application US/09764869
Fatent No. US20020061521A1
GENERAL INFORMATION:
TILEOF INFORMATION:
TILEOF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT APPLICATION ATE: 2001-01-17
Frior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SEQ ID NO 355
LENGTH: 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7034 CGTTAATTGTGTTATAATTTAACCAACATTAATGTTTCTGAACGGA 7081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 CTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGA 133
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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12.8%; Score 26.4; DB 10;
Best Local Similarity 52.8%; Pred. No. 49;
Matches 57; Conservative 0; Mismatches 51;
                                                                                                   CURRENT APPLICATION DATA:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFYCATION: Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVEY
REGISTATION NUMBER: 40.302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMPUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 8921 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (5)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (15)
OTHER INFORMATION: n equals a,t,g,
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STRANDEDNESS: double
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1828 GCAGCÍT 1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                             TYPE: DNA
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Sequence 4875, Application US/05938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Joel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Znu, Tong

TITLE OF, INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF, INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 ATTAICTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGAT 140
                                                                                                                                                                                                                    90 ATTCGTTGCGCTATGTTAAACCCACCTAAACGGTTGTTTGAAGGACACTGATTGTCCAGGT 149
                                                                                                                                                                                                                                                             253 AATCTTAGGGTTGGATAAAAGGGCCCTTCTCTTTGTCTAAAAAGAGTAATTCTCCATTT 194
                                                                                                                                                                               0; Gaps
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APPLICANT: Macdad, Mo. US20030009018Aliko
APPLICANT: Macdad, Mo. US20030009018Aliko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
FILE REFERENCE: 06501-105US1
CURRENT APPLICATION UNMBER: US/10/105,930
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PCT/JP00/06654
PRIOR APPLICATION NUMBER: JP 12000-240397
PRIOR PILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 77
COSTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1381 AĠAĊĊĊŦĠŤŦŤĊĊŦĀĀĀAĀĠŦŤŦĀĀĀCĀGĊĊĀĠĠŦĠĊĀĠĠŤŦĀĠŢĊ 1431
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                                                                                                                      Query Match 12.7%; Score 26.2; DB 10; Length 670; Best Local Similarity 51.5%; Pred. No. 17; Matches 52; Conservative 3; Mismatches 46; Indela no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 12.7%; Score 26.2; DB 9; Length 17
Local Similarity 52.3%; Pred. No. 27;
nes S8; Conservative 0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                            150 ATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTT 190
                                                                                                                                                                                                                                                                                                                                          LOCATION: (24)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-355
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10105930
Publication No. US20030009018A1
GENERAL INFORMATION:
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LOCATION: (98)...(1108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-938-842A-4875/c
                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1784
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US-10-105-930-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPE: DNA
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1948 AAATCGAĞTTGTAAAATAATGCTGCATAAATTATGGTCCCATATTTTĞGTCTTĞTTTTT 1889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gulukota, Kaidard J.
APPLICANT: Gulukota, Kaidard J.
APPLICANT: Gulukota, Kaidard J.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REPREBRUCE: GIN 6403
CURRENT APPLICATION NUMBER: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 3479;
                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.7%; Score 26.2; DB 9; Length 2000; Best Local Similarity 58.2%; Pred. No. 28; Mismatches 33; Indels 0; Matches 46; Conservative 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 26.2; DB 10; Length 3 50.4%; Pred. No. 37; tive 0; Mismatches 63; Indels
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4875
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 40
US-09-822-849A-298/c
US-09-822-849A-298/c
; Sequence 298, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agostino, Michael J.
Howes, Steven H.
                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 TICGTIGCGCIAIGITAAA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 †CAGATGCAAAAGTTAAAA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 598
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wong, Gordon G. APPLICANT: Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRCANISM: Homo sapiens
US-09-822-849A-298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fechtel, Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/214,188
FILING DATE: 08-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                  ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 620-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 16..1020
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703) 816-4000
703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1325 GAAGTACACTTATT 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 GAAGGACACTGATT 141
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 44
US-09-938-842A-4030/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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                                                                                    Sequence 1, Application US/09935464
Publication No. US20030027153A1
GENERAL INFORMATION:
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GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GE
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Sequence 1, Application US/09790988

Sequence 1, Application US/09790988

Sequence 1, Application US/09790988

Sequence 1, Application US/09790988

APPLICANT: WAIANABE, HIDEMI

APPLICANT: WAIANABE, HIDEMI

APPLICANT: HATTORI, MASAHIRA

APPLICANT: BAKAKI, YOSHIYUKI

ITILE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS

CURRENT APPLICATION NUMBER: US/09/790,988

CURRENT APPLICATION NUMBER: US/09/790,988

PRIOR FILING DATE: 2001-02-23

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 TAAGCCAGGITCIIGICCIAITAICIIGAIICGIIGCGCIAIGIIAAACCCACCI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.7%; Score 26.2; DB 9; Length 157875; Best Local Similarity 56.3%; Pred. No. 2.2e+02; Matches 49; Conservative 0; Mismatches 38; Indels 0;
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Publication No. US20030022260A1
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; ORGANISM: Buchnera sp.
US-09-790-988-1
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                                                            US-09-935-464-1/C
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Sequence 4030, Application US/09938842A

Sequence 4030, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Shu, Tong

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFREENCE: SCRIP1300-3

FILE CORRENT APPLICATION NUMBER: US 60/227,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 AGGITCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCCACCTAACCGTTGTTT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICANT: LA THANGUE, NICHOLAS B.
BERNARDS, RENE
HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.6%; Score 26; DB 9;
Best Local Similarity 59.5%; Pred. No. 28;
Matches 44; Conservative 0; Mismatches 3(
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SEQUENCE CHARACTERISTICS:
          COMPUTER READABLE FORM:
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US-09-886-055-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-070-927A-722
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TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
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                                                                                                                                                                                                                                                                                                                                    20 ACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCC 79
                                                                                                                                                                                                                                                                                                                                                                            144 AACTGATTATAGATTATAAGTAATAAAATTAGTAATGTTTACGTTACCAAGTTCTTTCA 85
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Pred. No. 17;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT APPLICATION TO 101-17
Frior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                   12.6%; Score 26; DB 9; Length 2000; 59.5%; Pred. No. 33; tive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4030
LENGTH: 2000
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Sequence No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2223, Application US/09764877 Patent No. US20020147140A1 GENERAL INFORMATION:
                                                                                                                                                                               TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.5%;
Best Local Similarity 60.9%;
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Best Local Similarity 59.5%
Matches 44; Conservative
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US-09-764-877-2223
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US-09-764-877-2223
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APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
APPLICANT: STRYER, LUBERT
TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
FILE REFERENCE: 078003-0277150
CURRENT FILING DATE: 2001-06-22
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEO ID NOS: 522
SOFTWARE: PATENTIN VOF: 2.1
SEQ ID NO 410
LENGTH: 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 TCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 Tr¢rcifircccraagrafirctrifgraaccgrcafggaaaaaaaafraafcrcgcfffraac 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 ichacardrendeinchtricchacaferhagehadradecthaddnucthreacae 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.5%; Score 25.8; DB 10; Length 1047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69; Indels
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,927A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
12.5%; Score 25.8; DE
Best Local Similarity 48.9%; Pred. No. 21;
Matches 66; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 722:
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
                                                                                                                                                                                                                                                                                   FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 410, Application US/09886055; Patent No. US20020132273A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                          FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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SOFTWARE: PatentIn ver. 3.0
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US-09-938-540-1/c
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APPLICANT:
APPLICANT:
                                                                                                                                                          Query Match
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                                                              90 ATTCGTIGCGCTAIGTTAAACCCACCTAACCGTIGTTIGAAGGACACTGATTGTCCAGGT 149
                                                                                                       879 AGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCCTGTAATCTACACGCT 938
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 TICTIGICCIATRAICTIGATICGTIGCGCTAIGTIAAACCCACCTAACCGTTGTTIGAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 İTCTİTCÖLTCİĞATCIGAATCAĞCTĞAĞCİĞCTGAGCAGAĞATATTAĞTĞCTĞTĞTĞGATA 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 GGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 GTAAGACTGCTGTGGGGGCTGAGGGAAGGGTATGAAGGCTGCTGGGGT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 32 Human secreted proteins FILE REFERENCE: P2044p1
FILE REFERENCE: P2044p1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: PCT/US00/26013
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.5%; Scor No. 29; 52.3%; Pred. No. 29; ... 0; Mismatches '
Best Local Similarity 56.5%; Pred. No. 29;
Matches 48; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
THE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                             150 ATCAAAAGTGCTGTGAAGGTTCCT 174
                                                                                                                                                                                      939 AAGAAACAAAGAAGTGAAGGCAGCT 963
                                                                                                                                                                                                                                                                                         Sequence 67, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NACKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.33
Matches 57; Conservative
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US-09-800-729-67
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US-09-800-729-67/c
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SEQ ID NO 67
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APPLICANT:
APPLICANT:
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447 ICCCCTGITAACCAAGTCAGTGACTTGTTCCTCTGACTGAATGTGTGGGACCACGATGAT 388
                                                                                                                                                                                                                                                  50 TCCTGTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGATAAA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 ATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527 Arrirgaagriggirgaagagagaaacarricciaacaacirgricaaagacrirriacr 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                               12.5%; Score 25.8; DB 9; Length 1107; 58.4%; Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No. US20020187523A1 1566162CB1
US-09-965-528-31
                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, Dyung Aina M.
APPLICANT: PATTERSON, CHANGER
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REPERENCE: PF-0701 USA
CURRENT APPLICATION NUMBER: US/09/965,528
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
                                                                                                                                                                                                   0; Mismatches
                                            TYPE: DNA ORYNEbacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 31, Application US/09965528
; Publication No. US20020187523A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 CCAGGTATCAAAAGTGCTGTGAAG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 ccaddgadacaraccraacrdgdaad 611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BURFORD, Neil
BANDMAN, Olga
BAUGHN, Mariah R.
AZIMZAI, Yalda
                                                                                                                                                                                                                                                                                                                                               110 CCCACCTAACCGTTGTT 126
                                                                                                                                                                                                                                                                                                                                                                                                   387 TCCATCGAGGCGTTGGT 371
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANG, Y. Tom
YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 31
LENGTH: 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                      Best Local Similarity
Matches 45; Conserv
                                                                                             US-09-738-626-1385
SEQ ID NO 1385
LENGTH: 1107
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2753 GTAAGACTGCTGTGGGGGCTGAGGGGTATGAAGGCTGCTGGGGGT 2705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2683 GTAAGACTGCTGTGTGGGGGAAGGGGTATGAAGGCTGCTGGGGT 2635
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                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 2960079CB1
US-10-044-090-333
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                              12.5%; Score 25.8; DB 12; 52.3%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATE: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
TITLE OF INVENTION: 32 Human secreted proteins
TITLE OF INVENTION: 32 Human secreted proteins
TITLE OF INVENTION: 2004-09-08
CURRENT FILING DATE: 2000-09-22
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
                                                CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 333
LENGTH: 3189
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US-09-822-846-104/C
Sequence 104, Application US/09822846
Sequence 104, Application No. US20030027139A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 68, Application US/09800729
; Patent No. US20020068319A1
                                                                                                                                                                                                                                                                                                                                                                                                  Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Homo sapiens
US-09-800-729-68
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Matches 57; Conservat
                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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US-09-800-729-68/c
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0
                                                           APPLICANT: Degussa AG
APPLICANT: Degussa AG
TITLE OF INVENTION: New nucleotide sequences which code for the ccpAl gene
FILE REFERENCE: 000059 BT
CURRENT APPLICATION NUMBER: US/09/938,540
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2612 Trchinccchchdatchaancagchaachachaacaaachannachchchdracha 2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 TICTIGICCIATIAICTIGATICGTIGCGCTATGTTAAACCCACCTAACCGTTGTTTGAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 recrerentance and refreshment to reconstruction of the 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728 rccccidirakccakarcakaraacridrrccrcraacraakrararakacaccacarak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 3098;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.4%; Pred. No. 35;
Matches 45; Conservative 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2552 gragacrecretregegercangegaadegerarieaagecrecreeder 2504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 1999-03-12
PRIOR PLLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOGTWARE: Patentin Ver. 2.0
SEQ ID NO 693
LENGTH: 3098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Indels
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                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 693, Application US/09925300 Patent No. US20020151681A1 GENERAL INFORMATION:
Sequence 1, Application US/09938540 Patent No. US20020151001A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: ccpAl-Gen
US-09-938-540-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 CCCACCTAACCGTTGTT 126
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-044-090-333/c
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US-09-925-300-693/c
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LENGTH: 1600
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
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No. 50; 57; Conservative 0; Mismatches 52; Indels 0;
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US-09-800-729-35

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APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakat
APPLICANT: Graham, James R.
APPLICANT: Greatics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
APPLICANT: Gloverics Institute, Inc.
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
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Pred. No. 55;
0; Mismatches 52; Indels 0;
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Patent No. US2002006319A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1;
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: PCT/US00/26013
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR RILING DATE: 1999-09-24
NUMBER FLING DATE: 1999-09-24
NUMBER: PATENT ON ON S: 217
SOFTWARE: PATENT OF VERY SECOND ON S: 217
                                           Merberg, David
Treacy, Maurica
Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
Spaulding, Vikki
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LOCATION: (6035)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
LOCATION: (6037)
Collins-Racie, Lisa A.
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Best Local Similarity 52.3%;
Matches 57; Conservative (
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                                                                                                                                                                                                                  Clark, Hilary
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ORGANISM: Homo sapiens
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US-09-800-729-35/c
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LENGTH: 4116
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OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: SITE (CATION: (6038) OTHER INFORMATION: n equals a,t,g, or c

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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
                                                                                                                                                  2813 TICTITCCCICIGATCIGAATCAGCIGAGCIGCTGAGCAGACATATTACTGCTGTGGATA 2754
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       Length 6065;
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                                                       Indels
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APPLICANT: Wahlestedt, Claes
APPLICANT: Wahlestedt, Claes
APPLICANT: Wahlestedt, Claes
CURENT PLIUG, BO
CURENT APPLICATION NUMBER: US/10/002,048A
CURENT FILIG DATE: 2001-11-02
PRIOR APPLICATION NUMBER: SE 0004035-2
PRIOR APPLICATION NUMBER: SE 0004035-2
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
FEQ ID NO 4
       DB 10;
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                                                     0; Mismatches
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     Score 25.8; I
Pred. No. 67;
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12.4%; Score 25.6; I
Best Local Similarity 55.7%; Pred. No. 17;
Matches 49; Conservative 0; Mismatches
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DATABASE ENTRY DATE: 1995-01-08
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
     12.5%;
Query Match
Best Local Similarity 52.3
Matches 57; Conservative
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OTHER INFORMATION:
PUBLICATION INFORMATION:
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LOCATION: (1)..(29)
OTHER INFORMATION:
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ORGANISM: human
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US-09-960-352-6148
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APPLICANT: Li, Haddong
APPLICANT: Li, Haddong
APPLICANT: Li, Haddong
APPLICANT: Li, Haddong
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
CURRENT ELING DATE: 2000-02-15
CURRENT FILING DATE: 1995-04-12
PRIOR PELLORION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
NUMBER OF SEQ ID NOS: 12485
SOFTWARE PARENT NOS: 12485
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CTHER INFORMATION: (1). (434)
CTHER INFORMATION: n = a or c or g or t
US-09-880-107-2920
                                                                                                       Sequence 2920, Application US/09880107

Sequence 2920, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: HORIE, Darci T.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REPERBUCE 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE PARCENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 12.4%; Score 25.6; DB 10; Length 434; Best Local Similarity 62.5%; Pred. No. 22; Marches 40; Conservative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 11050, Application US/09783590
; Parent No. US20020110850A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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US-09-783-590-11050
                                                                                      RESULT 60
US-09-880-107-2920/c
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154 AATT 151
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LENGTH: 434
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APPLICANT: Young, Paul
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·.
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                                                                                                                                                                                                                                                                                                                                               Gaps
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12.4%; Score 25.6; DB 10; Length 434;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 40; Conservative 0; Mismatches 24; Indels 0;
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                                                                                                                                                                                                                                 12.4%; Score 25.6; DB 10; Length 327; 51.8%; Pred. No. 19; tive 0; Mismatches 54; Indels 0;
                                                                                                                                             ) ORGANISM: Bos taurus
) OTHER INFORMATION: Clone ID: 26-LIB34-075-Q1-E1-G5
) US-09-960-352-6148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 669290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/23,617
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR PILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
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PRIOR FILING DATE: 2000-09-27
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) OTHER INFORMATION: n=a,t,g or c
US-09-954-456-2208
  CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 6148
LENGTH: 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                     Best Local Similarity 51.8
Matches 58; Conservative
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US-09-954-456-2208/c
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191 CGTT 194
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LENGTH: 434
                                                                                                                                                                                                                                                           Query Match
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                                                                                                                            TYPE: DNA
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61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
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APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
FILE REFERENCE: 7529/1614840.51
CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 742
SOFTWARE: PatentIn version 3.1
SEQ ID NO 715
LENGTH: 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Degenerate polynucleotide sequence of SEQ ID NO:21
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.4%; Score 25.6; DB 9; Length 633; Best Local Similarity 28.9%; Pred. No. 27; Matches 37; Conservative 24; Mismatches 67; Indels
            APPLICANT: Xu, Wenfeng,
APPLICANT: Xu, Wenfeng,
APPLICANT: No. US2003007253Alak, Julia E.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/253,561
PRIOR APPLICATION NUMBER: US 60/257,211
PRIOR APPLICATION NUMBER: US 60/267,211
NUMBER OF SEQ. ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1). (729)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-715
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12.4%; Score 25.6; Di
Best Local Similarity 50.8%; Pred. No. 28;
Matches 61; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 715, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (6.3.3)
; OTHER INFORMATION: n = A,T,C or G
US-09-995-898A-29
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
APPLICANT: Presnell, Scott R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Xenopus laevis
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US-09-910-943-715/c
                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 GIGGITCCAGGGITTCCTNGNTIGCCGGTTTCCAAAACGGGTTTCAAGATTCCTGTGGAA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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            THER INFORMATION: n equals a,t,g, or c
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US-09-783-590-11050
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
                                                                                                                                                   OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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US-09-995-898A-29
US-09-995-898A-29
; Sequence 29, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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                                                                                  OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: '?a,'
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NAME/KEY: misc feature
LOCATION: (439)
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
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LOCATION: (295)
                                      NAME/KEY: misc feature
                                                                                                                                                                                                                                                 'KEY: misc feature
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LOCATION: (443)
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DB 10; Length 729;
                                      59; Indels
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Carr, Grant J.
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SEQ ID NO 3
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US-09-995-898A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      806 TATGCTATATCGATAATATCGATGCTAGAATGAATGTTTGAAAAAGGCATATAAAAAA 865
                                                                                                                              279 TCTCGGAGIAGCTCGCTTAGTTTCGGGTAGTCAAACTGAAATTCGTTTTGCTTGATTATG 220
                                                                        135 ACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGGTATGGCTTGTTTCGTT 194
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Oblish, Kari L.
APPLICANT: Oblish, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000-101-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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; Sequence 8969, Application US/09815242
; Patent No. US/20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                     sequence 8813, Application US/09815242 patent No. US20020061569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 CTGTGAAGGTTC 172
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US-09-815-242-8813
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APPLICANT: Wangangoo Teber T.
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TITLE REFERENCE ELITRA OLD TO TEST THE PREFERENCE ELITRA OLD TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPERTY TO TEST THE PROPE
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                                                                                                                                                                                                                                                                                                             324 RWSNCCNIGGGINGARWSNGARIAYYINGAYTAYYINTIYGARGTNGARCCNGCNCCNCC 383
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                                                                                                                                                                                              1 AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTA 60
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                                                                                                         12.4%; Score 25.6; DB 9; Length 1473; 28.9%; Pred. No. 40; tive 24; Mismatches 67; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Presnell, Scott R.
APPLICANT: Xu, Wenfeng
APPLICANT: Xu, Wenfeng
APPLICANT: No. US20030027253Alak, Julia E.
APPLICANT: No. US20030027253Alak, Julia E.
APPLICANT: Grant, Francis J.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
FILE REFERENCE: 00-108
CURRENT APPLICATION NUMBER: US/09/995,898A
CURRENT FILING DATE: 2001-11-28
FRIOR APPLICATION NUMBER: US 60/253,561
FRIOR APPLICATION NUMBER: US 60/267,211
PRIOR APPLICATION NUMBER: US 60/267,211
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: S0
SOFTWARR: FastEEQ for Windows Version 3.0
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OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LCCATION: (1)...(1473)
; OTHER INFORMATION: n = A,T,C or G
US-09-995-898A-3
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                                                                                                                                                    Matches 37; Conservative
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Matches 37; Conservative
                                                                                                                                Local Similarity
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NGTNYTNG 391
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RESULT 68

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APPLICANT: Rosen et al.
TITLE DO INVENDATION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3301
                                                                                                                                                                                                                       Prior application data removed - consult PALM or file wrapper NUMBER OF PALEN IN NOS: 1792 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 359
                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.4%; Score 25.6; DB 10; Length ;
Best Local Similarity 62.5%; Pred. No. 48;
Matches 40; Conservative 0; Mismatches 24; Indels
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49.3%; Pred. No. 79;
tive 0; Mismatches
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
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APPLICANT: Charles A. Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3301, Application US/09764877 ; Patent No. US20020147140A1
                     Sequence 359, Application US/09764864
Patent No. US20020132753A1
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Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-359
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; ORGANISM: Homo sapiens
US-09-764-877-3301
                                                                        GENERAL INFORMATION:
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US-09-764-877-3301
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US-09-764-864-359
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09-833799-13a.rnpb

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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAP
TITLE OF INVENTION: HENATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
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                                                                                                                                                                                                                                                                                                                                                               191 ACTCTACCTGCCACTGTCCTATTATATTCATTCTTTTTGAAATGTCAACCCCAAGTTA 133
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                                                                                                                                                Query Match
12.3%; Score 25.4; DB 10; Length 326;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels 0;
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PRIOR FILING DATE: 2000-03-01
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PRIOR PILING DATE: 2000-03-17
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PRIOR PILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-05-04
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PRIOR FILING DATE: 2000-05-04
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OTHER INFORMATION: n=A,T,C or G
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OTHER INFORMATION: n=A,T,C or G
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                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-998-598-2252
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 72
US-09-796-692-7381
LENGTH: 326
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                                                                                                                                                                                                                                                                                                                                                                                 QQ
                                                                  TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 10059 CGCTGATCGCGCAGGTTTATACTACGCCGAAGAAGGTGCTTTAAGTATGATTTATT 10118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 CACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGT 193
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Sequence 2222, Application US/09998598
Patent No. US20020150922A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.651
CURRENT FILING DATE: 2001-11-16
WHMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO. 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 59.7%; Pred. No. 1.6e+02;
Matches 43; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OMERATING YSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-M9-2000
CLASSIFCATION NUMBER: 60/046,655
APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/046,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/046,031
FILING DATE: 1997-101-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
SEQUENCE DESCRIPTION: SEQ ID NO: 138: US-09-070-927A-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 28690 base pairs
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       Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                Steven Barash
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
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OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature LOCATION: (417)
OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature LOCATION: (419)
OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (412)
                                 OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (340)
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OTHER INPORMATION: n equals a,t,g, or of the control of the control (357)
OTHER INFORMATION: n equals a,t,g, or other information: n equals a,t,g, or other information of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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NAME/KEY: misc feature
LOCATION: (342)
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NAME/KEY: misc feature
LOCATION: (348)
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NAME/KEY: misc feature
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FION: (360)
   LOCATION: (335)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7280, Application US/09783590
| Sequence 7280, Application US/09783590
| Patent No. US20020110850A1
| GENERAL INPORMATION:
| APPLICANT: Li, Hadodny
| APPLICANT: Li, Hadodny
| APPLICANT: Ruben, Craig A.
| APPLICANT: Ruben, Steven M.
| TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2 FILE REFERENCE: PO-16.21
| CURRENT APPLICATION NUMBER: US/09/783,590
| CURRENT FILING DATE: 1995-04-12
| PRIOR FILING DATE: 1995-04-12
| PRIOR APPLICATION NUMBER: 08/420,856
| PRIOR FILING DATE: 1994-11-21
| NUMBER OF SEQ ID NOS: 12485
| SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                            0; Gaps
                                                                                                                                                                                                           60 ACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAA 118
                                                                                                                                                                                                                                                   136 ACTCTACCTGCACACTGTCCTATTATATATTCATTCTTTTTGAATGTCAACCTCCAAGTTA 194
                                                              Query Match
12.3%; Score 25.4; DB 9; Length 327;
Best Local Similarity 64.4%; Pred. No. 23;
Matches 38; Conservative 0; Mismatches 21; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (61)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (123)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (125)
COTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (128)
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NAME/KEY: misc feature
LOCATION: (150)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (185)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (327)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (61)
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OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature
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US-09-783-590-7280/c
US-09-796-692-7381
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LENGTH: 504
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SEQ ID NO 55
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APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Resnick, Richard J.
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6402
CURRENT APPLICATION NOWBER: US/09/822,830A
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARR: PatentIn Ver. 2.0
SSETURENT: NANA
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Best Local Similarity 55.3%; Pred. No. 28;
Matches 47; Conservative 0; Mismatches 38; Indels 0.
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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LOCATION: (456)
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OTHER INFORMATION: n equals a,t,g, or
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                                                                                                                                                INFORMATION: n equals a,t,g, or
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Papplicant: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
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CORGANISM: Homo sapiens
US-09-822-830A-205
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LOCATION: (455)
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Query Match
Best Local Similarity 52.3%; Pred. No. 39;
Matches 56; Conservative 0; Mismatches 51; Indels 0;
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Sequence 55, Application US/08927939;
Patent No. US2010006640A1
GENERAL INFORMATION:
APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauen Marie
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
FILE REPERENCE: 295.022US1
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
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SOFTWARE: FastSEQ for Windows Version 3.0
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US-08-927-939-55
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Human genome-deriv Human colon cancer

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                                                                                       February 15, 2003, 21:13:02; Search time 194 Seconds (without alignments) 2391.297 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 1008
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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RESULT 2
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Oligonucleotide fo
       (KCN6q
                Drosophila melanog
                       recepto
                              Drosophila melanog
                                      Drosophila melanog
                                            Human digestive sy
Human protein havi
                                                           Human colon cancer
                                                                                                               Human immune/haema
                                                                                                Human polynucleoti
        Human KCNQ5
                       thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene product has inhibitory activity against human leukocyte elastase (HLE) and may be isolated from psoriatic scales. The sequence may be expressed from a plasmid transformed expression system and may be useful in the prevention of tissue damage alsociated with emphysema, adult respiratory distress syndrome, psoriasis and bullous dermatoses. Other treatable conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leucocyte elastase inhibitor - is genetically engineered polypeptide for treatment of inflammatory, pulmonary and skin conditions
                                                                                                                                                                                                                                  Sequence encoding human leukocyte elastase inhibiting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                         Edge MD;
                                                                                                                                                                                                                                                Emphysemia; respiratory distress syndrome; atherosclerosis; arthritis; cystic fibrosis; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                        Schroder JM, Pioli D, Wiedow O,
                                                                                                                                                                                                                                                                                                     /*tag= a
/label= Elastase inhibitor
                                                                                                                                                  ALIGNMENTS
                                    ABL02548
AAK91348
                                                                                       AAI59408
AAI61194
                                                                                                       AAT42063
                                                                                                                     ABQ53920
ABQ53921
                                                                  ABA83379
                                                                         ABQ91970
                                                                                                              AAK59445
AAV59749
        AAC64370
                      AAL45900
                             ABL20270
                                                   AAD12603
                                                           AAH34853
                                                                                 ABQ91971
                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 13; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         (ICIL ) IMPERIAL CHEM INDS PLC.
                                                                                                                                                                                      AAQ06819 standard; DNA; 206 BP.
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89GB-0013346.
89GB-0013349.
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P-PSDB; AAR08217.
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13.6
13.6
13.6
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                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                      04-JUN-1990;
                                                                                                                                                                                                                   06-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                    02-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                   09-JUN-1989;
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28
27.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGGTA 180
                                                                                                                                                                                                                                                                                                                                                                                              61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                     1 AATICGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTGTTA 60
                                                                                                                                                                                                                                                                                                                                         1 AATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTA 60
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                                                                                                                                                                                                                                0;
include atherosclerosis, cystic fibrosis, bronchitis and acute non-lymphoblastic leukaemia. Abs raised to the polypeptide may be used in detection.
                                                                                                                                                                         Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elafin, elafin 25L gene, Pichia pastoris, expression vector, alcohol oxidase 1; controlling region; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pPIC9/ELF25L cDNA construct containing the elafin 25L gene.
                                                                                                                                                                                                                             Indels
                                                                                                                                                                      ; Score 206; DB 11;
; Pred. No. 5.6e-60;
0; Mismatches 0;
                                                                                                                 Sequence 206 BP; 51 A; 46 C; 44 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV28852 standard; cDNA to mRNA; 8598 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TGGCTTGTTTCGTTCCACAATAATAG 206
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949..1203
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1204..1374
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                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 206; Conservative
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controlling region (AOCR) which controls the expression of EL encoding gene; (2) a microbial host transformed with the vector; (3) DNA fragment for recombinant transformation comprising: (a) a first region homologous to the genomic DNA of the host; (b) a promoter region of (AOCR) gene; (c) a gene encoding signal peptide; (d) a linker designed to secrete a matured elafin; (e) a gene encoding EL; (f) selection marker gene; (g) stop codon, and (h) a second region homologous to a part of the genomic DNA of the host, and (4) a microbial host transformed with the DNA fragment of (3). The microbial hosts can be used to prepare EL commercially. The production of EL by the microbial hosts can be carried
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1264 Arccerrecerrisersaaccesceaaccerrerraaasacacreereser 1323
                                                                                                                                                                                                                                                                                                                                                                                                          1204 GCTCAAGAACCAGTTAAGGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCGATTATCCTG 1263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT 149
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                                                                                                                                                                                                                                                                                                                                                                  GCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1324 ATCAAAAAATGCTGCGAAGGTTCTTGCGGTATGGCATGCTTCGTTCCGCAGTAGT 1378
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                                                                                                                                                                                                                                                                                   61.7%; Score 127; DB 19; Length 8598; 82.9%; Pred. No. 1.4e-32; tive 0; Mismatches 30; Indels 0
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                                                                                                                                                                                                                                               Sequence 8598 BP; 2306 A; 2025 C; 1920 G; 2347 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoshida M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1, Page 23; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaji A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ56674 standard; DNA; 177 BP
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                                                                                                                                                                                                          on a large scale.
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AAQ56674
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The DNA
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                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAQ56674-76 encode elafin derivatives. The DP encoding wild type elafin is mutated, inserted into a suitable vector and then used to transform E. coli, yeast, Bacillus subtilis transformed cells. The modified elafin is expressed when the transformed cells are cultured. The modified elafin are drugs with elastase inhibitor activity. They have improved oxidation stability cover natural elafin and thus retain activity better under oxidative conditions.
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                                                                                                                             30 GCTCAAGAACCAGTTAAAAGGTCCTGTGTTAAAGGCCAGGTTCTTGTCCTATTATCTTG 89
                                                                                                                                                            1 gcacaggaaccagrinaaaggrccggrgrccaaccaaaccgggcrcrrgcccgarrarccrg 60
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                                                              Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant modified elafin with improved oxidation stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elafin; derivative; mutation; transformation; E. coli; yeast;
                                                              Score 125.4; DB 15; Length
Pred. No. 1.2e-32;
0; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis; elastase inhibitor; oxidation; ss.
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                                Sequence 177 BP; 39 A; 49 C; 48 G; 41 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     has pharmaceutical use as an elastase inhibitor
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                                                                                                                                                                                                                                                                                                                                                                         AAQ56676 standard; DNA; 177 BP
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                                                                              Best Local Similarity 82.3%;
Matches 144; Conservative
                                                                60.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                           AAQ56676;
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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30 GCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCCAGGTTCTTGTCCTATTATCTTG 89 

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The polymucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polymucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer.

ABK4450-ABK46237 represent coding sequences of human colon tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides encoding colon tumour proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Force: With the exception of SEQ ID No 1 and 2, the sequence data for this patent did not form part of the printed specification but was supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colon cancer polypeptides and polynucleotides, useful as vaccines, diagnosing, preventing, and treating colon cancer, and as markers the progression of cancer -
                                                                                                                                                  1 GCACAGGAACCAGTTAAAGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCGATTATCCTG 60
                                                                         ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT
                                                                                                                                                                                                                                                                   121 ATCAAAAATGCTGCGAAGGTTCTTGCGGTATGCCATGCTTCGTTCCGCAGTAGT 175
                                                                                                                                                                                                                        150 ATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAAT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 125.2; DB 24; Length 480; Pred. No. 2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon tumour; vaccine; colon cancer; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 480 BP; 113 A; 105 C; 139 G; 120 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA encoding colon tumour protein, SEQ ID No 1393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 1393; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK45842/c
ID ABK45842 standard; cDNA; 480 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000; 2000US-223283P.
28-MAR-2001; 2001US-279763P.
29-JUN-2001; 2001US-302051P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2001; 2001WO-US24218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunotherapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 King GE, Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-241739/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-FEB-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK45842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                        TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCCAG 147
88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 rearcederecearerrearececeraececeraecerrearasararaceareceas 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides comprising immunogenic portion of head and neck tumour protein useful for treating, diagnosing and monitoring cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAG 142
                                                                     148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                                                      251 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCCAGTGAGAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                                                                                                                                                                                                                                                                                                          Head tumour; neck tumour; lung cancer; vaccine; cancer therapy; ss.
                                                                                                                                                                                                                                                                                                      Human head/neck tumour related protein partial coding sequence #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 124.6; DB 2. Pred. No. 3.1e-32;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as head, neck and lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                               AAC68808 standard; cDNA; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-2000; 2000WO-US10687.
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20-APR-2000; 2000US-0533870.
                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                      21-FEB-2001
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                                                                                                                                                                                                                                     AAC68808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
                                                                                                                                                                                AAC68808/c
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34; Indels

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Matches 145; Conservative

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Local Similarity

311 AAGCGCAAGAGCCAGTCAAAGGTCCAGTNTCCACTAAGCCTGGCTCCTGCCCCATTATCT 312

28 ATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCT 87

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Emphysemia; respiratory distress syndrome; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene product has inhibitory activity against human leukocyte elastase (HLE) and may be isolated from psoriatic scales. The sequence may be expressed from a plasmid transformed expression system and may be useful in the prevention of tissue dange associated with emphysema, adult respiratory distress syndrome, psoriasis and bullous dermatoses. Other treatable conditions include atherosclerosis, cystic fibrosis, bronchitis and acute non-lymphoblastic leukkaemia.

Abs raised to the polypeptide may be used in detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human leucocyte elastase inhibitor - is genetically engineered polypeptide for treatment of inflammatory, pulmonary and skin conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.5%; Score 124.6; DB 11; Length 504;
                                                                                        Sequence encoding human leukocyte elastase inhibiting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edge MD;
                                                                                                                                                                                                                      label = Upstream in-frame coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wiedow O,
                                                                                                                                                                                                                                 121..328
/*tag= a
/label= Blastase inhibitor
                                                                                                                               arthritis; cystic fibrosis; leukaemia; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Christophers E, Schroder JM, Pioli D,
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 16, 45pp, English.
              BP.
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            AAQ06820 standard; cDNA; 504
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89GB-0013349.
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09-JUN-1989;
25-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                     04-JUN-1990;
                                                               06-MAR-1991
                                                                                                                                                                                                                                                                                                                  EP402068-A.
                                      AAQ06820;
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                                                                                                                                                        Homo
AAQ06820
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AB056306 to AB060787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the AB060776 to AB060787 uncleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and conference or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), in a cell. A probe/primer derived from (I) can be used for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antissnse therapy, to generate

The corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and disgnafest applications. (I) can be used to raise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 rearccionicarcinarionariccionarione 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molino GA;
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148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
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                                        276 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAG 334
                                                                                                                                                                                                                                                                                                                          Human; colon cancer; cancer; tissue profiling; forensic; mapping; genetic analysis; diagnostic; antisense therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies, and to screen for peptide analogues and antagonists.
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                                                                                                                                                                                                                                                                                Human colon cancer related nucleotide sequence SEQ ID NO:2513.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 571 BP; 136 A; 155 C; 131 G; 145 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carroll E,
                                                                                                                                                  ABQ58818 standard; cDNA; 571 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2001; 2001WO-US30732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2000; 2000US-237271P
                                                                                                                                                                                                                                     (first entry)
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Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200229086-A2
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                     02-AUG-2002
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                                                                                                                                                                                            ABQ58818;
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                                                                                                         RESULT 8
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Gaps

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34; Indels

Pred. No. 3.3e-32; 0; Mismatches

ilarity 81.0%; Conservative

Local Similarity

145;

Matches

TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147

88

셤 ò

28 ATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAAGGTTCTTGTCCTATTATCT 87

ABK83819;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in AAQS6674-76 encode elafin derivatives. The DN encoding wild type elafin is mucated, inserted into a sustable vector and then used to transform E. coli, yeast, Bacillus subtilis or animal cells. The modified elafin is expressed when the transformed cells are cultured. The modified elafin are drugs with elasstase inhibitor activity. They have improved oxidation stability cover natural elafin and thus retain activity better under oxidative conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 GCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGGCCAGGTTCTTGTCCTATTATCTTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCACAGGAACCAGTTAAAGGTCCGGTGTCGACCAAACCGGGCTCTTGCCCGATTATCCTG 60
                 328 GAATCAAGAAGTGCTGTGGAAGGCTCTTGCGGATGGCCTGTTTCGTTCCCCAGTGAAGA 386
148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAATAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 Arcaaaaargcreceaaegrrerrecegrarescarecrresrresearaer 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 ATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAAT 204
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant modified elafin with improved oxidation stability has pharmaceutical use as an elastase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15; Length 177;
                                                                                                                                                                                                                                                       Elafin, derivative, mutation, transformation, E. coli, yeast, Bacillus subtilis, elastase inhibitor; oxidation, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yoshida M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 177 BP; 39 A; 50 C; 48 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okawa N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 24; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaji A,
                                                                                                                    AAQ56675 standard; DNA; 177 BP.
                                                                                                                                                                                                                       Elafin derivative Val25 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                               93WO-JP01133
                                                                                                                                                                                                                                                                                                                                                                                                                                               92JP-0234085
                                                                                                                                                                                      23-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ishima Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TSUR ) TSUMURA & CO.
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                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amagaya S,
                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                      AAQ56675;
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ABK83819 standard; cDNA; 2309 BP.

RESULT 10 ABK83819 ID ABK8 XX

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The invention relates to detecting (MI) granulocyte (GC) activation (CGCA), by detecting the level of expression of gene (5) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated (GC, where differential expression of GS is indicative of GCA. That alters the expression of at least one gene in GS; (2) screening (MI) can agent capable of modulating GN2 by contracting GC with an agent capable of modulating GCA or an inflammation (especially contract) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the control of in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the control of inflammatory disease, by detecting the subject to a pathogen or sterile inflammatory disease, by detecting the subject to a pathogen or sterile inflammatory disease, by contacting a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, and a tissue having or sterile inflammatory disease, and a tissue having a subject, exposure of a subject to a pathogen or sterile inflammatory disease, and is useful for screening an agent that modulates the expression of gene (S) for modulating GA, MI is useful for screening an agent capable of modulating an inflammation (sepecially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile computation of sepecially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile computation injury, ARDS, adult respiratory distress syndrome, continity and disease, also bacterial enfection, protozoal infection, viral infection, indicating continuous distress syndrome, continuous disease, also bacterial enfecting for treating one of the ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting granulocyte activation by detecting differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                 viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury, remal reperfusion injury, ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; unlerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                      Human cDNA differentially expressed in granulocytic cells #390.
                                                                                                                              granulocytic cell; DNA chip; bacterial infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2001; 2001WO-US30821.
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                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENE LOGIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug toxicity
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                           1552 AAGCGCAAGAGCCAGTCAAAGGTCCAGTAAGCCTGGCTCCTGCCCCATATCT 1611
                                                                                               TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                  Gaps
                                                                28 ATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCCAGGTTCTTGTCCTATTATCT 87
                                                                                                                                         GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAA 203
                                 Score 123.2; DB 24; Length 2309;
Pred. No. 1.7e-31;
0; Mismatches 33; Indels 0;
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0
                Sequence 2309 BP; 595 A; 537 C; 603 G; 572 T; 2 other;
                                                                                                                                                                                                                                       Lung cancer related gene sequence SEQ ID NO:4153.
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                      ABL65816 standard; DNA; 2309
                                Query Match
Best Local Similarity 81.2%;
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-234567P.
2000US-234923P.
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2000US-236842P
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25-SEP-2000;
25-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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                                                                                                                                                                                                                                                                               gene; ds.
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The present invention describes a method (M1) for screening for anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 to ABL7010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has gyrostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Horrigan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCCCCAGTGA 1727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for anti-neoplastic agent involves exposing cells to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.8%; Score 123.2; DB 24; Length 2309; Best Local Similarity 81.2%; Pred. No. 1.7e-31; Matches 143; Conservative 0; Mismatches 33; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endress G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2309 BP; 595 A; 537 C; 603 G; 572 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lung cancer related gene sequence SEQ ID NO:4825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 4153; 44pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL66488 standard; DNA; 2309
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2000US-237604P.
2000US-237606P.
2000US-237173P.
2000US-237278P.
                                                           2000US-237294P.
2000US-237295P.
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2000US-237425P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Augustus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (AVAL-) AVALON PHARM
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                                                    02-OCT-2000; 2
02-OCT-2000; 2
03-OCT-2000; 2
03-OCT-2000; 2
03-OCT-2000; 2
03-OCT-2000; 2
                           02-OCT-2000;
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Soppet DR,
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ABL66488
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02-OCT-2000; 2000US-237316P. 03-OCT-2000; 2000US-237425P. 02-OCT-2000; 2000US-237278P. 02-OCT-2000; 2000US-237294P. 02-OCT-2000; 2000US-237295P. 03-OCT-2000; 2000US-237598P. 

stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wllm's tumour; adenocarcinoma; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; 2000US-236034P. 2000US-236109P. 2000US-236111P. 2000US-236842P. 2000US-236891P. 2000US-236028P. 2000US-236032P. 2000US-236033P. 2000US-235637P. 2000US-235638P. 2000US-235720P. 2000US-235840P. 2000US-235863P. 02-OCT-2000; 2000US-237172P. 02-OCT-2000; 2000US-237173P. 2000US-235077P. 2000US-235082P. 2000US-235711P. 2000US-234009P. 2000US-234923P. 2000US-234924P. 2000US-235280P. 2000US-234509P 2000US-234567P 30-MAY-2001; 2001WO-US10838 2000US-23 WO200194629-A2 28-SEP-2000; 28-SEP-2000; 28-SEP-2000; 28-SEP-2000; 29-SEP-2000; 29-SEP-2000; 25-SEP-2000; 26-SEP-2000; 26-SEP-2000; 20-SEP-2000; 20-SEP-2000; 22-SEP-2000; 22-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; Homo sapiens. 28-SEP-2000; 27-SEP-2000; 27-SEP-2000; 20-SEP-2000; 27-SEP-2000; 13-DEC-2001 gene; ds.

01-NOV-2000; 2000US-245084P (AVAL-) AVALON PHARM. 01-NOV-2000;

2000US-237608P

Carter KC, Ebner R, Endress G, Horrigan S; Augustus M, Weaver Z; Young PE, A Soppet DR,

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set

Claim 1; SEQ ID 4825; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in

expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 55% identical to (S), where a change in a expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which can the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the tractment of cancer such as colon, breast, stomach, lung, thyroid, cosophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine cancer, squamous call carcinoma, neuroendocrine and Wilm's tumour. 1612 rearcceerececarerreaarccccraaccecrecrreaasaaracresececas 1671 1552 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTAAGCCTGGCTCCTGCCCCATTATCT 1611 88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147 0; Gaps 28 AIGCICAAGAACCAGITAAAGGICCIGIGICIAAAGCCAAGGITCIIGICCIAIIAICI 87 Diagnosos and treatment of cancer - using candidate tumor suppressor which utilizes a biotinylation-based subtraction procedure instead of hydroxyapatite as previously used. In this procedure, a single strand phagemid cDNA library from normal cell polyA+ mRNA is hybridized with excess biotinylated tumor polyA+ mRNA, and the resulting double stranded sequences are removed by binding to 1672 GAATCAAGAAGIGCIGIGAAGGCTCTIGCGGAAIGGCCTGTTTCGTTCCCCAGTGA 1727 148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATAA 203 An adaptation of the subtractive hybridization technique was used 59.8%; Score 123.2; DB 24; Length 2309; 81.2%; Pred. No. 1.7e-31; live 0; Mismatches 33; Indels 0; Sequence 2309 BP; 595 A; 537 C; 603 G; 572 T; 2 other; CaN19; tumour suppressor gene; cancer; therapy; ss. Partial sequence of tumour suppressor gene U9. Claim 29; Page 37-38; 54pp; English. (DAND ) DANA FABER CANCER INST INC. genes or the corresp. antibodies. AAQ28757 standard; DNA; 321 BP 91US-0662216. 92WO-US01624 25-FEB-1993 (first entry) Matches 143; Conservative WPI; 1992-331663/40. Local Similarity 28-FEB-1992; 28-FEB-1991; Homo sapiens WO9215602-A. AAQ28757; Query Match Sager R; RESULT 13 AAQ28757 QQ ò ò

Sequence 737 BP; 205 A; 192 C; 182 G; 158 T; 0 other;

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streptavidin. The remaining single-stranded phagemid cDNAs are converted to double-stranded form and used to transform bacterial host cells. The resulting subtracted cDNA library is differentially screemed with total cDNA from normal and tumor cells. This method produced some 20 additional cloned cDNAs. Also found by this method were several genes which, on the basis of the partial DNA sequences appear to be novel sequences not previously entered into GENBANK. The portion of the cDNAs so sequenced represents part of the coding region and/or part of the 3' untranslated region of each cDNA (see Q28749-58).
                                                                                                                                                                                                                                                                           142 AAGCGCAAGAGCCAGTCAAAGGTCCAGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCT 201
                                                                                                                                                                                                                                                                                                           88 TGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAG 147
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                    ATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sodium ion, potassium ion, ATP-ase inhibitor peptide; cardiac;
lar disease; PCR; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence (AAQ44862) encodes the SPAI peptide which is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sodium ion, potassium ion ATP-ase inhibitor peptide and corresp.
DNA - useful to treat cardiac and vascular disease
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0
                                                                                                                                                                                              e 121; DB 13; Length 321; No. 4.6e-31;
                                                                                                                                                                                                                                                                                                                                                                     148 GTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCC 196
                                                                                                                                                                                                                                                                                                                                                                                        262 GAATCAAGAAGTGCTGTGAAGGCTCTTGCGGGATGGCCTGTTTCGTTCC 310
                                                                                                                                                                                                                          0; Mismatches 30; Indels
                                                                                                                                                              Sequence 321 BP; 81 A; 80 C; 84 G; 76 T; 0 other;
                                                                                                                                                                                               Score 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to mRNA; 737 BP
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                                                                                                                                                                                                               Pred.
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/product= SPAI
                                                                                                                                                                                            58.78;
                                                                                                                                                                                                          82.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                      139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ44862 standard; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EISA ) EISAI CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-097819/12.
                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPAI gene
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                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                        Matches
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as a drug for treating cardiac and vascular diseases. The peptide is found as a pre-sequence (AARS0335) which is amplified using primers (AAQ44863-67)

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Secretory leukoprotease inhibitor; human; gene; ds; protease inhibitor; malaria; emphysema; asthma; chronic obstructive pulmonary disease; SLPI; ovstic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease; glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel fusion protein useful for inhibiting protesse activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an
                                                                 61 CTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACC 120
                                                                                             428 CTAAGCGTGGCCACTGCCCTAGGATTCTTTTTCGTTGCCCGCTGAGCAATCCCTCTAACA 487
                                                                                                                                 121 GTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTA 180
                                                                                                                                                                   488 AGTGTTGGAGAGATTATGACTGTCCAGGGGTCAAGAGGTGCTGTGAAGGCTTTTGCGGGA 547
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding human secretory leukoprotease inhibitor (SDPI) protein.
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32.1%; Score 66.2; DB 15; Length 737; 66.4%; Pred. No. 2.5e-12; ive 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Secretory leukoprotease inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "No start or stop codon shown"
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                                                                                                                                                                                                    181 TGGCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                      548 AGGATTGTTTGTATCCCAAGTGA 570
                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                       ABK88016 standard; DNA; 321
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2001US-331966P.
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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/product=
                                   Conservative
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               Local Similarity
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20-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                         ABK88016;
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzhaimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the human secretory leukoprotease inhibitor used to create the fusion protein
                       is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiquenesis, gastric ulceration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AAGCCAGGTAAGTGTCCAGTTACGTCAATGTTTGATGTTGAACCCACCAAACTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 rergaaaregacegreaareraagacacerrgaagrerrerargearreserrerererereraag 297
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/standard_name= "Ribosome binding site"
inhibitor of protease activity. The fusion protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 321 BP; 92 A; 67 C; 80 G; 82 T; 0 other;
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'product= "SLAP1 fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.4; DB 24
Pred. No. 2.1e-05;
0; Mismatches 56
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note= "SLPI coding region'
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/note= "linking codon"
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58.5%;
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es 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention.
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/note= "AAT coding region"

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tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Into the control relates to a lover that process in the functionally protease inhibitor comprising an alphal-antitypesh or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriaais, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, and for treating herpes infection, corneal or epidermal ulceration, and for treating herpes infection, corneal or epidermal ulceration, and for treating herpes infection, corneal or epidermal ulceration, and for the activity is activity.
                                                                                                                                                                                                                                                                                                                                                            Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 padcicadinaandriciaarinacinacericaarieringarieringaacicaaaacini 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 rercaaargeaceercaareraasasasacrreaasierrisrareserarefersiaas 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 AAGCCAGGTTCTTGTCCTATTATCTTGATTGCGTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel fusion protein comprising a first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.4; DB 24; Length 1525; Pred. No. 3.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1525 BP; 467 A; 286 C; 314 G; 458 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence encoding rSLAP1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 73-73; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLAP1 fusion protein of the invention
                                                                                                                                                                                                                                                              Pemberton P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK88025 standard; DNA; 1525
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58.5%;
                                                                                                       18-DEC-2001; 2001WO-US49256.
                                                                                                                                                      18-DEC-2000; 2000US-256699P.
20-NOV-2001; 2001US-331966P.
                                                                                                                                                  2000US-256699P
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                                                                                                                                                                                                                   (ARRI-) ARRIVA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity F
                                                                                                                                                                                                                                                              Barr PJ, Gibson HL,
                                                                                                                                                                                                                                                                                                        2002-500631/53
                                                                                                                                                                                                                                                                                                                          P-PSDB; AAU99881
                      WO200250287-A2.
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                                                                 27-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibitor
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rSLAP1; gene; ds; Alzheimer's disease; tumour angiogenesis; malaria; emphysema; asthma; chronic obstructive pulmonary disease; cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema; human immunodeficiency virus; atopic dermatiis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; osteoporosis; Paget's disease; scleroderma; glomerulonephritis; hypertension

Homo sapiens.

Synthetic.

'standard\_name= "Ribosome binding site" 'product= "rSLAP1 fusion protein" 2..1193 /\*tag= e /note= "SLPI coding region" \*tag= c note= "AAT coding region" '\*tag= d
'note= "linking codon" Location/Qualifiers 194..1196 1197..1517 Ω .1520 \*tag= \*tag= misc\_feature misc\_feature misc\_feature CDS

WO200250287-A2

27-JUN-2002

18-DEC-2001; 2001WO-US49256

18-DEC-2000; 2000US-256699P. 20-NOV-2001; 2001US-331966P.

(ARRI-) ARRIVA PHARM INC.

Pemberton P; Barr PJ, Gibson HL,

WPI; 2002-500631/53. P-PSDB; AAU99884 Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease nhibitor

Example 3; Page 89-90; 134pp; English.

This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alphal-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active protein. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity by associated with a disorder cyclic fibrosis, others, asthma, chronic obstructive pulmonary disease, cystic fibrosis, ottis media, ottis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczena and psoriasis, in inflammantory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodonial disease, tumour metastasis and tumour angiogenesis, gastric ulceration, alaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The presents sequence represents the DNA encoding the 'SLAP1 fusion protein of the invention.

Sequence 1525 BP; 467 A; 287 C; 314 G; 457 T; 0 other;

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                                                                                                                                                                                                                                                   1434 TGTGAAATGGACGGTCAATGTAAGAGAGCTTGAAGTGTTGTATGGGTATGTGTAAG 1493
                                                                                                                                                  1374 AAGCCAGGTAAGTGTCCAGTTACTTACGGTCAATGTTTGATGTTGAACCCACCAAACTTC 1433
                                                                                                 63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                  123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                       Gaps
                                                       .
0
22.0%; Score 45.4; DB 24; Length 1525; 58.5%; Pred. No. 3.7e-05; ive 0; Mismatches 56; Indels 0;
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                                                 Conservative
                                                                                                                                                                                                                                                                                                     183 GCTTGTTTCGTTCCA 197
                    Best Local Similarity
Matches 79; Conserv
  Query Match
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RESULT 18 AAC97529

AAC97529 standard; DNA; 321 BP

AAC97529;

(first entry) 27-FEB-2001

DNA encoding a protease inhibitory peptide.

Serine protease inhibitor; cytostatic, anti-inflammatory, arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin; elastase; ds

Synthetic

US6132990-A

17-0CT-2000

91US-0712354. 07-JUN-1991;

89US-0293042. 84US-0678822. 85US-0803471. 02-DEC-1985

86US-0890526 29-JUL-1986

87US-0031846 87US-0082962 30-MAR-1987 

(AMGE-) AMGEN BOULDER INC.

Stetler GL, Bandyopadhyay PK, Eisenberg SP,

Thompson RC;

WPI; 2000-678667/66.

protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors New serine protease inhibitors and DNA sequences for treating a

Disclosure; Column 12-13; 47pp; English.

This invention relates to new purified and isolated mammalian serine procease inhibitors proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The procease inhibitors are capable of inhibiting chymotrypain and elastase. Sequences AAC97526 - AAC97534. AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB53122 represent the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors. The protease inhibitors have cytostatic and anti-inflammancry activity. The scrime protease inhibitor protein is useful for treating a protease-mediated condition, which includes protease mediated tissue

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elastase inhibitor; human polymorphonuclear leukocyte elastase inhibiting
          periodontitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elastase-inhibiting peptide of low serine protease-inhibiting activity contains C-terminal portion of human polymorphonuclear leukocyte
                                                                                                                                        63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                 178 AARCCNGGNAARTGNCCNGTNACNTAYGGNCARTGYCTNATGCTNAAYCCNCCNAAYTTY 237
                                                                                                                                                                                          TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                  238 TGNGARATGGAYGGNCARTGYAARCGNGAYCTNAARTGYTGYATGGGNATNTGYGGNAAR 297
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding fragment of human polymorphonuclear leukocyte elastase inhibiting protein.
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                                                                                    20.7%; Score 42.6; DB 21; Length 321; 42.5%; Pred. No. 0.00019; tive 16; Mismatches 61; Indels 0.
destruction, e.g. emphysema, arthritis, glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohtsuka
                                                             Sequence 321 BP; 60 A; 54 C; 60 G; 44 T; 103 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okada M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama T, Kamimura T, Masuda K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  AAN90354 standard; DNA; 194 BP.
                                                                                                  Local Similarity 42.5%;
tes 57; Conservative 1
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25.30
/*tag= c
56.61
/*tag= d
120.125
/*tag= e
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190..194
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                                                                                                                                                                                                                                             183 GCTTGTTTCGTTCC 196
                                                                                                                                                                                                                                                                     298 TCNTGYGTNTCNCC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-220549/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc feature
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                                                                                       Query Match
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                                                                                                                Matches
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                                                              The sequence encodes a fragment of human polymorphonuclear leukocyte elastase inhibiting protein (Asn 55-Ala 107). See AAP90126 for encoded peptide. Misc. features a-g are BamHI, SalI, MluI, NdeI, BglII, XhoI and PstI sites resp. See also AAP90384.
                                                                                                                                                                                                                                                                                                                                                                      93 cigigaaanggacggicagigiaaacgagarcigaangirigiangggiangigigiaa 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                              TAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCG 121
                                                                                                                                                                                                                                                                                                                                     TTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molino GA;
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                   33 TAAACCGGGTAAATGTCCGGTTACATATGGTCAGTGTCTGATGCTGAACCCGGCGGAACTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, colon cancer, cancer, tissue profiling, forensic; mapping, genetic analysis, diagnostic, antisense therapy; gene; ss.
                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer related nucleotide sequence SEQ ID NO:4416.
                                                                                                                                                                                          Length 194;
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                                                                                                                                                                                                                             60; Indels
                                                                                                                                                         Sequence 194 BP; 48 A; 42 C; 53 G; 51 T; 0 other;
                                                                                                                                                                                          Score 39; DB 10;
Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catino TJ,
                                                                                                                                                                                                                               0; Mismatches
                                    Disclosure; fig 2; 55pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ60721 standard; cDNA; 656
                                                                                                                                                                                            18.9%;
55.6%;
elastase inhibiting protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2001; 2001WO-US30732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                           Query Match
Best Local Similarity 55.00
The 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thiaglingam A, Lewis ME;
                                                                                                                                                                                                                                                                                                                                                                                                           182 GGCTTGTTTCGTTCC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                            153 ATCTTGTGTTTCTCC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Astle JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-426115/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200229086-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
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of cells from a patient. (1) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (1) can be used to raise antibodies, and to screen for peptide analogues and antagonists.
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Sequence 656 BP; 96 A; 91 C; 107 G; 256 T; 106 other;

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                                                            ATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCAC 198
                                                                                        285 ACTGNNCAGGAATCAAGAANTNNTGNGAAGGNTCTAGNGGGATGGCCNGATTNGTTCCCC 226
                                Gaps
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0
 Score 38; DB 24; Length 656;
Pred. No. 0.0088;
0; Mismatches 23; Indels
   18.4%;
                               44; Conservative
               Similarity
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                                                                                                                                                   225 ANNGANA 219
Query Match
Best Local S
Matches 44
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Murine SLPI sense riboprobe SEQ ID NO:20. ABQ73674 standard; DNA; 396 BP. 04-OCT-2002 ABQ73674; RESULT 21 

Murine; serum amyloid; SAA3; riboprobe; LST-1; follistatin-like 1; FST1; SLPI; secretory leukocyte protease inhibitor; legumain; SOCS3; rheumatoid arthritis; CISH3; RAGE; AGRR; LY117; hydroxymethyl glutarate; HMG-1; glucocorticoid leucine zipper; GLLZ; PTPN-18; GADD-45B; PRSC1; lipocalin 2; LCT2; glucose phosphate isomerase; GPI; Spil; serine protease inhibitor; TSG-6; ss.

ABQ73677 standard; DNA; 396 BP

Mus sp

WO200248310-A2.

20-JUN-2002.

17-DEC-2001; 2001WO-US48968

15-DEC-2000; 2000US-255861P

(GENE-) GENETICS INST LLC

Pittman DD, Feldman JL,

characteristic of rheumatoid arthritis in cell and reference level, by comparing expression levels of the genes determined in a cell with Determining difference between expression levels of genes WPI; 2002-583494/62.

Shields KM, Trepicchio WL;

Example 3; Page 88; 296pp; English.

reference level

The present invention describes a method (M1) for determining the difference between levels of expression of a number of genes characteristic of rheumatoid arthritis (RA) in cell and reference levels of expression of the genes, comprising: (a) providing RNA from a cell; (b) determining levels of RNA of a number of genes (G) characteristic of RA including a number of genes selected from SOCS3 (CISH3), RAGE (AGER), LST-1 (LY117), serum amyloid (SAA) 1-3, hydroxymethyl glutarate (HMG)-1, S100 A8, A9, and A12, secretory leukocyte protease inhibitor (SLPI); glucocorticoid leucine zipper (GLLZ), PTPN-18, GADD-45A and B, Legumain (PRSC1), follistatin-like 1 (FST1), lipocalin 2 (Lon2), glucose

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to obtain the levels of expression of the genes in the cell; and col comparing the levels of expression of the genes in the cell; and set of reference levels of expression of the genes, to determine the difference between levels of expression of the number of genes characteristic of RA in the cell and reference levels of expression of the genes. Wa is useful for determining whether a subject has or is likely to develop RA, or for determining whether a subject has or is effective in a subject having RA who is receiving the therapy. Mais effective in a subject having the stage of RA in a subject, for determining the stage of RA in a subject having RA, and for determining the likelihood of success of a particular therapy in subject having RA. The present sequence represents a mutine SLDI sense riboprobe, which is used in an example from the present invention.
phosphate isomerase (GPI), serine protease inhibitor (SpiL), and TSG-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 CCAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGTATGATGCTTAAC 303
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Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 396 BP; 94 A; 98 C; 118 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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53.3%;
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Murine, serum amyloid; SAA3; riboprobe, LST-1; follistatin-like 1; FST1; SLPI; secretory leukocyte protease inhibitor; legumain; SOCS3; rheumatoid arthritis; CISH3; RAGE; AGER; LY117; hydroxymethyl glutarate; HMG-1; glucocorticoid leucine zipper; GILZ; PTPN-18; GADD-45A; GADD-45B; PRSC1; lipocalin 2; Lon2; glucose phosphate isomerase; GPI; SpiL; serine protease inhibitor; TSG-6; ss. Murine SLPI antisense riboprobe SEQ ID NO:23. (first entry) 04-OCT-2002 Mus sp.

WO200248310-A2.

20-JUN-2002

17-DEC-2001; 2001WO-US48968. 

15-DEC-2000; 2000US-255861P.

(GENE-) GENETICS INST LLC

Trepicchio WL; Shields KM, Feldman JL, Pittman DD,

WPI; 2002-583494/62.

Determining difference between expression levels of genes characteristic of ineumatoid arthritis in cell and reference level, by comparing expression levels of the genes determined in a cell with reference level -

Example 3; Page 88; 296pp; English

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The present invention describes a method (MI) for determining the difference between levels of expression of a number of genes characteristic of expression of the genes, comprising: (A) in cell and reference levels of expression of the genes, comprising: (A) in cell and reference levels of expression of the genes, comprising: (A) providing RNA from a cell; (CAER), LST-1 (LY117), serum amyloid (SAA) 1-3, hydroxymethyl glutarate (HMG)-1, S100 A8, A9, and A12, secretory leukocyte protease inhibitor (SID); glucocorticoid leucine zipper (GILZ), prPN-18, GADD-45A and B, legumain (PRSC1), follistatin-like 1 (FST1), lipocalin 2 (LGC2), glucose phosphate isomerase (GPI), serine protease inhibitor (SpiL), and TSG-6 (C) comparing the levels of expression of the genes in the cell to a set of reference levels of expression of the genes in the cell to a set of reference levels of expression of the mumber of genes characteristic of RA in the cell and reference levels of expression of the genes, to determine the difference between levels of expression of the mumber of genes characteristic of RA in the cell and reference levels of expression of the genes, to determine the defective in a subject having RA who is receiving the therapy. MI is also useful for determining whether a subject has or is also useful for determining the efficacy of a therapy in a subject, for determining the efficacy of a therapy in a subject, for determining the likelihood of success of a particular therapy in subject having RA. The present sequence represents a murine SLDI antisense riboprobe, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 CCTCCCAATGTCTGCCAGAGGACGGGCAGTGTGACGGCAAATACAAGTGCTGTGAGGGT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; carcinoma cell; IMC-HA1; cancer; metastasis; CMAP; inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.8%; Score 34.6; DB 24; Length 396; llarity 53.3%; Pred. No. 0.1; Conservative 0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse IMC carcinoma cell IMC-HA1 clone 28-1#3 cDNA #1.
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tes 73; Conserv
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The present invention provides gene sequences associated with cancer metastasis which are isolated from mouse IMC carcinoma cells by detection of their higher expression in IMC-HM cell lines than in IMC-LM cell lines than in these cells. The gene sequences can be used for the screening of potential inhibitors of cancer metastasis by either: bringing into contact with the cancer metastasis associated protein (CMAP) and determining the degree of binding; or creating a transformant cell line which expresses CMAP and measuring the degree of expression of CMAP using an antibody recognising the protein, either in the presence or absence of the potential inhibitor. IMC-HM cells transformed with antisense CMAP DNA show a lowered ability to metastasise. The present sequence represents a specifically claimed gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 CCTCCCAATGTCTGCCAGAGGGACGGCAGTGTGACGGCAAATACAAGTGCTGTGAGGGT 387
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                                                                                                                                                                                               Protein associated with cancer metastasis and gene encoding it -useful for screening for potential inhibitors of cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; Length 684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 684 BP; 175 A; 176 C; 179 G; 154 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse IMC carcinoma cell IMC-HA1 clone 28-1#3 cDNA.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.8%; Score 34.6;
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                                                                                                                                                                                                                                                                                                  Claim 2; Page 46-47; 74pp; Japanese.
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                               Ohta M;
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                               Morita M,
                                                                                               WPI; 1999-080732/07.
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                                                                                                                                  P-PSDB; AAW98909.
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                               Arakawa H,
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Mus musculus,

08-APR-1997; 07-APR-1998;

WO9845431-A1 15-OCT-1998. 15

Page

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                                                                                                                                                                                                                                                                                                                                 The present invention provides gene sequences associated with cancer metastasis which are isolated from mouse IMC carcinoma cells by detection of their higher expression in IMC-HM cell lines than in IMC-LM cell lines than in IMC-LM cell lines using differential display of the mRNA in these cells. The gene sequences can be used for the screening of potential inhibitors of cancer metastasis by either: bringing into contact with the cancer metastasis associated protein (PMP) and determining the degree of binding; or creating a transformant cell line which expresses CMAP and measuring the degree of expression of CMAP using an antibody recognising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 ccadidideadeaadecrideaaggiecercaaacrcagecaagaigrargagecriaac 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the protein, either in the presence or absence of the potential inhibitor. IMC-HM cells transformed with antisense CMAP DNA show a lowered ability to metastasise. The present sequence represents a
                                                                                                                                                                    Protein associated with cancer metastasis and gene encoding it -
useful for screening for potential inhibitors of cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 cerecenarorer de casa de constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la constante de la c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically claimed gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.8%; Score 34.6; DB 20; Length 691; 53.3%; Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse IMC carcinoma cell IMC-HA1 clone #8.323 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                            74pp; Japanese.
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   Ohta M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohta M;
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   Morita M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arakawa H, Morita M,
                                                                                                                                                                                                                                                                            Claim 2; Page 41-42;
                                                                       WPI; 1999-080732/07
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                                                                                                    P-PSDB; AAW98908
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Arakawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The present invention provides gene sequences associated with cancer metastasis which are isolated from mouse IMC carcinoma cells by detection of their higher expression in IMC-HM cell lines than IMC-LM cell lines using differential display of the mRNA in these cells. The gene sequences can be used for the screening of potential inhibitors of cancer metastasis by either: bringing into contact with the cancer metastasis associated protein (CMAP) and determining the degree of binding; or creating a transformant cell line which expresses CMAP and measuring the degree of expression of CMAP using an antibody recognising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 CCAGTGTGGAGGAAGCCTGGGAGGTGCGTCAAAACTCAGGCAAGATGTATGATGCTTAAC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                   the protein, either in the presence or absence of the potential inhibitor. IMC-HM cells transformed with antisense CMAP DNA show a lowered ability to metastasise. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation; ss.
useful for screening for potential inhibitors of cancer metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 CCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 CCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757 cereceaargrefeceagaggacagaggecagigiaacggeaaracaagrefergagger
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                                                                                                                                                                                                                                                                                                                                                                                            Score 34.6; DB 20; Length 1114; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                specifically claimed gene sequence from the present invention
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                                                                                                                                                                                                                                                                                                                                                       Sequence 1114 BP; 271 A; 299 C; 290 G; 254 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                      Claim 2; Page 44-45; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                              16.8%;
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 53.3
Matches 73; Conservative
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AAI81895
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                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyneptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                   86 CTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCC 145
                                                                                                                                                                                                                                                                                                                                                                         200 criaatregrigiaccatritacariccaccagcaargregaagariccigrircrec 259
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                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                  26 ATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAAGCCAGGTTCTTGTCCTATTAT 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic sequence capable of directing microbial synthesis of serine protease inhibitor having similar properties to protein isolated from parotid secretions.
             Claim 1; SEQ ID NO 1955; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                 Score 33; DB 22; Length 416;
                                                                                                                                                                                                                                                                          55; Indels
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                                                                                                                                                                                                                        Sequence 416 BP; 102 A; 77 C; 73 G; 163 T; 1 other;
                                                                                                                                                                                                                                                              0.37;
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                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                              Pred. No.
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                                                                                                                                                                                                                                                  16.0%;
54.5%;
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85US-0803471.
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                                                                                                                                                                                                                                                                          66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trypsin-; inhibitor; ss.
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                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                inflammation.
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The sequence directs synthesis of a single chain polypeptide serine procease-inhibitor, which believed to have at least 2 active sites, a stries, a stries, a stries, a stries, a stries, a stries, and the other exhibiting activity against trypsin. See also AAN60464-69 and AAP60562-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 TGCGAAATGGACGGCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGCGGCAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence directs synthesis of a secretory leukocyte protease-inhibitor. See also AAN60463, AAN60465-69 and AAP60562. AAP60564-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New synthetic DNA sequences for directing microbial synthesis - for prodn. of single poly:peptide chain serine protease inhibitor having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease-inhibitor; parotid; leukocyte-elastase-inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic sequence capable of directing microbial synthesis of
                                                                                                                                                                                                                                                                                                                                                         15.6%; Score 32.2; DB 7; Length 324; illarity 51.8%; Pred. No. 0.63; Conservative 0; Mismatches 68: Indels Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thompson RC;
having leukocyte elastase and trypsin inhibitory sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                              Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretory leukocyte protease-inhibitor.
                                                           Disclosure; Page 14; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 rcrrcrcrccccccanaaa 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAN60464 standard; DNA; 324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandyopadh PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85WO-US02385.
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85US-0803471.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trypsin-; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1986-169458/26.
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAP60563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-DEC-1984;
02-DEC-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN60464;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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AAN60464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a DNA sequence (A) encoding an analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;
                                                                                                                      AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                              178 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 237
                                                                                                                                                                                                                                         TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                    TGCGAAATGGACGGCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGCGGCAAA 297
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis,
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      DB 7; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease inhibitor direct manufacturing DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thompson RC;
                                                                 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stetler GL,
   Score 32.2; DB Pred. No. 0.63; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscular dystrophy, and tumour invasion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX16194 standard; DNA; 324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                    298 rcircigirrccccccgraaa 318
                                                                                                                                                                                                                                                                                                                                                            183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84US-0678822.
86US-0890526.
86US-0903471.
90US-0563832.
94US-0279056.
   15.6%;
51.8%;
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                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPI; 1999-166640/14.
                               Local Similarity
ses 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acute leukemia; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUL-1986;
33-SEP-1986;
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Query Match
Best Local 5
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                                                                                                                                                                                                                                         123
                                                                                                                                                                                                                                                                                                    238
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                                                                 Matches
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         absence of biochemical stimuli. The present sequence represents a DNA sequence which is used to direct manufacture of recombinant serine protease inhibitors.
                                                                                                                                                                                       63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                           178 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 237
                                                                                                                                                                                                                                                            TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                               238 TGCGAAATGGACGCCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGCGCAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;
high degree of self assembly forming an active tertiary structure in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor direct manufacturing DNA sequence (SLPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis, muscular dystrophy, and tumour invasion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA sequence encoding mammalian serine protease inhibitor
                                                                                                                      DB 20; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandyopadhyay PK, Bisenberg SP, Stetler GL, Thompson RC;
                                                                                                                                                      68; Indels
                                                                                 Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 other;
                                                                                                                  15.6%; Score 32.2; DB 51.8%; Pred. No. 0.63; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Column 29; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                  298 rcircicirrrccccccraaa 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                 183 GCTTGTTTCGTTCCACAATAA 203
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86US-0903471.
90US-0563832.
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84US-0678822.
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                                                                                                                                                      Conservative
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                                                                                                                                 Local Similarity
nes 73; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acute leukemia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX16236;
                                                                                                                      Query Match
                                                                                                                                                                                                                                                            123
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 30
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                                                 allows (B) to be recombinantly produced in sufficient quantities and purities so as to provide economical pharmaceutical compositions. (B) is resistant to heat, acid, and a variety of proteolytic enzymes, is thermodynamically stable in extracellular conditions, and exhibits a high degree of self assembly forming an active terriary structure in the absence of biochemical stimil. The present sequence represents a DNA sequence which is used to direct manufacture of recombinant serine
caused by a disturbance in the native protease/protease inhibitor balance such as emphysema, arthritis, glomerulonephritis, peridontitis, muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A)
                                                                                                                                                                                                                                                                                                              63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                              123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGGTATG 182
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                              178 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                238 TGCGAAATGGACGGCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGCGGCAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin; elastase; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                           15.6%; Score 32.2; DB 20; Length 324; 51.8%; Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding a serine protease inhibitor peptide sequence.
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                            68;
                                                                                                                                                                                                          Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stetler GL,
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 34; Column 64-66; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 TCTTGTGTTTCCCCGGTAAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC97527 standard; DNA; 324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTGTTTCGTTCCACAATAA 203
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85US-0803471.
86US-0890526.
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87US-0082962.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOULDER INC.
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-678667/66.
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bandyopadhyay
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02-DEC-1985;
29-JUL-1986;
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protease inhibitors of the invention, and include oligonuclecting the sequences used in the isolation and characterisation of the protease primers AAC97535 - AAC97573 and AAC9582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB53089 - AAB53122 represent the protease inhibitors. Peptide sequences various other peptides used in the isolation of the protease inhibitors and various other peptides used in the isolation of the protease inhibitors. The protease inhibitors protease inhibitors protease inhibitors protease inhibitor protein; useful for treating a protease mediated condition, which includes protease mediated tissue destruction, e.g. emphysem, arthritis, glomerulonephitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the proteins, especially by recombinant methods.
This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534, AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 TGCGAAATGGACGGCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGCGGCAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secretory leukocyte protease inhibitor (SLPI) DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                            Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                   0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  15.6%; Score 32.2;
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84US-0678822.
85US-0803471.
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87US-0031846.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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29-JUL-1986;
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AAC97574 - AAC97581 and AAC97614 - AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97632 - AAC97633 - AAC97633 - AAC97632 - AAC97633 - AAC97632 - AAC97633 - AAC97632 - AAC97633 - AAC97632 - AAC97633 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632 - AAC97632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               various other peptides used in the isolation of the protease inhibitors. The protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating a protease-mediated condition, which includes protease mediated tissue destruction, e.g. emphysem, arthritis, glomerulonephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AAGCCAGGITCITGICCIAITAICITGAITCGITGCGCIAIGITAAACCCACCIAACCGI 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                       New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins, especially by recombinant methods.
                                                                                                                                                       Disclosure; Column 5; 47pp; English.
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85US-0803471.
86US-0890526.
87US-0031846.
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29-JUL-1986;
30-MAR-1987;
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AAC97579
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This invention relates to new purified and isolated mammalian serine protease inhibitors proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97534. AAC97581 and AAC97614 - AAC97641 represent DNA encoding the sportease inhibitors of the invention, and include oligonucleotide sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97573 and AAC9582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences AAB5302 represent the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors. The protease inhibitors have cytostatic and anti-inflammatory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The serine protease inhibitor protein is useful for treating a protease-mediated condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy or tumour invasion. It is also useful for modulating protease activity. The DNAs are useful for producing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recearatesaceccaeteraaceagaretesaarecrerateseratesecaar 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                             New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema or tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor protein; recombinant; leukocyte elastase;
trypsin; ds.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.6%; Score 32.2; DB 21; Length 324; 51.8%; Pred. No. 0.63;
                                                                                 Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "serine protease inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                              Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant serine protease inhibitor DNA
                                                                                                                                                                                                                                            Example 2; Column 30-32; 47pp; English.
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                                                                              Bandyopadhyay PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI67488 standard; DNA; 324 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 TCTTGTGTTTCCCCGGTAAAA 318
87US-0082962.
                                        (AMGE-) AMGEN BOULDER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .324
                                                                                                                       WPI; 2000-678667/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
04-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US6291662-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA167488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
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Matches
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                                                                                                                                                                                                                                                                                        The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight eysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents the coding strand of a DNA that directs the manufacture of a recombinant
                                                                                                                                                                                                                        New DNA sequences, useful in recombinant DNA techniques for directing
the production of a serine protease inhibitor protein, e.g. leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 aaacceegraaarecceegraaccrareeccaerercrearecreaacceeceaactre 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 TGCGAAATGGACGGCCAGTGTAAACGAGATCTGAAATGCTGTATGGGTATGTGCGGCAAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant secretory leukocyte protease inhibitor (SLPI) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.2; DB 22; Length 324; Pred. No. 0.63;
                                                                                                                                                               Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 324 BP; 87 A; 85 C; 88 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                               Bandyopadhyay PK, Eisenberg SP, Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                      Example 1; Column 4; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 rcrigicirrcccccggraaa 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI67489 standard; DNA; 324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 15.6%;
Local Similarity 51.8%;
                                                                               94US-0279056.
84US-0678222.
                                  98US-0158085
                                                         87US-0031846
                                                                     90US-0563832
                                                                                                      85US-0803471
                                                                                                                   86US-0890526
                                                                                                                                                                                                                                                                                                                                                                                                 serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73; Conservative
                                                                                                                                                                                       WPI; 2001-637974/73.
                                                                                                                                                                                                                                                elastase or trypsin
                                                                                                                                         (AMGE-) AMGEN INC.
                                                                                                                                                                                                    P-PSDB; AAG65993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6291662-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-2001.
                                  22-SEP-1998;
                                                                                                                   29-JUL-1986;
                                                                     06-AUG-1990
                                                                                           05-DEC-1984
                                                                                                        02-DEC-1985
            18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI67489;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA167489
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The invention relates to a DNA sequence encoding an analog of a mammalia serine protease inhibitor protein. The analog comprises at least eight oysterine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin. The present sequence represents the coding strand of a DNA that directs the manufacture of a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 receaaredaceeccaereraaceagreresaarecreracererecerarereceaa 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 324;
                                                                                                                                                                                                                                                                                                                         Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 324 BP; 86 A; 85 C; 87 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                         Bandyopadhyay PK, Eisenberg SP, Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secretory leukocyte protease inhibitor (SLPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32.2; DB; Pred. No. 0.63; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Column 5; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence of ompA-tc-met-SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX16272 standard; DNA; 420 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 TCTTGTGTTTCCCCGGTAAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.6%;
51.8%;
                                                                                90US-0563832.
94US-0279056.
84US-0678222.
98US-0158085.
                                                                                                                                                                       85US-0803471.
                                                       87US-0031846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 51.8
es 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-637974/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute leukemia; ds.
                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAG65996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
   22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-1999.
                                                                                                                      22-JUL-1994;
                                                                                                                                                                                                         29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5871956-A
                                                                                      06-AUG-1990;
                                                                                                                                              05-DEC-1984
                                                                                                                                                                       02-DEC-1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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The present invention describes a DNA sequence (A) encoding an analogue of a mammalian serine protease inhibitor (B). The DNA sequences and recombinant methods allow manufacture of a class of inhibitors of e.g. cathepsin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions caused by a disturbance in the native protease/protease inhibitor balance such as emphysema, arthritis, glomerulomephritis, peridontitis, muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A) burities so as to provide economical pharmaceutical compositions (B) is thermodynamically stable in extracellular conditions, and exhibits a high degree of self assembly forming an active textiary structure in the absence of blochemical stimuli. The present sequence represents the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          338 receaariceaccaererationalecaerereaarecreariererareaerarererereaa 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                            New DNA sequence encoding mammalian serine protease inhibitor useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 15.6%; Score 32.2; DB 20; Length 420; Local Similarity 51.8%; Pred. No. 0.69; He 73; Conservative 0; Mismatches AR Indale A.
                                                                                                                                                                                                                                   Bandyopadhyay PK, Eisenberg SP, Stetler GL, Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 420 BP; 123 A; 98 C; 112 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        muscular dystrophy, and tumour invasion
                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Column 37-40; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 TCTTGTGTTTCCCCGGTAAAA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC97624 standard; DNA; 436 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding ompA-tc-met-SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of ompA-tc-met-SLPI.
                                                                         84US-0678822.
86US-0890526.
86US-0903471.
90US-0563832.
94US-0279056.
                    94US-0279056
                                                         87US-0031846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                          WPI; 1999-166640/14.
                                                                                                                                                                                                (AMGE-) AMGEN INC.
                    22-JUL-1994;
                                                                                                                                                       22-JUL-1994;
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                                                                                              29-JUL-1986
                                                                                                                  03-SEP-1986
                                                                                                                                       06-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 37
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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97534.

AAC9754 - AAC97531 and AAC97614 - AAC97614 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide of sequences used in the isolation and characterisation of the proteins. Primers AAC97535 - AAC97533 and AAC975582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors. Peptide sequences CC AAB33102 represent the protease inhibitors. Peptide sequences CC AAB33102 represent the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors have cytostatic and anti-inflammatory activity. The serine protease inhibitor protein is useful for treating a protease enhibitor protein is useful for treating a content and secular dystrophy or tumour invasion. It is also useful continis, muscular dystrophy or tumour invasion. It is also useful continied in the invention in the invention of the protease activity. The DNAs are useful for producing the continied in the invention of the protease activity. The DNAs are useful for producing the continied in the invention of the protease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AAGCCAGGITCTIGICCTAITAICTIGAITCGITGCGCIAIGITAAACCCACCTAACCGI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCGGAACTTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 recgaraticacicacióraraceagarcicaariciórareceratereces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease-mediated condition or tissue destruction e.g. emphysema or
tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New serine protease inhibitors and DNA sequences for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.6%; Score 32.2; DB 21; Length 436; 51.8%; Pred. No. 0.7;
                                                                                                                                                                                                                                                                                                                                                                                          Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 436 BP; 128 A; 102 C; 116 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                          Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Column 39-40; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          Bandyopadhyay PK, Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 rcrrcrcrcccccccraaaa 418
                                                                                                                                                                                                              85US-0678822.
85US-0803471.
86US-0890526.
                                                                                                                                                   91US-0712354.
                                                                                                                                                                                              89US-0293042
                                                                                                                                                                                                                                                                             87US-0031846
87US-0082962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI67583 standard; DNA; 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN BOULDER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 51.8
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-678667/66.
                                                                                                                                                   07-JUN-1991;
                                                             US6132990-A.
                                                                                                        17-OCT-2000
                                                                                                                                                                                                                                    02-DEC-1985
                                                                                                                                                                                                                                                           29-JUL-1986
                                                                                                                                                                                                                                                                               30-MAR-1987
                                                                                                                                                                                                                                                                                                  04-AUG-1987
                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA167583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI67583
ID AAI6
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Eisenberg SP,
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                                                                                                                                               87US-0031846.
84US-0678822.
86US-0890526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC97622 standard; DNA; 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.8%;
                                                                                                                         94US-0279056
                                                                                                                                                                                 86US-0903471.
                                                                                                                                                                                             90US-0563832
                                                                                                                                                                                                       94US-0279056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 GCTTGTTTCGTTCCACAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 TCTTGTGTTTCCCCGGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of ompA-SLPI.
                                                                                                                                                                                                                                                                            WPI; 1999-166640/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                              INC.
                                                                                                                                                                                                                                                     Bandyopadhyay PK,
                                                                                                                                                                                                                             (AMGE-) AMGEN
                                            Homo sapiens
                                                                                                                         22-JUL-1994;
                                                                              US5871956-A.
                                                                                                                                                30-MAR-1987;
                                                                                                                                                                      29-JUL-1986;
03-SEP-1986;
                                                                                                                                                                                             06-AUG-1990;
                                                                                                                                                                                                       22-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73;
                                                                                                   L6-FEB-1999
                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC97622
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                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dalgarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. leukocyte elastase or trypsin. The present sequence represents the DNA sequence coding for ompA-tc-met-secretory leukocyte protesse
                                                                                                                                                                                                                                                                                                                      the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                              New DNA sequences, useful in recombinant DNA techniques for directing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 receaaarecaceceacrereraaccacartercaaarecrerarecerares
                                Serine protease inhibitor protein; recombinant; leukocyte elastase;
trypsin; secretory leukocyte protease inhibitor; SLPI; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 436;
                                                                                                                                                                                                                                                                   Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 436 BP; 128 A; 102 C; 116 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                   Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 32.2; 51.8%; Pred. No. 0.
            DNA sequence coding for ompA-tc-met-SLPI.
                                                                                                                                                                                                                                                                                                                                                              Example 3; Column 37-38; 37pp; English.
                                                                                                                                                                                                                                                                   Bandyopadhyay PK, Eisenberg SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 GCTTGTTTCGTTCCACAATAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 TCTTGTGTTTCCCCGGTAAAA 418
                                                                                                                                                                        90US-0563832.
94US-0279056.
84US-0678222.
85US-0803471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX16271 standard; DNA; 460
                                                                                                                                        98US-0158085
                                                                                                                                                               87US-0031846
                                                                                                                                                                                                                       86US-0890526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of ompA-SLPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                         WPI; 2001-637974/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                             (AMGE-) AMGEN
                                                                       Homo sapiens
                                                                                           US6291662-B1
                                                                                                                                        22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-1999
                                                                                                                                                                        06-AUG-1990;
22-JUL-1994;
                                                                                                                                                                                                                       29-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                            02-DEC-1985
                                                                                                                                                               30-MAR-1987
                                                                                                                                                                                                05-DEC-1984
                                                                                                                  18-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX16271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XEXEXEX
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purities so as to provide economical pharmaceutical compositions. (B) is resistant to heat, acid, and a variety of proteolytic enzymes, is thermodynamically stable in extracellular conditions, and exhibits a high degree of self assembly forming an active tertiary structure in the absence of blochemical stimuli. The present sequence represents the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of a mammalian sering processe inhibitor (B). The DNA sequences and recombinant methods allow manufacture of a class of inhibitors of e.g. cathepsin G, elastase, and trypsin, with different specificities. The recombinant serine protease product can be directed to act intracellularly or extracellularly and is useful in treating conditions caused by a disturbance in the native protease/protease inhibitor balance such as emphysema, arthritis, glomerulonephitis, peridontiis, muscular dystrophy, tumour invasion, sepsis, and acute leukemia. (A) allows (B) to be recombinantly produced in sufficient quantities and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a DNA sequence (A) encoding an analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 receararegacegeceagreraaceagarereaariecreraregerareregeaar 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 361
Serine protease inhibitor; human; emphysema; arthritis; peridontitis; muscular dystrophy; tumour invasion; glomerulonephritis; sepsis; acute leukemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 AAGCCAGGIICTIGICCTATTAICTIGATICGTIGCGCTAIGTIAAACCCACCTAACCGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA sequence encoding mammalian serine protease inhibitor useful for recombinantly producing inhibitors with different specificities and treating diseases such as emphysema, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 460 BP; 123 A; 114 C; 125 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscular dystrophy, and tumour invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Column 37-38; 37pp; English.
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This invention relates to new purified and isolated mammalian serine protease inhibitor proteins which comprise at least 8 cysteine residues and no more than 107 amino acids. The protease inhibitors are capable of inhibiting chymotrypsin and elastase. Sequences AAC97526 - AAC97531, AAC97574 and AAC97641 represent DNA encoding the protease inhibitors of the invention, and include oligonucleotide protease unbibitors of the invention, and include oligonucleotide requences used in the isolation and characterisation of the proteins. Finers AAC97535 - AAC97537 and AAC95582 - AAC97613 are used in the construction of DNA encoding the protease inhibitors of the invention and various other peptides used in the isolation of the protease inhibitors have cytostatic and anti-inflammatory activity. The protease inhibitors protein is useful for treating a protease inhibitor protein is useful for treating a protease inhibitor protein is useful for treating a protease acidited condition, which includes protease mediated tissue destruction, e.g. emphysema, arthritis, glomerulonephritis, producing the proteins eared and proteins muscular dystrophy or tumour invasion. It is also useful represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCGGCGGAACTTC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 IGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 recgaraticak ceccaciórara ceacatercara recretare de recesera de 121
                                                                                                               Serine protease inhibitor; cytostatic; anti-inflammatory; arthritis; protease mediated tissue destruction; emphysema; glomerulonephritis; periodontitis; muscular dystrophy; tumour invasion; chymotrypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New serine protease inhibitors and DNA sequences for treating a protease-mediated condition or tissue destruction e.g. emphysema tumor invasion and for recombinant production of inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32.2; DB 21; Length 460;
Pred. No. 0.72;
0; Mismatches 68; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thompson RC;
                                                                            DNA encoding OmpA secretory leukocyte protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 460 BP; 123 A; 114 C; 125 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stetler GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins, especially by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Column 37-38; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eisenberg SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 GCTTGTTTCGTTCCACAATAA 203
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51.8%;
                                                                                                                                                                                                                                                                                                                                                                                              84US-0678822
85US-0803471
                                                                                                                                                                                                                                                                                                                                                                                                                                     86US-0890526.
87US-0031846.
                                                                                                                                                                                                                                                                                                                                       91US-0712354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87US-0082962
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOULDER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-678667/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bandyopadhyay
                                                                                                                                                                              elastase; ds
                                       27-FEB-2001
                                                                                                                                                                                                                                                                                                                                       07-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1986;
30-MAR-1987;
                                                                                                                                                                                                                                                                                                17-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                            03-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1984
02-DEC-1985
                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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or

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New DNA sequences, useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, e.g. leukocyte elastase or trypsin -
                                                                                                                   Serine protease inhibitor protein; recombinant; leukocyte elastase; trypsin; secretory leukocyte protease inhibitor; SLPI; ds.
                                                                                                                                                                                                                                                                                                         Stetler GL, Thompson RC
                                                                                                  DNA sequence coding for ompA SLPI.
                                                                                                                                                                                                                                                                                                         Bandyopadhyay PK, Eisenberg SP,
                                            AAI67582 standard; DNA; 460 BP.
422 TCTTGTGTTTCCCCGGTAAAA 442
                                                                                                                                                                                                                               90US-0563832.
94US-0279056.
84US-0678222.
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                                                                                                                                                                                                                                                                      86US-0890526
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                           WPI; 2001-637974/73
                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN
                                                                                                                                                                 US6291662-B1
                                                                                                                                                                                                     22-SEP-1998;
                                                                                 11-FEB-2002
                                                                                                                                                                                                                                          22-JUL-1994;
                                                                                                                                                                                                                                                  05-DEC-1984;
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                                                                                                                                                                                                                                                           02-DEC-1985
                                                                                                                                                                                    18-SEP-2001
                                                              AAI67582;
                           RESULT 41
                                    AAI67582
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Example 3; Column 36; 37pp; English.

The invention relates to a DNA sequence encoding an analog of a mammalian serine protease inhibitor protein. The analog comprises at least eight cysteine residues and possesses serine protease inhibitor activity, and at least one operational element consisting of a promoter, an operator, a leader sequence, a Shine-Dajarno sequence, a ribosome binding site or a terminator codon. The DNA is useful in recombinant DNA techniques for directing the production of a serine protease inhibitor protein, .g. leukocyte elastase or trypsin. The present sequence represents the NA sequence coding for ompA-secretory leukocyte protease inhibitor

Sequence 460 BP; 123 A; 114 C; 125 G; 98 T; 0 other;

ö TGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGGTATG 182 63 AAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGT 122 302 AAACCGGGTAAATGCCCGGTAACCTATGGCCAGTGTCTGATGCTGAACCCGCCGAACTTC 361 362 receaaaredaceeccaereraaaceagarereaaarecrerareeerarerececcaaa 421 Gaps .. 0 15.6%; Score 32.2; DB 22; Length 460; 51.8%; Pred. No. 0.72; 68; Indels 0; Mismatches 183 GCTTGTTTCGTTCCACAATAA 203 73; Conservative Local Similarity Query Match 123 Matches

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Gaps

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422 TCTTGTGTTTCCCCGGTAAAA 442

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RESULT 43
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTAC 61
                                                                                                                              Staphylococcus aureus DNA for cellular proliferation protein #34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 23; Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98; Indels
                                                                                                                                                                 Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; Seg ID No 4199; 511pp; English.
                 AAS51617 standard; DNA; 546 BP.
                                                                                                                                                                                                                                                                                                                                                                                           23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                             2000US-191078P.
                                                                                          13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU33758
                                                                                                                                                                                                                                                              WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2000;
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                                                                                                                                                                                                                                                                                                    27-SEP-2001
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AAS51617/c
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the companies. Their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are setherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella premunoniae, Pseudomonasa aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Con essential prokaryotic cellular proliferation protein.

Con essential prokaryotic cellular proliferation protein.

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Con fund directly from MIPO at a contained in electronic form the principle directly from MIPO at a contained in electronic forming in the principle directly from MIPO at a contained in electronic forming in the principle directly from MIPO at a contained in electronic forming in the property of the principle directly from AIPO at a contained in electronic forming in the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the principle data for the property of the p
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252 TACCACATACCATGATTCATCTGTCATGATTAATTCCACTAAAACATATCCAGGAATGT 193
                                                                                                                                  192 TITITIAACGGIIGITITAGCITIACCATCITIAACTIGAGTITCTICTICTICCGGIAT 133
                                                                               TIGITIGAAGGACACIGATIGICCAGGIAICAAAAAGIGCIGIGAAGGIICCIGCGGIAI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus DNA for cellular proliferation protein #1029.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                     AAS54717 standard; DNA; 549 BP.
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2000US-207727P.
2000US-242578P.
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2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-611495/70.
                                                                                                                                                                                             182 GGCTTGTTT 190
                                                                                                                                                                                                                                                   132 GACTACTCT 124
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26-MAY-2000;
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22-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS54717;
                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCG 121
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14-AUG-2000; 2000US-0225758.
14-AUG-2000; 2000US-0225759.
18-AUG-2000; 2000US-022679.
22-AUG-2000; 2000US-022679.
22-AUG-2000; 2000US-0226868.
22-AUG-2000; 2000US-0227182.
23-AUG-2000; 2000US-0227182.
23-AUG-2000; 2000US-0228924.
01-SEP-2000; 2000US-0228934.
01-SEP-2000; 2000US-0228934.
01-SEP-2000; 2000US-0228934.
01-SEP-2000; 2000US-0228959.
05-SEP-2000; 2000US-0228959.
06-SEP-2000; 2000US-0228959.
06-SEP-2000; 2000US-022896.
06-SEP-2000; 2000US-022896.
08-SEP-2000; 2000US-0231242.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231289.
14-SEP-2000; 2000US-0231289.
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25-SEP-2000; 2000US-0234997.
26-SEP-2000; 2000US-0234999.
27-SEP-2000; 2000US-0235984.
27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235834.
29-SEP-2000; 2000US-0235835.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236368.
29-SEP-2000; 2000US-0236369.
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14-SEP-2000; 20000S-0232399.
14-SEP-2000; 20000S-0233400.
14-SEP-2000; 20000S-0233401.
14-SEP-2000; 20000S-023363.
14-SEP-2000; 20000S-023364.
14-SEP-2000; 20000S-0233654.
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02-0CT-2000; 2000US-0237037.
02-0CT-2000; 2000US-0237038.
02-0CT-2000; 2000US-0237040.
13-0CT-2000; 2000US-0239935.
13-0CT-2000; 2000US-0239935.
20-0CT-2000; 2000US-0239937.
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20-OCT-2000; 2000US-0241785.
20-OCT-2000; 2000US-0241786.
20-OCT-2000; 2000US-0241808.
20-OCT-2000; 2000US-0241809.
20-OCT-2000; 2000US-0241809.
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2000US-0241221.
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2000US-0246476
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2000US-0246478.
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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                                                                                                       312 ATTTGGCTTAGACCCTGCACACAGAACCTACAAAACCAGTAACGCCTGGTGTATTTCT 253
                                                                                                                                  62 TAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCAACCTAACCG 121
                                                                                                                                                        252 TACCACATACCATGATTCATCTGTCATGATTAATTCCACTAAAACATATCCAGGGAATGT 193
                                                                                                                                                                                  122 IIGITIGAAGGACACIGATIGICCAGGIAICAAAAAGGCIGGGAAGGIICCIGCGGIAI 181
                                                                                                                                                                                                         192 TİTİTİAACGGTIGTİTTAGCİTTACCATCTTTAACTİGAGTİTCTTCİİÇTİCĞGIAY 133
                                                                                  2 ATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTAC 61
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20301.
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                .;
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                                 Ouery Match 15.6%; Score 32.2; DB 23; Length 549; Best Local Similarity 48.1%; Pred. No. 0.77; Matches 91; Conservative 0; Mismatches 98; Indels 0
           Sequence 549 BP; 207 A; 73 C; 122 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                      AAK65489 standard; DNA; 16605 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000US-0214898.

07-JUL-2000; 2000US-0216647.

07-JUL-2000; 2000US-0216680.

11-JUL-2000; 2000US-0217497.

11-JUL-2000; 2000US-0217497.

14-JUL-2000; 2000US-0217497.

14-JUL-2000; 2000US-021890.

26-JUL-2000; 2000US-0220963.

14-AUG-2000; 2000US-0220963.

14-AUG-2000; 2000US-0226118.
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2000US-0190076

2000US-0198123

2000US-0205515

2000US-0214886

2000US-0214886
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2000US-0225447.
2000US-0225757.
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                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                                                                                   182 GGCTTGTTT 190
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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07-JUN-2000;
28-JUN-2000;
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09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 20301; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Barash SC, Ruben SM;
                                                       2000US-0249208.
2000US-0249209.
2000US-0249211.
2000US-0249211.
2000US-0249212.
2000US-0249213.
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                                                                                                                                                                  2000US-0249215.
2000US-0249216.
2000US-0249217.
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08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
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2000US-0250391.
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2000US-0251988.
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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4064 TGGGGCCTTATAGCTGGGACACTGACGCTCAAAATACCAGGAGCTGCTGGAATGGGTATT 4123
                                         115 CTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCT 174
                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41861.
                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                               AAK87049 standard; DNA; 16605 BP.
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14-AUG-2000; 2000US-0225270.

14-AUG-2000; 2000US-022547.

14-AUG-2000; 2000US-0225757.

14-AUG-2000; 2000US-0225757.

14-AUG-2000; 2000US-0225759.

18-AUG-2000; 2000US-0225759.

22-AUG-2000; 2000US-0225779.

22-AUG-2000; 2000US-0225779.
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07-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-021487.
11-JUL-2000; 2000US-0214487.
14-JUL-2000; 2000US-0218290.
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26-JUL-2000; 2000US-0220964.
14-AUG-2000; 2000US-0224518.
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16-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0190076.
18-APR-2000; 2000US-0198123.
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28-JUN-2000, 2000US-0214886.
30-JUN-2000, 2000US-0215135.
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14-AUG-2000; 2000US-0225266.
14-AUG-2000; 2000US-0225267.
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2000US-0229345
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14-AUG-2000; 2000US-0225213
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                                                                                                                            4124 GTAATATGTATGGT 4137
                                                                                                    175 GCGGTATGGCTTGT 188
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01-SEP-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16605 BP; 4009 A; 3696 C; 4212 G; 4688 T; 0 other;
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Matches

Query Match Best Local Similarity 52.23 Matches 70; Conservative

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PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0220437.
PR 08-SEP-2000; 2000US-0211243.
PR 08-SEP-2000; 2000US-0211244.
PR 08-SEP-2000; 2000US-0211244.
PR 08-SEP-2000; 2000US-0211244.
PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
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PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
PR 14-SEP-2000; 2000US-021390.
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PR 14-SEP-2000; 2000US-021390.
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PR 25-SEP-2000; 2000US-021390.
PR 25-SEP-2000; 2000US-021390.
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PR 25-SEP-2000; 2000US-021390.
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PR 25-SEP-2000; 2000US-021499.
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PR 25-SEP-2000; 2000US-021499.
PR 25-SEP-2000; 2000US-021499.
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PR 25-SEP-2000; 2000US-021499.
PR 25-SEP-2000; 2000US-021499.
PR 25-SEP-2000; 2000US-021499.
PR 25-SEP-2000; 2000US-
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
compression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and canner metatesases of haematopoietic decisions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to AAK87694 represent human immune/heematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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                              2000US-0249217.
2000US-0249218.
2000US-0249244.
2000US-0249245.
2000US-0249265.
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2000US-0249299.
2000US-0249300.
2000US-0250160.
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2000US-0251030.
2000US-0251988.
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2000US-0251479.
2000US-0251856.
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2000US-0251989.
2000US-0251990.
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05-JAN-2001; 2001US-0259678.
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17-NOV-2000;
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4064 TGGGGCCTTATAGCTGGGACACTGACGCTCAAATACCAGGAGCTGCTGGAATGGGTATT 4123

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원 상 원

55 TGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCAC 114

Query Match
Best Local Similarity 52.2%; Pred. No. 4.4;
Matches 70; Conservative 0; Mismatches 64; Indels 0;

0; Gaps

BP.

ABA18664 standard; DNA; 3496

ABA18664;

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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                   prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 ACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAAC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 AATAAGAGTGATTCTTGTGTATTGATCTTGTATCCTGCCACTATCTTAAATTCACTTAAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                   Human prostate expression marker cDNA 53531.
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                                                                                                                                                                                       pharmacogenomic marker; gene; ss
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1 Similarity 63.9%;
46; Conservative
                                  ABV53540 standard; cDNA; 612
                                                                                                                                                                                                                                                                                                                                                                              2000US-189862P.
2000US-207454P.
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                                                                                                  (first entry)
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Best Local Similarity
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25-MAY-2000;
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                                                                  ABV53540;
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RESULT 47 ABA18664/c

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immunosuppressive, antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarchritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                           nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                       Human nervous system related polynucleotide SEQ ID NO 10995.
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2000US-0217496.
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2000US-0231413
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                                     (first entry)
                                                                                                                                                                                WO200159063-A2.
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18-AUG-2000; 2
22-AUG-2000; 2
22-AUG-2000; 2
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14-AUG-2000;
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01-SEP-2000;
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                                                                                                                                                            Homo sapiens.
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07-JUN-2000;
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26-JUL-2000;
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                                                                              Human;
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26-SEP-2000; 2000US-02343484.
27-SEP-2000; 2000US-0235834.
29-SEP-2000; 2000US-0235834.
29-SEP-2000; 2000US-0235836.
29-SEP-2000; 2000US-0236369.
29-SEP-2000; 2000US-0236369.
29-SEP-2000; 2000US-0236369.
29-SEP-2000; 2000US-0236369.
29-SEP-2000; 2000US-023639.
29-SEP-2000; 2000US-023639.
20-OCT-2000; 2000US-0237031.
20-OCT-2000; 2000US-023935.
20-OCT-2000; 2000US-023937.
20-OCT-2000; 2000US-023937.
20-OCT-2000; 2000US-024180.
20-OCT-2000; 2000US-024180.
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20-OCT-2000; 2000US-024677.
08-NOV-2000; 2000US-024652.
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08-NOV-2000; 2000US-024652.
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17-NOV-2000; 2000US-0249264.
17-NOV-2000; 2000US-0249265.
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17-NOV-2000; 2000US-0249217
17-NOV-2000; 2000US-0249218
17-NOV-2000; 2000US-0249244
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17-NOV-2000; 2
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25-SEP-2000;
25-SEP-2000;
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21-SEP-2000;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The disquesis, treatment and prevention of: (a) cancer, e.g. breast on the disquesis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone warrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune characters e.g. Addison's disease, allergies, autoimmune contiss, (c) cardiovascular disorders such as mycoardial ischaemias; (c) cardiovascular disorders such as mycoardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.

CC (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal and parasitic infections.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1085 GITCTGGITCTAGGICAAGGCACAAATAGIGTATTITCATTTTCCTGITCTACATGCTTA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 GCTCAAGAACCAGTTAAAAGGTCCTGTGTCTAAGCCAGGTTCTTGTCCTATTATCTTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 ATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1025 ATAGTCAGTGAAATATTTTGCCCAAGAGCCCATGCTATGTTGGATTTTAATTACAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 10995; 1701pp + Sequence Listing; English.
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Best Local Similarity 49.4%; Pred. No. 6.2;
Matches 79; Conservative 0; Mismatches 81; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3496 BP; 1089 A; 587 C; 579 G; 1241 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 ATCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        965 AAATAAAAGCTCTGCTGATGGTCAGGCAAAATTATTGCT 926
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                01-DEC-2000; 2000US-0250391.

01-DEC-2000; 2000US-02510160.

05-DEC-2000; 2000US-0251030.

05-DEC-2000; 2000US-0251988.

06-DEC-2000; 2000US-0251479.

06-DEC-2000; 2000US-0251868.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-0251869.

08-DEC-2000; 2000US-025189.

08-DEC-2000; 2000US-025189.

08-DEC-2000; 2000US-025199.

08-DEC-2000; 2000US-025199.
                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
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149 996

18-SEP-2002 (first entry)

Mycoplasma genitalium genome.

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Costeoblast formation or osteoporosis; or osteoblast formation or osteoporosis; or costeoblast formation or osteoporosis; or costeoblast formation or osteoporosis; or costeoblast formation or osteoporosis; or conditions or monitoring the progression of bone tissue deposition.

Specific conditions include postmenopausal osteoporosis, glucocorticoid osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drugal-induced abnormalities in bone formation or bone loss, conditions that involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis), skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome or fibrous dysplasia. The present sequence is that of an osteoblast differentiation associated CDNA marker of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of genes and their expression profiles associated with osteoblast differentiation for screening modulators bone formation, for diagnosing or treating e.g. osteoporosis, or as markers for the differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 AGGICCIGIGICIACIAAGCCAGGIICTIGICCIAITAICITGATICGIIGCGCIAIGII 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to genes and their expression profiles are used
                                         Human; osteoblast; stem cell differentiation; bone tissue deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (a) screening modulators of precursor stem cell differentiation into osteoblasts, or bone tissue deposition;
(b) diagnosing abnormal deposition of bone tissue, abnormal rate of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Jaiswal N, Einstein R, Houghton A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63769 CAGGCCACTGCGCTTCAGCCTGGGTGACAGCCAAGACCTTATCTCAAAAAG 63820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 AAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAG 158
Human osteoblast differentiation related cDNA SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 86; 78pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 580073
                                                                     osteoporosis; osteopathic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                   Axelrod DW, Cook JS,
                                                                                                                                                                                                                                                                        18-DEC-2000; 2000US-255882P. 24-APR-2001; 2001US-285691P.
                                                                                                                                                                                                                                 18-DEC-2001; 2001WO-US48276.
                                                                                                                                                                                                                                                                                                                                                        (PROC ) PROCTER & GAMBLE CO.
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                                                                                                                                                                                                                                                                                                                                         (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-557663/59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     process
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"Previously identified as MORF-19823, MORF-20080 and MORF-20081, the encoded protein shows 33.04 percentage identity to 5,10-methylene-tetrahydrofolate dehydrogenase (folD) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Previously identified as MORF-20078, the encoded protein shows 35.43 percentage identity to the Bacillus subtilis hypothetical protein covered in accession number GB:D26185_102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded protein shows 31.50 percentage identity to the ribosomal protein S6 modification protein (rimK) from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MORF-20093, the encoded protein shows 46.84 percentage identity to GTP-binding protein from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note = "Previously identified as MORF-20092, the encoded protein shows 45.96 percentage identity to fructose-bisphosphate aldolase (tsr) from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Previously identified as MORF-20084, the encoded protein shows 32.23 percentage identity to transport ATP-binding protein (msbA) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Previously identified as MORF-20099, the encoded protein shows 26.82 percentage identity to ATP-dependent nuclease (addA) from B. subtilis"
                                                                                                                                                                                                                                                                                      /note= "Previously identified as MORF-20076, the encoded protein shows 27.59 percentage identity to thymidylate kinase (CDC8) from Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Previously identified as MORF-20079, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Previously identified as MORF-20080, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Previously identified as MORF-19826 and
                                             M. genitalium; DNAA; DNA gyrase; origin of replication; megabase shotgun sequencing method; open reading frame; ORF; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded protein shows 25.73 percentage identity to DNA primase (dnaE) from Clostridium acetobutylicum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (14396..15217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (13570..14247)
                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= i
/label= MG032
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/label= MG012
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/label= MG023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= MG009
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/label= MG006
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                                                                                                                                                                                                                     .9184
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                                                                                                                                    Mycoplasma genitalium
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06-OCT-2000 (first entry)
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                 /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system permease protein C (potC) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Previously identified as MORF-20110, the encoded protein shows 26.51 percentage identity to spermidine/putrescine transport system permease protein (potB) from E. coli"
                                                                                                                                                                                                                                                                                                             /note= "Previously identified as MORF-19831 and MORF-20106, the encoded protein shows 43.20 percentage identity to glycerol-3-phosphate dehydrogenase (GUT2) from S. cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Previously identified as MORF-19832 and MORF-20108, the encoded protein shows 41.92 percentage identity to spermidine/ putrescine transport ATP-binding protein (potA) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Previously identified as MORF-20111, the encoded protein shows 29.45 percentage identity to spermidine/putrescine transport
                                                                                                                                                                    /note= "Previously identified as MORF-20102, the encoded protein shows 30.71 percentage identity to histidyl-tRNA synthetase (hisS) from Mycobacterium leprae"
                                                                                                                                                                                                                                                                                                                                                                               /note= "The encoded protein shows 48.86 percentage identity to phosphohistidinoprotein-hexose phosphotransferase (ptsH) from Mycoplasma
         /*tag= j
/label= MG033
/note= "Previously identified as MORF-20100, the
encoded protein shows 35.90 percentage
identity to glycerol uptake facilitator
(glpF) from B. subtilis"
complement (39873..40514)
                                                                                                 /note= "Previously identified as MORF-20101, the encoded protein shows 48.13 percentage identity to thymidylate kinase (tdk) from B. subtilis"
                                                                                                                                                                                                                                         /note= "Previously identified as MORF-20105, the encoded protein shows 46.83 percentage identity to glycerol kinase (glpK) from E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Previously identified as MORF-20112, the encoded protein shows 36.60 percentage identity to staloglycoprotease (gcp) from Pasteurella haemolytica" ent (56970..58310)
                                                                                                                                                                                                             complement (44751..46277)
                                                                                                                                                                                                                                                                                  complement (46268..47422)
                                                                                                                                                                                                                                                                                                                                                                                                                 capricolum"
                                                                                        /label= MG034
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                                                                                                                                                                                                                                                                                                    'label= MG039
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/label= MG042
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/label= MG043
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'label= MG046
 39242..39904
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276182 AACTAGTTAAGGAAACTGAAATTAGAAAACCAATTGGTTCTCCTTTTATTGTCTATTTT 276241
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                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 GCGCTATGTTAAACCCACCTAACCGTTGTTGAAGGACACTGATTGTCCAGGTATCAAAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                  /note= "Previously identified as MORF-20114 and MORF-20115, the encoded protein shows 44.78 percentage identity to purine-nucleoside phosphorylase (deoD) from E. coli" 59083..59754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Previously identified as MORF-19845, the encoded protein shows 28.84 percentage identity to glutamic acid specific protease (SPase) from Staphylococcus aureus"
                                                                                                                                                                                                                                                                                                                                                                                           /note= "Previously identified as MORF-20117, the encoded protein shows 81.03 percentage identity to deoxyribose-phosphate aldolase (deoC) from Mycoplasma pneumoniae"
                       "Previously identified as MORF-19834, MORF-20114 and MORF-20115, the encoded proshows 43.02 percentage identity to signal recognition particle protein (ffh) from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 AACCAGITAAAAGGICCIGIGICIACIAAGCCAGGIICTIGICCIAITAICIIGAIICGII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Previously identified as MORF-20136, the encoded protein shows 34.8 percentage identity to ribosomal protein S2 (rpS2) from Spirulina plantensis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Previously identified as MORF-20122,
encoded protein shows 30.25 percent
identity to the protein disclosed in
GB:D26185_99 from B. subtilis"
complement (65713..66249)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST, SEQ ID NO: 11985.
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (64898..65731)
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Pred. No. 41
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/label= MG057
/label= MG048
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'label= MG049
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/label= MG050
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/label= MG067
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                                                                                                                                               58117..59079
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                                                                                                                                                                                                                                                                                                  The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and cenomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 AGAAAGGGTTAAAGGCTGATGGTACCTAAAGCCTGGTACTTGAATTTTTGATCAAGATAAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 TIGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 cieccijaagijereticaltaeaekaaajgajeeragataatigajagareergigeite 266
                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 450 BP; 114 A; 89 C; 103 G; 140 T; 4 other;
                                                                                                                                                                               Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 11985; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein cDNA, SEQ ID NO: 213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.7%; Score 30.2; 50.3%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 AAAGTGCTGTGAAGGTTCCTGCGGTAT 181
     gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AACTGGATTTYTAGATAGAAGCTGGAT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH64937 standard; cDNA; 1489 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.3%;
                                                                                                      21-FEB-2000; 2000EP-0200610.
                                                                                                                               99US-0122487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.39
Matches 74; Conservative
                                                                                                                                                                                                         WPI; 2000-500381/45.
                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                              26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2001
                             Homo sapiens
                                                      EP1033401-A2
                                                                              06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENSET; ss.
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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing that expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the used as DNA probes in diagnostic assays to detect and quantitate the used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to detentine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and activity. The present eventual and activity. The production of antibodies and in assays modulators (agonists and activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; kinase; enzyme; homeodomain-interacting protein kinase; testis;
brain medulloblastoma; infant brain; schizophrenic brain; retina; gene;
germinal center B cell; colon; liver; chromosome 1; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 AGAAAGGGTTAAAAGGCTGATGGTACCTAAAGCCTGGTACTTGAATTTTGATCAAGATAAG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 TIGCGCIAIGIIAAACCCACCIAACCGIIGIITGAAGGACACIGAIIGICCAGGIAICAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 ciécerraagrierericarracaéaaargarecragaraarraaragarecréregrie 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Full length GENSET human nucleic acids encoding potentially secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 AGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antagonists) of GENSET polypeptide expression and activity. present sequence is a GENSET nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jobert S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 30.2; DB; Pred. No. 5.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 766-767; 921pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 AACTGGATTTCTAGATAGAAGCTGGAT 291
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50.38;
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06-MAR-2000; 2000US-0187470.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J,
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WO200142451-A2.
                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
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/*tag= i | standard name= "Single nucleotide polymorphism" | standard name= "Single nucleotide polymorphism" | standard name= "Single nucleotide polymorphism" | state. | 2 | state. | 2 | state. | 2 | state. | 2 | state. | 2 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | state. | 3 | 
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/standard_name= "Single nucleotide polymorphism"
replace(5330,G)
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/standard_name= "Single nucleotide polymorphism"
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/standard_name= "Single nucleotide polymorphism"
replace(11773,G)
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gandard name= "Single nucleotide polymorphism"
replace(12886,G)
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3566._14639
                                                                                /product= "Human kinase"
/note= "Contains 14 introns"
2490..3565
SNP; single nucleotide polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                 replace (14130..14131, A-)
                                              Location/Qualifiers
2490..33161
                                                                                                                                                                                                replace (4452, T)
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/number= 3
18502..18686
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18687..18998
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26596..26730
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/ number = 13
/ nounber = 13
/ note = "12403-12436 is the location given in the
specification, but this location does not concur with
the protein encoded by this sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "32004-32171 is the location given in the specification, but this location does not concur with the protein encoded by this sequence" 32172..32402
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/note= "32441-22617 is the location given in the specification, but this location does not concur with the protein encoded by this sequence" 32618..32672
                                                                                                           /cons_gplice= (5'site:YES,3'site:NO)
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                                                                                                                                                                                                                                      /number= 10
/cons splice= (5'site:NO,3'site:YES)
/note= "The location for this exon was given as
31075-31157 in the specification"
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/number= 8
26731..29338
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/number= 12
32403..32436
/*tag= af
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/number= 10
31651.31857
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/*tag= z
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32004..32171
/*tag= ad
/number= 12
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/*tag= aj
/number= 15
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1858..32003
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/number= 9
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/number= 9
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number= 13
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Beasley EM;
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Matches
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                                                                                                      The present sequence is the gene for a human kinase, which is related to the homeodomain-interacting protein kinase subfamily. The kinase and its DNA sequence can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate kinase activity in cells and tissues that express the kinase. Experimental data indicates expression of the human kinase in testis, brain medulloblastomas, infant brain, schizophrenic brain, retina, germinal center B cells, colon and liver. The human kinase gene is
                        Human kinase protein, related to homeodomain-interacting protein kinase subfamily, useful as a model for developing human therapeutic targets and serves as a target for human therapeutics
                                                                                                                                                                                                                                                                                                                                                                  12268 crccadarccadarccadarccadarrcagarrccacarrardargagagarranariggana 12209
                                                                                                                                                                                                                                                                                                                                                                                                                        12208 ACAGATCTTTCCGTGAAGAACCATCTAACTGGCCGTGTCTCCTCACAGAATACCCAGGTT 12149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene library containing sequences with specific 3'-ends and no polyA tail, encoding proteins involved in a wide range of cellular processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell metabolism; energy metabolism; fatty acid metabolism; synthesis; phospholipid metabolism; purine; pyrimidine; nucleoside; nucleotide; replication; transcription; translation; transport protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                               91 TTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTA 150
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                          31 CTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAAGTTCTTGTCCTATTATCTTGA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; liver; gene library; amino acid synthesis; binding protein;
                                                                                                                                                                                                                                                                                  14.7%; Score 30.2; DB 24; Length 36159; 49.1%; Pred. No. 17; cive 0; Mismatches 83; Indels 0;
                                                                                                                                                                                                                                                          Sequence 36159 BP; 8425 A; 6177 C; 6348 G; 10756 T; 4453 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine replication associated protein encoding cDNA SEQ ID 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12148 rcrcaaacracrrcaagreararcrecrrarrerrerrer 12106
                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 TCAAAAAGTGCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 97; 251pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAK53717 standard; cDNA; 344 BP
                                                                                  Claim 22; Fig 3; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2001; 2001DE-2003510
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                                                                                                                                                                                                                                                                                                                80; Conservative
                                                                                                                                                                                                                                     located on chromosome 1.
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                                                                                                                                                                                                                                                                                                     Local Similarity
     P-PSDB; ABB83490.
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                                                                                                                                                                                                                                                                                        Query Match
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purines/pyrimidines/nucleosides/nucleotides, DNA replication/transcription/translation, or is a transport/binding protein. (A) are produced that correspond to the 3'-end of mRNA but without the polyA tail. They can be prepared more efficiently and with less effort than conventional libraries. AAK53436-AAK54275 represent fragments of the gene library described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTGAAGGACACTGATT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 riagcigarcitrirccccardritaracaaccaraardrecricgcresacciders 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blackcurrant, fruit-specific promoter, RIB7 gene, transgenic plant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
This invention describes a novel gene library (A) comprises a gene
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                       sequence (or its part) encoding a protein involved in amino acid synthesis, cellular/energy metabolism, metabolism of fatty acids/phospholipids, synthesis or breakdown of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/codon_start= 3156
/coton_startive ATG translational start codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 344;
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blackcurrant and other non-climacteric fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 344 BP; 73 A; 78 C; 70 G; 123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blackcurrant fruit-specific RIB7 gene promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 GICCAGGIATCAAAAGIGCIGIGAAGGIICCIGCGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 Arcredaraccadadarrrcidrererececedade 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 29.8; 56.7%; Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT68952 standard; DNA; 5150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55; Conservative
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3156
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9717452-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATA_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2569 CTATTTAAACAAGACTICTAAGTTGTTTCAGGGATTATTATTCATATTTATCAATAAA 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating or diagnosing tumor or cancer (e.g. prostate cancer or breast cancer), or as vaccines for treating or preventing these diseases
                                                                                                                                                                                                                                                                                                                                                                                                  100 CTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAAGT 159
                                                                                                                                                                                                                                                                                                                                           Gaps
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expressed at negligible levels in other tissues of the blackcurrant plant. Its promoter region can be used to drive fruit-specific expression of cloned downstream DNA sequences in transgenic blackcurrant or other non-climacteric fruit as a means of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy;
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I, Leshkowitz D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 699; 186pp + Sequence Listing; English.
                                                                                                                                                                                               Sequence 5150 BP; 1599 A; 1069 C; 899 G; 1583 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J, Garcia PD, Kassam A, Lamson G, Drmanac R, kov R, Dickson M, Drmanac S, Labat I, Leshkow: Garcia V, Jones WL, Stache-Crain B, Scott EM;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate expressed polynucleotide SEQ ID NO 699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2509 ACTGAGAACTTTTCTCCGTGTTCTTCTTCTTACGAGAATA 2467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GCTGTGAAGGTTCCTGCGGTATGGCTTGTTTCGTTCCACAATA 202
                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                                                                                                                           46;
                                                                                                                                                                                                                                                                    Score 29.4; I
Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                               blackcurrant or other non-climacter
manipulating the ripening process.
                                                                                                                                                                                                                                                                14.3%;
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13-MAR-2001; 2001US-275688P.
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                                                                                                                                                                                                                                                                                                                                     57; Conservative
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                                                                                                                                                                                                                                                                                                  Similarity
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Crkvenjakov R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2002
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                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HXSE-)
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Transcription antitermination factor; NusG; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivities; osteomyelltis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis;
specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence encodes S. aureus NusG (transcription antitermination factor). The polynucleotides of the invention are used to detect Staphylococcus nucleic acids in a biological sample from an animal for diagnosing Staphylococcus infections. The polypeptides of the invention
                                                                                                                                                                                 291 ACTATITIAAATCATCTGGCTTACTAACAAACTITTTCCTGCATGTACTTCTTTCTGTG 350
                                                                                                                                                                                                                  98 CGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCAAAAA 157
                                                                                                                                                                                                                                                 351 TGTGATTTCAAATTAATTTTAATGTTTACTAAAACAAAGTTATCTACCATTTATTAAA 410
                                                                                                                                                 38 ACCAGITAAAGGICCIGIGICIACIAAGCCAGGIICIIGICCIAITAICIIGAIICGIIG 97
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. aureus DNA encoding transcription antitermination factor, NusG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the
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                                                                                   Score 29.2; DB 24; Length 756;
                                                                                                                  78; Indels
                                              Sequence 756 BP; 236 A; 138 C; 158 G; 214 T; 10 other;
                                                                                                                                                                                                                                                                                  158 GIGCIGIGAAGGIICCIGCGGIAIGGCIIGIIIC 191
                                                                                                                                                                                                                                                                                                                   411 ACTCAATTGTAGGCCAGGCGTGGTGGCTTACGTC 444
                                                                                                   Pred. No. 9;
0; Mismatches
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/product= "NusG"
                                                                                                                                                                                                                                                                                                                                                                                                   AAS00193 standard; DNA; 549 BP
                                                                                   14.2%;
                                                                                                   Local Similarity 49.4%;
les 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-2000; 2000WO-US23773.
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                                                                                                 Similarity
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                                                                               Query Match
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                                                                                                                Matches
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AAS00193/c
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             from an animal to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to a member of the Staphylococcus genus and for preventing or attenuating an infection caused by a member of the Staphylococcus genus e.g wound infection, cellulitis, burn infection, eyelid infection, food poisoning, joint infection, neonateal conjunctivitis, osteomyelitis, skin infection, scaled skin syndrome (also known as toxic epidermal neorosis, Ritter's disease and Lyell's disease), toxic shock syndrome and endocarditis. The polynucleotides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in in vitro and in vivo diagnostic and therapeutic methods.
used to detect anti-Staphylococcus antibodies in a biological sample
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                                                                                                                                                                                                                                                                                                                                                                                                     315 ATTTGGCTTAGACCCTGCACCTGCAGAACCTACAAACCAGTAACGCCTGGTGTATTTCT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAAACCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 TACCACATACCATGATTCATCTGTCATGATTAATTCCACTAAAACATATCCAGGGAATGT 196
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                   2 ATTCGAGCTCGGTACCATACCTGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTAC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus DNA for cellular proliferation protein #1363.
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                                                                                                                                                                                                                                                                                             14.1%; Score 29; DB 22; Length 549; 51.1%; Pred. No. 9.3; tive 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense, ds, prokaryotic cellular proliferation gene, antibiotic, antibacterial, drug design.
                                                                                                                                                                                                                                                            Sequence 549 BP; 206 A; 73 C; 125 G; 145 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS55051 standard; DNA; 549 BP.
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2000US-207727P.
2000US-242578P.
2000US-253625P.
                                                                                                                                                                                                                                                                                                                ilarity 51.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 rrrrrrakcagrc 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus.
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Matches 68; Conserv
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26-MAY-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential comparation of proteins. The prokaryotes used are Bacherichia coll, Staphylococus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to soreen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 ATTTGGCTTAGACCCTGCACCTGCAGAACCTACAAACCAGTAACGCCTGGTGTATTTCT 253
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                                                                                                                                                                                                                                                                                                                             of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             14.1%; Score 29; DB 23; Length 549;
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 549 BP; 208 A; 73 C; 122 G; 146 T; 0 other;
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0; Mismatches
Claim 27; Seq ID No 8688; 511pp; English.
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23-MAY-2000; 2000US-206848P.
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23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
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16-FEB-2001; 2001US-269308P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Conservative
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26-SEP-2000;
       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel annibiotics, the essential genes themselves and the discovery of novel annibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella Inventionias areupinosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen a wide variety of organisms. The present sequence encodes an essential prockaryotic cellular proliferation protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                  New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.1%; Score 29; DB 23; Length 549; 51.1%; Pred. No. 9.3;
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                                                                                                                                   Claim 27; Seq ID No 8956; 511pp; English.
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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 Xu HH;
                                 WPI; 2001-611495/70.
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                                                P-PSDB; AAU37460
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Yamamoto RT,
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16-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0199874.
19-MAY-2000; 2000US-019123.
19-MAY-2000; 2000US-0209467.
28-JUN-2000; 2000US-0214886.
30-JUN-2000; 2000US-0216647.
07-JUL-2000; 2000US-0216647.
11-JUL-2000; 2000US-0217680.
11-JUL-2000; 2000US-0217687.
11-JUL-2000; 2000US-0217687.
11-JUL-2000; 2000US-0217687.
11-JUL-2000; 2000US-02174967.
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23-AUG-2000; 2000US-0227009.
30-AUG-2000; 2000US-022824.
01-SEP-2000; 2000US-0229343.
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01-SEP-2000; 2000US-0229345.
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05-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0239437.
06-SEP-2000; 2000US-0231242.
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14-AUG-2000, 2000US-0225268.
14-AUG-2000, 2000US-0225270.
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26-JUL-2000; 2000US-0220964
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14-AUG-2000; 2000US-0225266
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14-AUG-2000; 2000US-0225757.
14-AUG-2000; 2000US-0225758.
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18-AUG-2000; 2000US-0226279.
22-AUG-2000; 2000US-0226681.
22-AUG-2000; 2000US-0226888
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08-SEP-2000; 2000US-0231244
08-SEP-2000; 2000US-0231413
08-SEP-2000; 2000US-0231414
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08-SEP-2000; 2000US-0232081
12-SEP-2000; 2000US-0231968
14-SEP-2000; 2000US-0232397.
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14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232400.
14-SEP-2000; 2000US-02332401.
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02-OCT-2000; 2000US-0237039
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
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                                                                  2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
2000US-0246474.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) collynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of hematopoietic-derived cells. AAK64703 concers and cancer metastases of hematopoietic antigen genomic construction the present invention. AAK64950 and AAM82169.
                                                                                                                                                                                                                                                                                                        sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9370 gcricartritraaridegerrertraarrecagariatraeaccritaearecagaerr 9429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 TATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23387.
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 IGCATATGCTCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAAGCCAGGTTCTTGTCCTAT 82
                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 32145;
                                                                                                                                                                                                                                                                                                                                                        Sequence 32145 BP; 8777 A; 7496 C; 7117 G; 8755 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 42;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                14.1%; Score 29; 49.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCAGGTATCAAAAGTGCTGTGAAGGTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK68575 standard; DNA; 32145 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0190876.
18-APR-2000; 2000US-019076.
19-MAY-2000; 2000US-0190876.
19-MAY-2000; 2000US-0209467.
28-JUN-2000; 2000US-0215135.
07-JUL-2000; 2000US-0215135.
07-JUL-2000; 2000US-0216135.
07-JUL-2000; 2000US-021647.
07-JUL-2000; 2000US-0216487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
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2000US-0217496

11-JUL-2000;

Disclosure; SEQ ID NO 23303; 3071pp + Sequence Listing; English

25-SEP-2000; 2000US-023434; 25-SEP-2000; 2000US-0234999. 25-SEP-2000; 2000US-0234999. 27-SEP-2000; 2000US-0235834; 27-SEP-2000; 2000US-0235834; 29-SEP-2000; 2000US-0235836; 29-SEP-2000; 2000US-0235636; 29-SEP-2000; 2000US-0236369; 29-SEP-2000; 2000US-0236369; 29-SEP-2000; 2000US-0236369; 29-SEP-2000; 2000US-023637; 02-OCT-2000; 2000US-0237039; 02-OCT-2000; 2000US-0237039; 02-OCT-2000; 2000US-0237039; 02-OCT-2000; 2000US-023935; 02-OCT-2000; 2000US-0241869; 20-OCT-2000; 2000US-0241869; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241806; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241806; 20-OCT-2000; 2000US-0241806; 20-OCT-2000; 2000US-0241806; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241809; 20-OCT-2000; 2000US-0241806; 2000US-0244617. 06-SEP-2000; 2000US-0230431.
06-SEP-2000; 2000US-023304318.
08-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-023131143.
08-SEP-2000; 2000US-0231311413.
08-SEP-2000; 2000US-0232081.
12-SEP-2000; 2000US-0232081.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-0232398.
14-SEP-2000; 2000US-02323063. 2000US-0218290. 2000US-0220963. 2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0227009 2000US-0228924 2000US-0229383 2000US-0229344 2000US-0229345 2000US-0229509 2000US-0229509 14 - JUL - 2000; 2 6 - JUL - 2000; 2 6 - JUL - 2000; 2 6 - JUL - 2000; 2 14 - AUG - 2000; 

2000US-0246477 2000US-0246478 2000US-0246523 2000US-0246525 2000US-0246525 2000US-0246527 2000US-0246527 2000US-0246527 2000US-0246610 2000US-0246610 2000US-0246610 2000US-0246610 2000US-024610 2000US-0249208 2000US-0249210 2000US-0249213 2000US-0249213 2000US-0249213 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249214 2000US-0249216 2000US-0249216 2000US-0249297. 2000US-0249299. 2000US-0249300. 2000US-0250160. 2000US-02510301. 2000US-02510301. 2000US-0249244. 2000US-0249245. 2000US-0249264. 2000US-0249265. 2000US-0256719. 2000US-0251479. 2000US-0251856. 2000US-0251868 2000US-0251869 2000US-0251989 2000US-0251990 2000US-0254097 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 10-DEC-2000; 2 00-DEC-2000; 2 05-DEC-2000; 2 05-DEC-2000; 2 06-DEC-2000; 2 08-DEC-2000; 2 08-DEC-2000; 2 08-DEC-2000; 2 88 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 200 - NOV - 2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 17-NOV-2000; 2 

(HUMA-) HUMAN GENOME SCI INC

Ruben SM Barash SC, Rosen CA,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 23387; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations of deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,

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Indels

1.9e+02; thes 65;

Mismatches

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Conservative

68;

Matches

Pred. No.

51.1%;

Best Local Similarity

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0
                                                                                                       represent sequences used in the exemplification of the present invention.
                 cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                 9310 rrccrcrccrcractracccarcrararcrcrrrrraacaagrcrcrrrraafcarrarcrararcrarr 9369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9370 GCTCATTTTTTAATGGGGTTGTTTAATTGCAGATATTAGACCTTAGATGGATCCAGAGTT 9429
diagnose and treat immune/haematopoietic-related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                        83 TATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTG 142
                                                                                                                                                                                                                                                                                                                              82
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequence useful in the identification or Lactococcus
lactis and related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese; ds.
                                                                                                                                                                                                                                                                                                                           TGCATATGCTCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTAT
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                    DB 22; Length 32145; 42;
                                                                                                                                                             Sequence 32145 BP; 8777 A; 7496 C; 7117 G; 8755 T; 0 other;
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                       75;
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                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9430 rgcaaararrrgrcrcarrrrgraggrr 9458
                                                                                                                                                                                                                    Score 29;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 TCCAGGTATCAAAAAGTGCTGTGAAGGTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sorokine A, Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 1; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA90521 standard; DNA; 2365589
                                                                                                                                                                                                                    14.18;
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                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-043418/06.
                                                                                                                                                                                                                                           Similarity
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Local S....
74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2001
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                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                          Matches
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Db 2287134 GTTACGACAGGTGCGATAGGGGTAACTTCTGTATCTGCGACTTAAGTCGCCTATGTAAAA 2287075
                                     Db 2287194 AAGAGGTAAATTATGGAAATGAATTTGAAAAAAAAAATCTTTGTCTTATCAACTTTACTT 2287135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding factors, basic helix-loop, helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant, transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain, AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to novel plant transcription factors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide encoding a plant transcription factor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                             94 GITGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACACTGATTGTCCAGGTATCA 153
34 AAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTC 93
                                                                                                                                                                                                                                                                                                                                                                                                                            Eucalyptus grandis transcription factor DNA sequence #219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Pages 103-104; 747pp; English.
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                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                        AAC56088 standard; DNA; 1677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2000; 2000WO-US06112.
                                                                                                                                                                                                     Db 2287074 ACAAGITCAGITA 2287062
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                154 AAAAGTGCTGTGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McGrath A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-579369/54
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                                                                                                                                                                                                                                                                  RESULT 62
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DB 21; Length 1677;

Score 28.8;

14.08;

Query Match

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sequence (ABA90221) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of woment and composition of woments.

The present invention is related to a Lactococcus lactis nucleotide

production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent
WO200177334 (published 18-OCT-2001) which is available in electronic
format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 2365589 BP; 765914 A; 415261 C; 420487 G; 763927 T; 0 other;

14.1%; Score 29;

Query Match

DB 24; Length 2365589;

Sequence 1677 BP; 424 A; 371 C; 433 G; 449 T; 0 other;

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Length 464;

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Incleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contracting the probes with a collection of detectably labelled nucleic acids the probes with a collection of detectably labelled nucleic acids carived from mRNA of human breast. And then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence at a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the contraction, but was obtained in electronic format directly contraction.
                                                                                      1278 GIGAGICCICGACTGTCIGCCIGICTIALIALALIGACITGITITCCGAIGTTAAAAAGT 1337
                                                   GTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                      .,
                                                                                                                                                                                                                                                                                                                                                                                                        Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 2185; 327pp + sequence listing; English.
                     Indels
                                                                                                                                                                                                                                                                                                                                                                Human breast cell single exon nucleic acid probe #2185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            irom WIPO at ftp.wipo.int/pub/published_pct_sequences.
                 37;
 Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                              1338 CCTAGTCAATGAGAAGAGAGATTGCTT 1365
                                                                                                                          114 CCTAACCGTTGTTTGAAGGACACTGATT 141
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30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0631366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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58.0%;
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                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             disease; cancer; ss.
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Best Local Similarity
Matches 51; Conserv
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Sequence 464 BP; 112 A; 126 C; 88 G; 138 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                               TCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACAC 136
                                                                                             293 récretriceacagarraridecrecrecrecaagecerreacretagaargaagecre 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2243; 639pp + sequence listing; English.
                                   46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                        Human foetal liver single exon nucleic acid probe #2243.
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                                                                                                                             137 TGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGG 178
                                                                                                                                                            rdarrirccrescarcarscarsacrisasaassircasistics 394
   Score 28.4; DB 22;
Pred. No. 14;
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                                 0; Mismatches
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ilarity 54.9%; Pred. No. 14;
Conservative 0; Mismatches
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2000US-0207456.
2000US-0608408.
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1 Similarity 54.9%;
56; Conservative
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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Query Match
Best Local Similarity
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30-JUN-2000;
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                               Matches
                                                                                                                                                             353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 TCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACAC 136
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                                                                                                                                                            Probe #2155 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                   Human, gene expression, heart, microarray, vascular system, probe, cardiovascular disease, hypertension, cardiac arrhythmia, congenital heart disease, ss.
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    353 réartricérédearcardachdadadéreagierée 394

              353 TGATTTTCCTGGCATCATGCATGACTGAGAGGTCAGTGTGG 394
137 TGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
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                                                                                    ABA23689 standard; DNA; 464 BP
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2000US-0608408.
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                       23-JAN-2002 (first entry)
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30-JUN-2000;
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                                                                                                              ABA23689;
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Matches
                                                             RESULT 65
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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                   Human, brain expressed exon, gene expression analysis; probe; microarray, Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                             Human brain expressed single exon probe SEQ ID NO: 2199.
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AAK02208 standard; DNA; 464 BP
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26-MAY-2000; 2000US-0207456.
30-UTN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532366.
21-SFP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
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                                                                                                                                                                                                                                                                                                     epilepsy; cancer; ss.
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                                                           AAK02208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe #2168 for gene expression analysis in human cervical cell sample.
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                      Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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 Human bone marrow expressed single exon probe SEQ ID NO: 2212.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 464 BP; 112 A; 126 C; 88 G; 138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 TGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGG 178
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                                                                                                                                                                                                                                                                                                          analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Pred. No. 14;
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2000US-0234687.
2000US-0236359.
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2000US-0207456.
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                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                           WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                          WO200157276-A2
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                                                       Homo sapiens
                                                                                                                                                                                              27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                30-JUN-2000;
                                                                                                                                                                         03-AUG-2000;
21-SEP-2000;
                                                                                                                                         04-FEB-2000;
                                                                                                                                                    26-MAY-2000;
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                                                                                                09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa calls. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 ICCIATTATCTTGATTCGTTGCGTATGTTAAACCCACCTAACCGTTGTTGAAGGACAC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 464 BP; 112 A; 126 C; 88 G; 138 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                             26-MAY-2000; 2000US-0207456.
30-UIN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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54.9%;
30-JAN-2001; 2001WO-US00670.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000, 2000US-0608408.
33-AUG-2000, 2000US-0532366.
21-SEP-2000, 2000US-0234687.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG, Hanzel DK,
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Best Local Similarity
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13.8%; Score 28.4; D. 54.9%; Pred. No. 14; ative 0; Mismatches
25; SEQ ID No 2139; 322pp; English.
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26-MAY-2000; 2000US-207456P.
30-UTN-2000; 2000US-0608408.
03-AUG-2000; 2000US-23468P.
21-SEP-2000; 2000US-23468P.
27-SEP-2000; 2000US-23468P.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                         56; Conservative
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  Claim
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                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for prodicting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                   Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                  analyzing gene expression in human placenta
                                                                                                                                                          Claim 25; SEQ ID No 2275; 654pp; English.
                                                                                                                                                                                                                                                                                     Score 28.4;
Pred. No. 14
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                                                                     Chen W, Rank DR;
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26-MAY-2000; 2000US-0207456.
30-UTN-2000; 2000US-0608408.
03-MUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                           (MOLE-) MOLECULAR DYNAMICS INC
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1 Similarity 54.9%;
56; Conservative (
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                  04-OCT-2000; 2000GB-0024263.
       27-SEP-2000; 2000US-0236359.
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                                                                      Hanzel DK,
                                                                                              WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                        Query Match
                                                                       Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe breast. The probes at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, discorders of development, inflammatory diseases of the breast, fibrocytic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 464 BP; 112 A; 126 C; 88 G; 138 T; 0 other;
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probes, Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acide expressed in the human lung; measuring gene expression in a cample derived from human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising of a collection of detectably labeled nucleic acids derived from human lung cample array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, and (b) detecting specific hybridisation of detectably captured fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarray; having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases (COPD), interstital lung disease (LLD), familial idiopathic pulmonary disease. Hermannsky-pulmake syndrome, sarcoideds, pulmonary disease. Hermannsky-pulmake syndrome, sarcoideds, pulmonary diseases. Niemann-Pick disease. Hermannsky-pulmake syndromes and succession of the exons in the strain of the exons
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                                                                                                                                                The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertension
Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 TCCTATTATCTTGATTCGTTGCGCTATGTTAAACCCACCTAACCGTTGTTTGAAGGACAC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 recircificeaeaantarificerecieciecaageeerricaergradaarggaageerg 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosfs, ulunonary alveolar proteinosis, karagener syndrome, fibrocystic pulmonary dysplasia, primary cilary dyskinesis, pulmonary hypertens and hyaline membrane disease. The present sequence is a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the printed specification, but was obtained in electronic cormat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 464 BP; 112 A; 126 C; 88 G; 138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 TGATTGTCCAGGTATCAAAAGTGCTGTGAAGGTTCCTGCGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 reartriccredearcardcardachadaadarcadadaga 394
                                  measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                       Claim 1; SEQ ID No 2107; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA16089 standard; DNA; 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          haemosiderosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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08-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer differentially expressed nucleotide sequence #94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colon cancer; detect; differential expression; human; treatment; detect mutation; non-invasive diagnostic method; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-2000 (first entry)
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differentially expressing a number course sequence miles in the sequence and the expression levels in normal cells. The nucleotide sequence can be used as a source to primers and probes. The nucleotide sequence can be used as a source the phenotype of a cell by detecting the differential expression of the sequence relative to a normal cell. The probes derived from the sequence and also be used to determine the phenotype of cells in a sample. Probes and antibodies which hybridise to the nucleotide sequence can also be used to determine the phenotype of a cell. The primers are useful for used to determine the phenotype of a cell. The primers are useful for detecting a mutation in a test nucleotide sequence and also for detecting by the nucleotide sequence can also be used in a method to detect colon cancer. The diagnostic method is non-invasive and accurate for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopoiesis; myeloid deficiency; lymphoid cell deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, ss, gene, secreted protein, immune deficiency, viral infection, bacterial infection, fungal infection; autoimmune disorder, burn, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 TCAAGCTACAGGTAAAGGCTCTACCACCATTAAGGTATTGACTTATCCTATGAATTTGAT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 TCAAGAACCAGTTAAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCCTATTATCTTGAT 91
                                                                                                                                                                                                                                                                                           Astle JH, Burgess CC, Carroll E; ord DM, Lewis ME, Molino GA, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and proteins for identifying therapeutic agents useful for treating and diagnosing cancer, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a human nucleotide sequence which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.8%; Score 28.4; DB 21; Length 658; 62.9%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 658 BP; 195 A; 125 C; 130 G; 189 T; 19 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA for novel secreted protein, SEQ ID 510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 162; 345pp; English.
                                                                                                                                                                                                                                                                                                                 Dwivedi P, Ford DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK34741 standard; cDNA; 1636 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon cancer at an early stage.
                                                                                                                                             99WO-US19424.
                                                                                                                                                                                       98US-0098639
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                                                                                                                                                                                                                                                                                         Endege WO, Steinmann KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Conservative
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                                                                                                                                                                                                                                               (FARB ) BAYER CORP.
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                                                          WO200012702-A2.
                     Homo sapiens.
                                                                                                                                             30-AUG-1999;
                                                                                                                                                                                  31-AUG-1998;
                                                                                                                                                                                                          27-JAN-1999;
                                                                                                    09-MAR-2000
                                                                                                                                                                                                                                                                                                                                  Schlegel R;
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98WO-US25149.
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                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                          Steininger RJ, Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Conservative
                                                                                                                                                                                                                                                                                              Jacobs K,
                                                                                                                                                                                                                                                                                                                                        WPI; 1999-357809/30.
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                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY17228
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                                                                                                                                                                                                                                                                                Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2002
                                                                                                                                                                          24-NOV-1998;
                                                                                       Homo sapiens
                                                                                                                  WO9926961-A1
                                                                                                                                                                                                                      26-NOV-1997;
                                                                                                                                                03-JUN-1999
                                                                                                                                                                                                                                                                                                echtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS59216;
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                                                                                                                                                                                                                                                                                                                                                                The invention relates to 625 polymucleotides which have been derived from a variety of human tissue sources and which encode novel secreted proteins, their complements and sequences that hybridise to them.

C Also included are a vector comprising the polymucleotide, a host cell transformed with the vector, the proteins encoded by the conjunction of the proteins and identification of modulators of the proteins or the expression of the polymucleotides.

CC modulators of the proteins or the expression of the polymucleotide.

CC modulators can lso be used as probes for the identification of the polymucleotides can be used as probes for the identification.

CC and isolation of full length cDNA and genomic DNA. The polymucleotides and isolation of full length cDNA and genomic PNA. The protein cs useful in the treatment of various immune deficiencies and disorders (e.g. theumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating conditions (e.g. asthma). They are also useful for treating diseases, parkinson's disease), liver fibrosis, coaquiation disorders (e.g. hemophila), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of definitions incisions and ulcers. The proteins are also useful for tissue regeneration, for wound healing and in the treatment of definitions and conditions and ulcers. The proteins are also useful for definitions and ulcers. The proteins are also the proteins are also regulating heamatopolesis, for treating myeloid or lymphoid cell
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0
                                                                                                                                                                                                                                                                 Six hundred and twenty five polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1104 TCAAGCTACAGGTAAAGGCTCTACCACCATTAAGGTATTGACTTATCCTATGAATTTGAT 1045
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                                                                                                                                                                                            Resnick RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 TCAAGAACCAGTTAAAGGTCCTGTGTCTACTAAGCCAGGTTCTTGTCTTATTATCTTGAT 91
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                                                                                                                                                                                            Howes SH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein encoding DNA (clone yb8-1).
                                                                                                                                                                                              Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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Pred. No. 22
                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 273; 339pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX60810 standard; DNA; 1656 BP
                                                                                                                                                                                              Fechtel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding a secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%;
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                                                                                                      29-MAR-2001; 2001WO-US10295.
                                                                                                                                     06-APR-2000; 2000US-194941P
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                                                                                                                                                                (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Conservative
                                                                                                                                                                                                             Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1044 TCTTTCTTCT 1035
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                                                                                                                                                                                                                                       WPI; 2002-179323/23
                                                                                                                                                                                              Clark HF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                               WO200177290-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-1999
                   Homo sapiens
                                                                                                                                                                                                             Gulukota K,
                                                                            18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX60810;
                                                                                                                                                                                              Wong GG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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The invention relates to secreted proteins (AAY17219-228) encoded by CC polynucleotides obtained from human fetal kidney, adult lung, adult kidney, adult brain, adult blood, adult testes, and fetal brain and murine adult bone marrow cDNA libraries. The secretd protein nucleic acid sequences (X6801-811) correspond to clones bd306-7, g3283-6, C 411 clones are deposited as ATCC 98699; The PNS and proteins are corresponded activities which would make them suitable corresponds, although no supportaing medical conditions in humans and animals, although no supportaing data is given. Suggested activities include nutritional activity, cytokine and cell conditions in humans and include nutritional activity, immune stimulating (e.g. as vaccines) or suppressing activity, immune stimulating e.g. as vaccines) or suppressing activity, hematopoiesis regulating activity, chemotactic/chemotactic activity, inhibin activity, calluting inhibin activity, chemotactic/chemotactic activity, and tumour inhibition activity. The PNS are allowed the parent activity and tumour inhibition activity. The PNS are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
Secreted protein; kidney; lung; brain; blood; testis; bone marrow; nutritional activity; cytokine; cell proliferation; immune stimulation; hematopoiesis regulation; tissue growth; thrombolytic; gene therapy; anti-inflammatory; tumour invasion; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins-Racie LA, Evans C;
avallie ER, McCoy JM, Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA encoding a secreted protein yb8_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%; Score 28.4; I
62.9%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 39; Page 125-126; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark HF, Collingacobs K, Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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nootropic, neuroprotective, antianthritic, antimicrobial, vulnerary, cytostatic, antidabetic; virucide, antimicrobial, vulnerary, cytostatic, antidabetic; virucide, antimicrobial, antidaminary, antidhematic, antitumor, antidler; osteopathic, tranquiliser, cerebroprotective; cytokine; cell proliferation; cell differentiation; mmune deficiency; severe combined immunodeficiency; SCID, tumour, autoimmune disorder; multiple sclerosis; rheumatoid arthritis, graft-versus-host disease; myeloid deficiency; wound healing; ulcer; periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease; parkinson's disease; Huntingfon's disease; infection; cardiac disease; stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen; secreted protein; ss; antiinflammatory; immunosuppressive; food supplement

WO200175068-A2.

11-OCT-2001

22-MAR-2001; 2001WO-US09369.

30-MAR-2000; 2000US-0539330. 04-DEC-2000; 2000US-0729674.

(GEMY ) GENETICS INST INC.

Evans C; Wong GG; Jacobs K, McCoy JM, Lavallie E, Collins-racie LA, E Treacy M, Agostino MJ, Steininger RJ, Spaulding V, Clark H, Fechtel K, Merberg D;

WPI; 2001-639363/73. P-PSDB; AAU38998.

Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke) -

Claim 13; Page 471; 619pp; English.

The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myloid or Iymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers; as well as in treatment of periodontal disease, osteoperosis or osteoparthitis, mediated by of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, Alzhaimer's, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence encodes a secreted protein of the invention

Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 other;

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·.
                                    Gaps
                                   .,
 13.8%; Score 28.4; DB 22; Length 1656; 62.9%; Pred. No. 22; tive 0; Mismatches 26; Indels 0;
                                 44; Conservative
Query Match
Best Local Similarity
                                 Matches
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1023 TCAAGCTACAGGTAAAGGCTCTACCACCATTAAGGTATTGACTTATCCTATGAATTTGAT 964
                                                                 92 TCGTTGCGCT 101
                                                                 ò
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Search completed: February 15, 2003, 22:16:54 Job time : 811 secs

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